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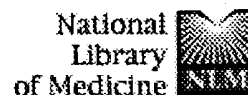
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☐ **1:** Tintinger GR, Anderson R.   Related Articles, Links

Counteracting effects of NADPH oxidase and the Na+/Ca2+ exchanger on membrane repolarisation and store-operated uptake of Ca2+ by chemoattractant-activated human neutrophils.
Biochem Pharmacol. 2004 Jun 15;67(12):2263-71.
PMID: 15163557 [PubMed - indexed for MEDLINE]

☐ **2:** Craner MJ, Newcombe J, Black JA, Hartle C, Cuzner ML, Waxman   Related Articles, Links
SG.

Molecular changes in neurons in multiple sclerosis: altered axonal expression of Nav1.2 and Nav1.6 sodium channels and Na+/Ca2+ exchanger.
Proc Natl Acad Sci U S A. 2004 May 25;101(21):8168-73. Epub 2004 May 17.
PMID: 15148385 [PubMed - indexed for MEDLINE]

☐ **3:** El-Armouche A, Jaeckel E, Boheler KR, Boknik P, Hertle B,   Related Articles, Links
Neumann J, Eschenhagen T.

Ouabain treatment is associated with upregulation of phosphatase inhibitor-1 and Na+/Ca(2+)-exchanger and beta-adrenergic sensitization in rat hearts.
Biochem Biophys Res Commun. 2004 May 21;318(1):219-26.
PMID: 15110776 [PubMed - indexed for MEDLINE]

☐ **4:** Palty R, Ohana E, Hershfinkel M, Volokita M, Elgazar V, Beharier   Related Articles, Links
O, Silverman WF, Argaman M, Sekler I

Lithium-calcium exchange is mediated by a distinct potassium-independent sodium-calcium exchanger.
J Biol Chem. 2004 Jun 11;279(24):25234-40. Epub 2004 Apr 01.
PMID: 15060069 [PubMed - indexed for MEDLINE]

☐ **5:** Osborne NN, Wood JP, Chidlow G, Casson R, DeSantis L, Schmidt   Related Articles, Links
KG.

Effectiveness of levobetaxolol and timolol at blunting retinal ischaemia is related to their calcium and sodium blocking activities: relevance to glaucoma.
Brain Res Bull. 2004 Feb 15;62(6):525-8. Review.
PMID: 15036567 [PubMed - indexed for MEDLINE]

☐ **6:** Diaz-Horta O, Van Eylen F, Herchuelz A.   Related Articles, Links

Na/Ca exchanger overexpression induces endoplasmic reticulum stress, caspase-12 release, and apoptosis.
Ann N Y Acad Sci. 2003 Dec;1010:430-2.
PMID: 15033764 [PubMed - indexed for MEDLINE]

☐ **7:** Hegde M, Roscoe J, Cala P, Gorin F.   Related Articles, Links

Amiloride kills malignant glioma cells independent of its inhibition of the sodium-hydrogen exchanger.
J Pharmacol Exp Ther. 2004 Jul;310(1):67-74. Epub 2004 Mar 09.
PMID: 15010500 [PubMed - in process]

h   cb   hg   e   e   e   fcg   e   ch   b   e

8: Roberts DE, McNicol A, Bose R.   Related Articles, Links

Mechanism of collagen activation in human platelets.
J Biol Chem. 2004 May 7;279(19):19421-30. Epub 2004 Feb 23.
PMID: 14981087 [PubMed - indexed for MEDLINE]

9: Yasumura Y, Takemura K, Sakamoto A, Kitakaze M, Miyatake K.   Related Articles, Links

Changes in myocardial gene expression associated with beta-blocker therapy in patients with chronic heart failure.
J Card Fail. 2003 Dec;9(6):469-74.
PMID: 14966788 [PubMed - indexed for MEDLINE]

10: Seemann G, Sachse FB, Weiss DL, Dossel O.   Related Articles, Links

Quantitative reconstruction of cardiac electromechanics in human myocardium: regional heterogeneity.
J Cardiovasc Electrophysiol. 2003 Oct;14(10 Suppl):S219-28.
PMID: 14760927 [PubMed - indexed for MEDLINE]

11: Varro A, Biliczki P, Iost N, Virag L, Hala O, Kovacs P, Matyus P, Papp JG.   Related Articles, Links

Theoretical possibilities for the development of novel antiarrhythmic drugs.
Curr Med Chem. 2004 Jan;11(1):1-11. Review.
PMID: 14754422 [PubMed - indexed for MEDLINE]

12: Ikeda M, Nagashima T, Bhattacharjee AK, Kondoh T, Kohmura E, Tamaki N.   Related Articles, Links

Quantitative analysis of hyperosmotic and hypothermic blood-brain barrier opening.
Acta Neurochir Suppl. 2003;86:559-63.
PMID: 14753506 [PubMed - indexed for MEDLINE]

13: Rosker C, Graziani A, Lukas M, Eder P, Zhu MX, Romanin C, Groschner K.   Related Articles, Links

Ca(2+) signaling by TRPC3 involves Na(+) entry and local coupling to the Na(+)/Ca(2+) exchanger.
J Biol Chem. 2004 Apr 2;279(14):13696-704. Epub 2004 Jan 21.
PMID: 14736881 [PubMed - indexed for MEDLINE]

14: Amran MS, Homma N, Hashimoto K.   Related Articles, Links

Pharmacology of KB-R7943: a Na+-Ca2+ exchange inhibitor.
Cardiovasc Drug Rev. 2003 Winter;21(4):255-76. Review.
PMID: 14647531 [PubMed - indexed for MEDLINE]

15: Cai X, Lytton J.   Related Articles, Links

Molecular cloning of a sixth member of the K+-dependent Na+/Ca2+ exchanger gene family, NCKX6.
J Biol Chem. 2004 Feb 13;279(7):5867-76. Epub 2003 Nov 18.
PMID: 14625281 [PubMed - indexed for MEDLINE]

16: Rizzuto R.   Related Articles, Links

Calcium mobilization from mitochondria in synaptic transmitter release.
J Cell Biol. 2003 Nov 10;163(3):441-3. Review.
PMID: 14610050 [PubMed - indexed for MEDLINE]

17: Hill JA.   Related Articles, Links

Electrical remodeling in cardiac hypertrophy.
Trends Cardiovasc Med. 2003 Nov;13(8):316-22. Review.
PMID: 14596946 [PubMed - indexed for MEDLINE]

18: Reeves JP, Condrescu M.   Related Articles, Links

Allosteric activation of sodium-calcium exchange activity by calcium: persistence at low calcium concentrations.
J Gen Physiol. 2003 Nov;122(5):621-39.
PMID: 14581586 [PubMed - indexed for MEDLINE]

19: Ohana E, Segal D, Palty R, Ton-That D, Moran A, Sensi SL, Weiss JH, Hershfinkel M, Sekler I.   Related Articles, Links

A sodium zinc exchange mechanism is mediating extrusion of zinc in mammalian cells.
J Biol Chem. 2004 Feb 6;279(6):4278-84. Epub 2003 Oct 27.
PMID: 14581475 [PubMed - indexed for MEDLINE]

20: Khan SA, Hare JM.   Related Articles, Links

The role of nitric oxide in the physiological regulation of Ca2+ cycling.
Curr Opin Drug Discov Devel. 2003 Sep;6(5):658-66. Review.
PMID: 14579515 [PubMed - indexed for MEDLINE]

21: Weber CR, Piacentino V 3rd, Houser SR, Bers DM.   Related Articles, Links

Dynamic regulation of sodium/calcium exchange function in human heart failure.
Circulation. 2003 Nov 4;108(18):2224-9. Epub 2003 Oct 13.
PMID: 14557358 [PubMed - indexed for MEDLINE]

22: Sergeeva OA, Amberger BT, Eriksson KS, Scherer A, Haas HL.   Related Articles, Links

Co-ordinated expression of 5-HT2C receptors with the NCX1 Na+/Ca2+ exchanger in histaminergic neurones.
J Neurochem. 2003 Nov;87(3):657-64.
PMID: 14535948 [PubMed - indexed for MEDLINE]

23: Bers DM, Eisner DA, Valdivia HH.   Related Articles, Links

Sarcoplasmic reticulum Ca2+ and heart failure: roles of diastolic leak and Ca2+ transport.
Circ Res. 2003 Sep 19;93(6):487-90. No abstract available.
PMID: 14500331 [PubMed - indexed for MEDLINE]

24: Bernecker OY, del Monte F, Hajjar RJ.   Related Articles, Links

Gene therapy for the treatment of heart failure--calcium signaling.
Semin Thorac Cardiovasc Surg. 2003 Jul;15(3):268-76. Review.
PMID: 12973704 [PubMed - indexed for MEDLINE]

25: Malli R, Frieden M, Osibow K, Zoratti C, Mayer M, Demaurex N, Graier WF.   Related Articles, Links

Sustained Ca2+ transfer across mitochondria is Essential for mitochondrial Ca2+ buffering, sore-operated Ca2+ entry, and Ca2+ store refilling.
J Biol Chem. 2003 Nov 7;278(45):44769-79. Epub 2003 Aug 26.
PMID: 12941956 [PubMed - indexed for MEDLINE]

26: Schuh K, Quaschning T, Knauer S, Hu K, Kocak S, Roethlein N, Neyses L.   Related Articles, Links

Regulation of vascular tone in animals overexpressing the sarcolemmal calcium pump.
J Biol Chem. 2003 Oct 17;278(42):41246-52. Epub 2003 Aug 04.
PMID: 12900399 [PubMed - indexed for MEDLINE]

27: Kang K, Schnetkamp PP.   Related Articles, Links

Signal sequence cleavage and plasma membrane targeting of the retinal rod NCKX1 and cone NCKX2 Na+/Ca2+ - K+ exchangers.
Biochemistry. 2003 Aug 12;42(31):9438-45.
PMID: 12899631 [PubMed - indexed for MEDLINE]

☐ **28:** Gupta A, Gupta S, Tiwary AK.

Spermicidal efficacy of H2-receptor antagonists and potentiation with 2',
4'-dichlorobenzamil hydrochloride: role of intrasperm Ca2+.
Contraception. 2003 Jul;68(1):61-4.
PMID: 12878289 [PubMed - indexed for MEDLINE]

☐ **29:** Kiang JG, McClain DE, Warke VG, Krishnan S, Tsokos GC.

Constitutive NO synthase regulates the Na+/Ca2+ exchanger in human T
cells: role of [Ca2+]i and tyrosine phosphorylation.
J Cell Biochem. 2003 Aug 1;89(5):1030-43.
PMID: 12874836 [PubMed - indexed for MEDLINE]

☐ **30:** Doggrell SA, Hancox JC.

Is timing everything? Therapeutic potential of modulators of cardiac Na(+)
transporters.
Expert Opin Investig Drugs. 2003 Jul;12(7):1123-42. Review.
PMID: 12831348 [PubMed - indexed for MEDLINE]

☐ **31:** Kawano S, Otsu K, Shoji S, Yamagata K, Hiraoka M.

Ca(2+) oscillations regulated by Na(+)-Ca(2+) exchanger and plasma
membrane Ca(2+) pump induce fluctuations of membrane currents and
potentials in human mesenchymal stem cells.
Cell Calcium. 2003 Aug;34(2):145-56.
PMID: 12810056 [PubMed - indexed for MEDLINE]

☐ **32:** Reddy HK, Wasson S, Koshy SK, Komatireddy R.

Structural correlates of electrical remodeling in ventricular hypertrophy.
Cardiovasc Res. 2003 Jun 1;58(3):495-7. No abstract available.
PMID: 12798420 [PubMed - indexed for MEDLINE]

☐ **33:** Moreau R, Daoud G, Masse A, Simoneau L, Lafond J.

Expression and role of calcium-ATPase pump and sodium-calcium
exchanger in differentiated trophoblasts from human term placenta.
Mol Reprod Dev. 2003 Jul;65(3):283-8.
PMID: 12784250 [PubMed - indexed for MEDLINE]

☐ **34:** Blank ME, Ehmke H.

Aquaporin-1 and HCO3(-)-Cl- transporter-mediated transport of CO2
across the human erythrocyte membrane.
J Physiol. 2003 Jul 15;550(Pt 2):419-29. Epub 2003 May 16.
PMID: 12754312 [PubMed - indexed for MEDLINE]

☐ **35:** Wald FA, Figueroa Y, Oriolo AS, Salas PJ.

Membrane repolarization is delayed in proximal tubules after ischemia-
reperfusion: possible role of microtubule-organizing centers.
Am J Physiol Renal Physiol. 2003 Aug;285(2):F230-40. Epub 2003 Apr 22.
PMID: 12709392 [PubMed - indexed for MEDLINE]

☐ **36:** Kang K, Bauer PJ, Kinjo TG, Szerencsei RT, Bonigk W, Winkfein
RJ, Schnetkamp PP.

Assembly of retinal rod or cone Na(+)/Ca(2+)-K(+) exchanger oligomers
with cGMP-gated channel subunits as probed with heterologously
expressed cDNAs.
Biochemistry. 2003 Apr 22;42(15):4593-600.
PMID: 12693957 [PubMed - indexed for MEDLINE]

☐ **37:** Bolli R.

h   cb   h g   e   e   e   fcg   e   ch   b   e

The role of sodium-hydrogen ion exchange in patients undergoing coronary artery bypass grafting.
J Card Surg. 2003 Jan-Feb;18 Suppl 1:21-6. Review.
PMID: 12691376 [PubMed - indexed for MEDLINE]

38: Schillinger W, Ohler A, Emami S, Muller F, Christians C, Janssen   Related Articles, Links
PM, Kogler H, Teucher N, Pieske B, Seidler T, Hasenfuss G.

The functional effect of adenoviral Na+/Ca2+ exchanger overexpression in rabbit myocytes depends on the activity of the Na+/K+-ATPase.
Cardiovasc Res. 2003 Mar 15;57(4):996-1003.
PMID: 12650877 [PubMed - indexed for MEDLINE]

39: Weisser-Thomas J, Piacentino V 3rd, Gaughan JP, Margulies K,   Related Articles, Links
Houser SR.

Calcium entry via Na/Ca exchange during the action potential directly contributes to contraction of failing human ventricular myocytes.
Cardiovasc Res. 2003 Mar 15;57(4):974-85.
PMID: 12650875 [PubMed - indexed for MEDLINE]

40: Allen DG, Xiao XH.   Related Articles, Links

Role of the cardiac Na+/H+ exchanger during ischemia and reperfusion.
Cardiovasc Res. 2003 Mar 15;57(4):934-41. Review.
PMID: 12650871 [PubMed - indexed for MEDLINE]

41: Schillinger W, Fiolet JW, Schlotthauer K, Hasenfuss G.   Related Articles, Links

Relevance of Na+-Ca2+ exchange in heart failure.
Cardiovasc Res. 2003 Mar 15;57(4):921-33. Review. No abstract available.
PMID: 12650870 [PubMed - indexed for MEDLINE]

42: Piper HM, Meuter K, Schafer C.   Related Articles, Links

Cellular mechanisms of ischemia-reperfusion injury.
Ann Thorac Surg. 2003 Feb;75(2):S644-8. Review.
PMID: 12607706 [PubMed - indexed for MEDLINE]

43: Muller-Ehmsen J, Nickel J, Zobel C, Hirsch I, Bolck B, Brixius K,   Related Articles, Links
Schwinger RH.

Longer term effects of ouabain on the contractility of rat isolated cardiomyocytes and on the expression of Ca and Na regulating proteins.
Basic Res Cardiol. 2003 Mar;98(2):90-6.
PMID: 12607130 [PubMed - indexed for MEDLINE]

44: Piacentino V 3rd, Weber CR, Chen X, Weisser-Thomas J,   Related Articles, Links
Margulies KB, Bers DM, Houser SR.

Cellular basis of abnormal calcium transients of failing human ventricular myocytes.
Circ Res. 2003 Apr 4;92(6):651-8. Epub 2003 Feb 20.
PMID: 12600875 [PubMed - indexed for MEDLINE]

45: Pogwizd SM.   Related Articles, Links

Clinical potential of sodium-calcium exchanger inhibitors as antiarrhythmic agents.
Drugs. 2003;63(5):439-52. Review.
PMID: 12600224 [PubMed - indexed for MEDLINE]

46: Kinjo TG, Szerencsei RT, Winkfein RJ, Kang K, Schnetkamp PP.   Related Articles, Links

Topology of the retinal cone NCKX2 Na/Ca-K exchanger.
Biochemistry. 2003 Mar 4;42(8):2485-91.
PMID: 12600216 [PubMed - indexed for MEDLINE]

47: Prinsen CF, Cooper CB, Szerencsei RT, Murthy SK, Demetrick   Related Articles, Links

h   cb   h g   e   e   e   fcg   e   ch   b   e

DJ, Schnetkamp PP.

The retinal rod and cone Na+/Ca2+-K+ exchangers.
Adv Exp Med Biol. 2002;514:237-51. Review.
PMID: 12596925 [PubMed - indexed for MEDLINE]

48: Lakatta EG, Maltsev VA, Bogdanov KY, Stern MD, Vinogradova TM. Related Articles, Links

Cyclic variation of intracellular calcium: a critical factor for cardiac pacemaker cell dominance.
Circ Res. 2003 Feb 21;92(3):e45-50. Review.
PMID: 12595348 [PubMed - indexed for MEDLINE]

49: Mohler PJ, Schott JJ, Gramolini AO, Dilly KW, Guatimosim S, duBell WH, Song LS, Haurogne K, Kyndt F, Ali ME, Rogers TB, Lederer WJ, Escande D, Le Marec H, Bennett V. Related Articles, Links

Ankyrin-B mutation causes type 4 long-QT cardiac arrhythmia and sudden cardiac death.
Nature. 2003 Feb 6;421(6923):634-9.
PMID: 12571597 [PubMed - indexed for MEDLINE]

50: Nattel S. Related Articles, Links

Human genetics: Lost anchors cost lives.
Nature. 2003 Feb 6;421(6923):587, 589-90. No abstract available.
PMID: 12571577 [PubMed - indexed for MEDLINE]

51: Gabellini N, Bortoluzzi S, Danieli GA, Carafoli E. Related Articles, Links

Control of the Na+/Ca2+ exchanger 3 promoter by cyclic adenosine monophosphate and Ca2+ in differentiating neurons.
J Neurochem. 2003 Jan;84(2):282-93.
PMID: 12558991 [PubMed - indexed for MEDLINE]

52: Del Monte F, Johnson CM, Stepanek AC, Doye AA, Gwathmey JK. Related Articles, Links

Defects in calcium control.
J Card Fail. 2002 Dec;8(6 Suppl):S421-31.
PMID: 12555155 [PubMed - indexed for MEDLINE]

53: Duan J, Zhang HY, Adkins SD, Ren BH, Norby FL, Zhang X, Benoit JN, Epstein PN, Ren J. Related Articles, Links

Impaired cardiac function and IGF-I response in myocytes from calmodulin-diabetic mice: role of Akt and RhoA.
Am J Physiol Endocrinol Metab. 2003 Feb;284(2):E366-76.
PMID: 12531745 [PubMed - indexed for MEDLINE]

54: Abramov AY, Duchen MR. Related Articles, Links

Actions of ionomycin, 4-BrA23187 and a novel electrogenic Ca2+ ionophore on mitochondria in intact cells.
Cell Calcium. 2003 Feb;33(2):101-12.
PMID: 12531186 [PubMed - indexed for MEDLINE]

55: Winkfein RJ, Szerencsei RT, Kinjo TG, Kang K, Perizzolo M, Eisner L, Schnetkamp PP. Related Articles, Links

Scanning mutagenesis of the alpha repeats and of the transmembrane acidic residues of the human retinal cone Na/Ca-K exchanger.
Biochemistry. 2003 Jan 21;42(2):543-52.
PMID: 12525183 [PubMed - indexed for MEDLINE]

56: del Monte F, Hajjar RJ. Related Articles, Links

Targeting calcium cycling proteins in heart failure through gene transfer.
J Physiol. 2003 Jan 1;546(Pt 1):49-61. Review.

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☐ 57: Moreau R, Simoneau L, Lafond J.   Related Articles, Links

Calcium fluxes in human trophoblast (BeWo) cells: calcium channels, calcium-ATPase, and sodium-calcium exchanger expression.
Mol Reprod Dev. 2003 Feb;64(2):189-98.
PMID: 12506351 [PubMed - indexed for MEDLINE]

☐ 58: Terracciano C.   Related Articles, Links

Functional consequences of Na/Ca exchanger overexpression in cardiac myocytes.
Ann N Y Acad Sci. 2002 Nov;976:520-7.
PMID: 12502606 [PubMed - indexed for MEDLINE]

☐ 59: Bers DM, Weber CR.   Related Articles, Links

Na/Ca exchange function in intact ventricular myocytes.
Ann N Y Acad Sci. 2002 Nov;976:500-12.
PMID: 12502604 [PubMed - indexed for MEDLINE]

☐ 60: Weber CR, Piacentino V 3rd, Margulies KB, Bers DM, Houser SR. Related Articles, Links

Calcium influx via I(NCX) is favored in failing human ventricular myocytes.
Ann N Y Acad Sci. 2002 Nov;976:478-9. No abstract available.
PMID: 12502599 [PubMed - indexed for MEDLINE]

☐ 61: Piacentino V 3rd, Margulies KB, Houser SR.   Related Articles, Links

Ca influx via the Na/Ca exchanger maintains sarcoplasmic reticulum Ca content in failing human myocytes.
Ann N Y Acad Sci. 2002 Nov;976:476-7. No abstract available.
PMID: 12502598 [PubMed - indexed for MEDLINE]

☐ 62: Piacentino V 3rd, Weber CR, Gaughan JP, Margulies KB, Bers DM, Houser SR   Related Articles, Links

Modulation of contractility in failing human myocytes by reverse-mode Na/Ca exchange.
Ann N Y Acad Sci. 2002 Nov;976:466-71. Review.
PMID: 12502596 [PubMed - indexed for MEDLINE]

☐ 63: Sipido KR, Volders PG, Schoenmakers M, De Groot SH, Verdonck F, Vos MA.   Related Articles, Links

Role of the Na/Ca exchanger in arrhythmias in compensated hypertrophy.
Ann N Y Acad Sci. 2002 Nov;976:438-45. Review.
PMID: 12502593 [PubMed - indexed for MEDLINE]

☐ 64: Murphy E, Cross HR, Steenbergen C.   Related Articles, Links

Is Na/Ca exchange during ischemia and reperfusion beneficial or detrimental?
Ann N Y Acad Sci. 2002 Nov;976:421-30. Review.
PMID: 12502591 [PubMed - indexed for MEDLINE]

☐ 65: Tortiglione A, Pignataro G, Minale M, Secondo A, Scorziello A, Di Renzo GF, Amoroso S, Caliendo G, Santagada V, Annunziato L.   Related Articles, Links

Na+/Ca2+ exchanger in Na+ efflux-Ca2+ influx mode of operation exerts a neuroprotective role in cellular models of in vitro anoxia and in vivo cerebral ischemia.
Ann N Y Acad Sci. 2002 Nov;976:408-12. No abstract available.
PMID: 12502588 [PubMed - indexed for MEDLINE]

h   cb   hg   e   e   e   fcg   e   ch   b   e

66: Lytton J, Li XF, Dong H, Kraev A. Related Articles, Links

K+-dependent Na+/Ca2+ exchangers in the brain.
Ann N Y Acad Sci. 2002 Nov;976:382-93.
PMID: 12502585 [PubMed - indexed for MEDLINE]

67: Bose R, Li Y, Roberts D. Related Articles, Links

Na+/Ca2+ exchange in activated and nonactivated human platelets.
Ann N Y Acad Sci. 2002 Nov;976:350-3. No abstract available.
PMID: 12502580 [PubMed - indexed for MEDLINE]

68: Roberts DE, Bose R. Related Articles, Links

Reverse mode Na+/Ca2+ exchange in the collagen activation of human
platelets.
Ann N Y Acad Sci. 2002 Nov;976:345-9. No abstract available.
PMID: 12502579 [PubMed - indexed for MEDLINE]

69: Gabellini N, Bortoluzzi S, Danieli GA, Carafoli E Related Articles, Links

The gene promoter of human Na+/Ca2+ exchanger isoform 3 (SLC8A3) is
controlled by cAMP and calcium.
Ann N Y Acad Sci. 2002 Nov;976:282-4. No abstract available.
PMID: 12502570 [PubMed - indexed for MEDLINE]

70: Jordan MC, Quednau BD, Roos KP, Ross RS, Philipson KD, Related Articles, Links
Nicholas SB.

Cyclosporin A regulates sodium-calcium exchanger (NCX1) gene
expression in vitro and cardiac hypertrophy in NCX1 transgenic mice.
Ann N Y Acad Sci. 2002 Nov;976:259-67.
PMID: 12502568 [PubMed - indexed for MEDLINE]

71: Schulze DH, Polumuri SK, Gille T, Ruknudin A. Related Articles, Links

Functional regulation of alternatively spliced Na+/Ca2+ exchanger (NCX1)
isoforms.
Ann N Y Acad Sci. 2002 Nov;976:187-96. Review.
PMID: 12502560 [PubMed - indexed for MEDLINE]

72: Rahamimoff H, Ren X, Kimchi-Sarfaty C, Ambudkar S, Kasir J. Related Articles, Links

NCX1 surface expression: a tool to identify structural elements of
functional importance.
Ann N Y Acad Sci. 2002 Nov;976:176-86.
PMID: 12502559 [PubMed - indexed for MEDLINE]

73: Dong H, Dunn J, Lytton J. Related Articles, Links

Electrophysiological studies of the cloned rat cardiac NCX1.1 in
transfected HEK cells: a focus on the stoichiometry.
Ann N Y Acad Sci. 2002 Nov;976:159-65. No abstract available.
PMID: 12502557 [PubMed - indexed for MEDLINE]

74: Lytton J, Dong H. Related Articles, Links

Rat heart NCX1.1 stoichiometry measured in a transfected cell system.
Ann N Y Acad Sci. 2002 Nov;976:137-41.
PMID: 12502552 [PubMed - indexed for MEDLINE]

75: Yoo SS, Leach S, Lytton J. Related Articles, Links

Studies on the oligomeric state of the sodium/calcium + potassium
exchanger NCKX2.
Ann N Y Acad Sci. 2002 Nov;976:94-6. No abstract available.
PMID: 12502543 [PubMed - indexed for MEDLINE]

76: Cai X, Zhang K, Lytton J.   Related Articles, Links

Topological studies of the rat brain K+-dependent Na+/Ca2+ exchanger NCKX2.
Ann N Y Acad Sci. 2002 Nov;976:90-3. No abstract available.
PMID: 12502542 [PubMed - indexed for MEDLINE]

77: Van Eylen F, Kamagate A, Herchuelz A.   Related Articles, Links

Characterization and functional activity of a truncated Na/Ca exchange isoform resulting from a new splicing pattern of NCX1.
Ann N Y Acad Sci. 2002 Nov;976:81-4. No abstract available.
PMID: 12502539 [PubMed - indexed for MEDLINE]

78: Mejia-Elizondo R, Espinosa-Tanguma R, Saavedra-Alanis VM.   Related Articles, Links

Molecular identification of the NCX isoform expressed in tracheal smooth muscle of guinea pig.
Ann N Y Acad Sci. 2002 Nov;976:73-6. No abstract available.
PMID: 12502537 [PubMed - indexed for MEDLINE]

79: Kraev A, MacLennan D.   Related Articles, Links

Toward comparative genomics of calcium transporters.
Ann N Y Acad Sci. 2002 Nov;976:53-9. Review. No abstract available.
PMID: 12502533 [PubMed - indexed for MEDLINE]

80: Szerencsei RT, Winkfein RJ, Cooper CB, Prinsen C, Kinjo TG,   Related Articles, Links
Kang K, Schnetkamp PP.

The Na/Ca-K exchanger gene family.
Ann N Y Acad Sci. 2002 Nov;976:41-52. Review.
PMID: 12502532 [PubMed - indexed for MEDLINE]

81: Bers DM, Pogwizd SM, Schlotthauer K.   Related Articles, Links

Upregulated Na/Ca exchange is involved in both contractile dysfunction and arrhythmogenesis in heart failure.
Basic Res Cardiol. 2002;97 Suppl 1:I36-42. Review.
PMID: 12479232 [PubMed - indexed for MEDLINE]

82: Reuter H, Philipson KD.   Related Articles, Links

Sodium-calcium exchanger overexpression in the heart--insights from a transgenic mouse model.
Basic Res Cardiol. 2002;97 Suppl 1:I31-5. Review.
PMID: 12479231 [PubMed - indexed for MEDLINE]

83: McDonough AA, Velotta JB, Schwinger RH, Philipson KD, Farley   Related Articles, Links
RA.

The cardiac sodium pump: structure and function.
Basic Res Cardiol. 2002;97 Suppl 1:I19-24. Review.
PMID: 12479229 [PubMed - indexed for MEDLINE]

84: Powis DA, Marley PD.   Related Articles, Links

Ions, channels, and receptors.
Ann N Y Acad Sci. 2002 Oct;971:95-9. Review.
PMID: 12438098 [PubMed - indexed for MEDLINE]

85: Gabellini N, Bortoluzzi S, Danieli GA, Carafoli E.   Related Articles, Links

The human SLC8A3 gene and the tissue-specific Na+/Ca2+ exchanger 3 isoforms.
Gene. 2002 Sep 18;298(1):1-7.
PMID: 12406570 [PubMed - indexed for MEDLINE]

h   cb   hg   e   e   e   fcg   e   ch   b   e

86: Saksena S, Ammar MS, Tyagi S, Elsharydah A, Gill RK, Ramaswamy K, Dudeja PK   Related Articles, Links

Mechanisms of calcium transport in human colonic basolateral membrane vesicles.
Dig Dis Sci. 2002 Oct;47(10):2306-15.
PMID: 12395904 [PubMed - indexed for MEDLINE]

87: Petrova R, Yamamoto Y, Muraki K, Yonekura H, Sakurai S, Watanabe T, Li H, Takeuchi M, Makita Z, Kato I, Takasawa S, Okamoto H, Imaizumi Y, Yamamoto H.   Related Articles, Links

Advanced glycation endproduct-induced calcium handling impairment in mouse cardiac myocytes.
J Mol Cell Cardiol. 2002 Oct;34(10):1425-31.
PMID: 12393002 [PubMed - indexed for MEDLINE]

88: Fink K, Meder WP, Clusmann H, Gothert M.   Related Articles, Links

Ca2+ entry via P/Q-type Ca2+ channels and the Na+/Ca2+ exchanger in rat and human neocortical synaptosomes.
Naunyn Schmiedebergs Arch Pharmacol. 2002 Nov;366(5):458-63. Epub 2002 Sep 06.
PMID: 12382075 [PubMed - indexed for MEDLINE]

89: Li XF, Kraev AS, Lytton J.   Related Articles, Links

Molecular cloning of a fourth member of the potassium-dependent sodium-calcium exchanger gene family, NCKX4.
J Biol Chem. 2002 Dec 13;277(50):48410-7. Epub 2002 Oct 11.
PMID: 12379639 [PubMed - indexed for MEDLINE]

90: Cai X, Zhang K, Lytton J.   Related Articles, Links

A novel topology and redox regulation of the rat brain K+-dependent Na+/Ca2+ exchanger, NCKX2.
J Biol Chem. 2002 Dec 13;277(50):48923-30. Epub 2002 Oct 10.
PMID: 12377762 [PubMed - indexed for MEDLINE]

91: Chu SL, Zhu DL, Xiong MM, Wang GL, Zhang WZ, Zhou HF, Shen D, Gao PJ, Zhan YM, Jin L.   Related Articles, Links

Linkage analysis of twelve candidate gene loci regulating water and sodium metabolism and membrane ion transport in essential hypertension.
Hypertens Res. 2002 Jul;25(4):635-9.
PMID: 12358153 [PubMed - indexed for MEDLINE]

92: Kiedrowski L, Czyz A, Li XF, Lytton J.   Related Articles, Links

Preferential expression of plasmalemmal K-dependent Na+/Ca2+ exchangers in neurons versus astrocytes.
Neuroreport. 2002 Aug 27;13(12):1529-32.
PMID: 12218699 [PubMed - indexed for MEDLINE]

93: Deval E, Levitsky DO, Marchand E, Cantereau A, Raymond G, Cognard C.   Related Articles, Links

Na(+)/Ca(2+) exchange in human myotubes: intracellular calcium rises in response to external sodium depletion are enhanced in DMD.
Neuromuscul Disord. 2002 Oct;12(7-8):665-73.
PMID: 12207936 [PubMed - indexed for MEDLINE]

94: Lee SH, Kim MH, Park KH, Earm YE, Ho WK.   Related Articles, Links

K+-dependent Na+/Ca2+ exchange is a major Ca2+ clearance mechanism in axon terminals of rat neurohypophysis.
J Neurosci. 2002 Aug 15;22(16):6891-9.
PMID: 12177187 [PubMed - indexed for MEDLINE]

h   cb   hg   e   e   e   fcg   e   ch   b   e

95: Dillmann WH.   Related Articles, Links

Cellular action of thyroid hormone on the heart.
Thyroid. 2002 Jun;12(6):447-52. Review.
PMID: 12165105 [PubMed - indexed for MEDLINE]

96: Dunn J, Elias CL, Le HD, Omelchenko A, Hryshko LV, Lytton J.   Related Articles, Links

The molecular determinants of ionic regulatory differences between brain
and kidney Na+/Ca2+ exchanger (NCX1) isoforms.
J Biol Chem. 2002 Sep 13;277(37):33957-62. Epub 2002 Jul 12.
PMID: 12118014 [PubMed - indexed for MEDLINE]

97: Muller JG, Thompson JT, Edmonson AM, Rackley MS, Kasahara   Related Articles, Links
H, Izumo S, McQuinn TC, Menick DR, O'Brien TX.

Differential regulation of the cardiac sodium calcium exchanger promoter
in adult and neonatal cardiomyocytes by Nkx2.5 and serum response
factor.
J Mol Cell Cardiol. 2002 Jul;34(7):807-21.
PMID: 12099720 [PubMed - indexed for MEDLINE]

98: Bautista DM, Hoth M, Lewis RS.   Related Articles, Links

Enhancement of calcium signalling dynamics and stability by delayed
modulation of the plasma-membrane calcium-ATPase in human T cells.
J Physiol. 2002 Jun 15;541(Pt 3):877-94.
PMID: 12068047 [PubMed - indexed for MEDLINE]

99: Mizuno S, Demura Y, Ameshima S, Okamura S, Miyamori I,   Related Articles, Links
Ishizaki T.

Alkalosis stimulates endothelial nitric oxide synthase in cultured human
pulmonary arterial endothelial cells.
Am J Physiol Lung Cell Mol Physiol. 2002 Jul;283(1):L113-9.
PMID: 12060567 [PubMed - indexed for MEDLINE]

100: Cullinane AB, Coca-Prados M, Harvey BJ.   Related Articles, Links

Extracellular ATP effects on calcium signaling in cultured human non-
pigmented ciliary body epithelium.
Curr Eye Res. 2001 Dec;23(6):448-54.
PMID: 12045895 [PubMed - indexed for MEDLINE]

101: Sharon D, Yamamoto H, McGee TL, Rabe V, Szerencsei RT,   Related Articles, Links
Winkfein RJ, Prinsen CF, Barnes CS, Andreasson S, Fishman
GA, Schnetkamp PP, Berson EL, Dryja TP.

Mutated alleles of the rod and cone Na-Ca+K-exchanger genes in patients
with retinal diseases.
Invest Ophthalmol Vis Sci. 2002 Jun;43(6):1971-9.
PMID: 12037007 [PubMed - indexed for MEDLINE]

102: Diaz-Horta O, Kamagate A, Herchuelz A, Van Eylen F.   Related Articles, Links

Na/Ca exchanger overexpression induces endoplasmic reticulum-related
apoptosis and caspase-12 activation in insulin-releasing BRIN-BD11
cells.
Diabetes. 2002 Jun;51(6):1815-24.
PMID: 12031969 [PubMed - indexed for MEDLINE]

103: Su YH, Vacquier VD.   Related Articles, Links

A flagellar K(+)-dependent Na(+)/Ca(2+) exchanger keeps Ca(2+) low in
sea urchin spermatozoa.
Proc Natl Acad Sci U S A. 2002 May 14;99(10):6743-8.
PMID: 12011436 [PubMed - indexed for MEDLINE]

104: Thayer SA, Usachev YM, Pottorf WJ.   Related Articles, Links

Modulating Ca2+ clearance from neurons.
Front Biosci. 2002 May 1;7:d1255-79. Review.
PMID: 11991858 [PubMed - indexed for MEDLINE]

105: Ranu HK, Terracciano CM, Davia K, Bernobich E, Chaudhri B,   Related Articles, Links
Robinson SE, Bin Kang Z, Hajjar RJ, MacLeod KT, Harding SE.

Effects of Na(+)/Ca(2+)-exchanger overexpression on excitation-
contraction coupling in adult rabbit ventricular myocytes.
J Mol Cell Cardiol. 2002 Apr;34(4):389-400.
PMID: 11991729 [PubMed - indexed for MEDLINE]

106: Bers DM.   Related Articles, Links

Cardiac Na/Ca exchange function in rabbit, mouse and man: what's the
difference?
J Mol Cell Cardiol. 2002 Apr;34(4):369-73. No abstract available.
PMID: 11991726 [PubMed - indexed for MEDLINE]

107: Sipido KR, Volders PG, Vos MA, Verdonck F.   Related Articles, Links

Altered Na/Ca exchange activity in cardiac hypertrophy and heart failure:
a new target for therapy?
Cardiovasc Res. 2002 Mar;53(4):782-805. Review.
PMID: 11922890 [PubMed - indexed for MEDLINE]

108: Dong H, Dunn J, Lytton J.   Related Articles, Links

Stoichiometry of the Cardiac Na+/Ca2+ exchanger NCX1.1 measured in
transfected HEK cells.
Biophys J. 2002 Apr;82(4):1943-52.
PMID: 11916852 [PubMed - indexed for MEDLINE]

109: Billman GE.   Related Articles, Links

KB-R7943. Kanebo.
Curr Opin Investig Drugs. 2001 Dec;2(12):1740-5. Review.
PMID: 11892938 [PubMed - indexed for MEDLINE]

110: Kiyosue T.   Related Articles, Links

Removal of intracellular Mg(2+) activates cardiac Na(+)/Ca(2+)
exchanger.
Cardiovasc Res. 2002 Feb 1;53(2):290-1. No abstract available.
PMID: 11827677 [PubMed - indexed for MEDLINE]

111: Van Eylen F, Horta OD, Barez A, Kamagate A, Flatt PR,   Related Articles, Links
Macianskiene R, Mubagwa K, Herchuelz A.

Overexpression of the Na/Ca exchanger shapes stimulus-induced
cytosolic Ca(2+) oscillations in insulin-producing BRIN-BD11 cells.
Diabetes. 2002 Feb;51(2):366-75.
PMID: 11812743 [PubMed - indexed for MEDLINE]

112: Bose R, Li Y, Woo V.   Related Articles, Links

Sodium-calcium exchange in platelets of diabetics.
Proc West Pharmacol Soc. 2001;44:183-4. No abstract available.
PMID: 11793976 [PubMed - indexed for MEDLINE]

113: Berna N, Arnould T, Remacle J, Michiels C.   Related Articles, Links

Hypoxia-induced increase in intracellular calcium concentration in
endothelial cells: role of the Na(+)-glucose cotransporter.
J Cell Biochem. 2001;84(1):115-31.
PMID: 11746521 [PubMed - indexed for MEDLINE]

□ 114: Schotten U, Greiser M, Benke D, Buerkel K, Ehrenteidt B, Stellbrink C, Vazquez-Jimenez JF, Schoendube F, Hanrath P, Allessie M. Related Articles, Links

Atrial fibrillation-induced atrial contractile dysfunction: a tachycardiomyopathy of a different sort.
Cardiovasc Res. 2002 Jan;53(1):192-201.
PMID: 11744028 [PubMed - indexed for MEDLINE]

□ 115: Yamamura K, Tani M, Hasegawa H, Gen W. Related Articles, Links

Very low dose of the Na(+)/Ca(2+) exchange inhibitor, KB-R7943, protects ischemic reperfused aged Fischer 344 rat hearts: considerable strain difference in the sensitivity to KB-R7943.
Cardiovasc Res. 2001 Dec;52(3):397-406.
PMID: 11738056 [PubMed - indexed for MEDLINE]

□ 116: Zhu L, Yu Y, Chua BH, Ho YS, Kuo TH. Related Articles, Links

Regulation of sodium-calcium exchange and mitochondrial energetics by Bcl-2 in the heart of transgenic mice.
J Mol Cell Cardiol. 2001 Dec;33(12):2135-44.
PMID: 11735260 [PubMed - indexed for MEDLINE]

□ 117: Van Wagoner DR, Bond M. Related Articles, Links

Reperfusion arrhythmias: new insights into the role of the Na(+)/Ca(2+) exchanger.
J Mol Cell Cardiol. 2001 Dec;33(12):2071-4. No abstract available.
PMID: 11735253 [PubMed - indexed for MEDLINE]

□ 118: Verkerk AO, Veldkamp MW, Baartscheer A, Schumacher CA, Klopping C, van Ginneken AC, Ravesloot JH. Related Articles, Links

Ionic mechanism of delayed afterdepolarizations in ventricular cells isolated from human end-stage failing hearts.
Circulation. 2001 Nov 27;104(22):2728-33.
PMID: 11723027 [PubMed - indexed for MEDLINE]

□ 119: Campean V, Kricke J, Ellison D, Luft FC, Bachmann S. Related Articles, Links

Localization of thiazide-sensitive Na(+)-Cl(-) cotransport and associated gene products in mouse DCT.
Am J Physiol Renal Physiol. 2001 Dec;281(6):F1028-35.
PMID: 11704553 [PubMed - indexed for MEDLINE]

□ 120: Loffing J, Loffing-Cueni D, Valderrabano V, Klausli L, Hebert SC, Rossier BC, Hoenderop JG, Bindels RJ, Kaissling B Related Articles, Links

Distribution of transcellular calcium and sodium transport pathways along mouse distal nephron.
Am J Physiol Renal Physiol. 2001 Dec;281(6):F1021-7.
PMID: 11704552 [PubMed - indexed for MEDLINE]

□ 121: Kimchi-Sarfaty C, Kasir J, Ambudkar SV, Rahaminoff H. Related Articles, Links

Transport activity and surface expression of the Na+-Ca2+ exchanger NCX1 are inhibited by the immunosuppressive agent cyclosporin A and by the nonimmunosuppressive agent PSC833.
J Biol Chem. 2002 Jan 25;277(4):2505-10. Epub 2001 Nov 07.
PMID: 11700317 [PubMed - indexed for MEDLINE]

□ 122: McMillan DR, Kayes-Wandover KM, Richardson JA, White PC. Related Articles, Links

Very large G protein-coupled receptor-1, the largest known cell surface protein, is highly expressed in the developing central nervous system.
J Biol Chem. 2002 Jan 4;277(1):785-92. Epub 2001 Oct 17.

PMID: 11606593 [PubMed - indexed for MEDLINE]

123: Rogister F, Laeckmann D, Plasman P, Van Eylen F, Ghyoot M, Maggetto C, Liegeois J, Geczy J, Herchuelz A, Delarge J, Masereel B.   Related Articles, Links

Novel inhibitors of the sodium-calcium exchanger: benzene ring analogues of N-guanidino substituted amiloride derivatives.
Eur J Med Chem. 2001 Jul-Aug;36(7-8):597-614.
PMID: 11600230 [PubMed - indexed for MEDLINE]

124: Qiu Z, Chen J, Nicoll DA, Philipson KD.   Related Articles, Links

A disulfide bond is required for functional assembly of NCX1 from complementary fragments.
Biochem Biophys Res Commun. 2001 Oct 5;287(4):825-8.
PMID: 11573936 [PubMed - indexed for MEDLINE]

125: Aleksandrova EA.   Related Articles, Links

[Calcium-transporting systems and calcium regulation in cardiomyocytes]
Usp Fiziol Nauk. 2001 Jul-Sep;32(3):40-8. Review. Russian.
PMID: 11565424 [PubMed - indexed for MEDLINE]

126: Takuma K.   Related Articles, Links

[Delayed apoptosis and its regulation in astrocytes]
Yakugaku Zasshi. 2001 Sep;121(9):663-9. Review. Japanese.
PMID: 11558150 [PubMed - indexed for MEDLINE]

127: [No authors listed]   Related Articles, Links

Abstracts of the American Physiological Society Conferences. Cellular and Molecular Physiology of Sodium-Calcium Exchange, Banff, Alberta, Canada, October 10-14, 2001. Genome and Hormones: An Integrative Approach to Gender Differences in Physiology, Pittsburgh, Pennsylvania, USA, October 17-20, 2001.
Physiologist. 2001 Aug;44(4):219-86. No abstract available.
PMID: 11534550 [PubMed - indexed for MEDLINE]

128: Kubo H, Margulies KB, Piacentino V 3rd, Gaughan JP, Houser SR.   Related Articles, Links

Patients with end-stage congestive heart failure treated with beta-adrenergic receptor antagonists have improved ventricular myocyte calcium regulatory protein abundance.
Circulation. 2001 Aug 28;104(9):1012-8.
PMID: 11524394 [PubMed - indexed for MEDLINE]

129: Radvakova I, Mirossay A, Mojzis J, Mirossay L.   Related Articles, Links

The effect of 5'-(N,N-dimethyl)-amiloride on cytotoxic activity of doxorubicin and vincristine in CEM cell lines.
Physiol Res. 2001;50(3):283-7.
PMID: 11521739 [PubMed - indexed for MEDLINE]

130: Van Eylen F, Kamagate A, Herchuelz A.   Related Articles, Links

A new Na/Ca exchanger splicing pattern identified in situ leads to a functionally active 70kDa NH(2)-terminal protein.
Cell Calcium. 2001 Sep;30(3):191-8.
PMID: 11508998 [PubMed - indexed for MEDLINE]

131: Conway SJ, Koushik SV.   Related Articles, Links

Cardiac sodium-calcium exchanger: a double-edged sword.
Cardiovasc Res. 2001 Aug 1;51(2):194-7. Review. No abstract available.

h   cb   h g   e   e   e   fcg   e   ch   b   e

PMID: 11470457 [PubMed - indexed for MEDLINE]

132: Balasubramanyam M, Balaji RA, Subashini B, Mohan V.   Related Articles, Links

Evidence for mechanistic alterations of Ca2+ homeostasis in Type 2 diabetes mellitus.
Int J Exp Diabetes Res. 2001;1(4):275-87.
PMID: 11467418 [PubMed - indexed for MEDLINE]

133: Park SL, Park EJ, Kim NH, Baek WK, Lee YT, Lee CJ, Suh CK.   Related Articles, Links

Hypoxia delays the intracellular Ca2+ clearance by Na+-Ca2+ exchanger in human adult cardiac myocytes.
Yonsei Med J. 2001 Jun;42(3):333-7.
PMID: 11456400 [PubMed - indexed for MEDLINE]

134: Lipsius SL, Huser J, Blatter LA.   Related Articles, Links

Intracellular Ca2+ release sparks atrial pacemaker activity.
News Physiol Sci. 2001 Jun;16:101-6. Review.
PMID: 11443225 [PubMed - indexed for MEDLINE]

135: Houser SR, Piacentino V 3rd, Mattiello J, Weisser J, Gaughan JP.   Related Articles, Links

Functional properties of failing human ventricular myocytes.
Trends Cardiovasc Med. 2000 Apr;10(3):101-7. Review.
PMID: 11427996 [PubMed - indexed for MEDLINE]

136: Lee VM, Halligan AW, Ng LL.   Related Articles, Links

Leucocyte intracellular pH and Na+/H+ exchanger isoform-1 activity in postpartum women with pre-eclampsia.
BJOG. 2001 Jun;108(6):615-22.
PMID: 11426897 [PubMed - indexed for MEDLINE]

137: Kawamoto T, Kimura H, Kusumoto K, Fukumoto S, Shiraishi M, Watanabe T, Sawada H.   Related Articles, Links

Potent and selective inhibition of the human Na+/H+ exchanger isoform NHE1 by a novel aminoguanidine derivative T-162559.
Eur J Pharmacol. 2001 May 18;420(1):1-8.
PMID: 11412833 [PubMed - indexed for MEDLINE]

138: Pogwizd SM, Schlotthauer K, Li L, Yuan W, Bers DM.   Related Articles, Links

Arrhythmogenesis and contractile dysfunction in heart failure: Roles of sodium-calcium exchange, inward rectifier potassium current, and residual beta-adrenergic responsiveness.
Circ Res. 2001 Jun 8;88(11):1159-67.
PMID: 11397782 [PubMed - indexed for MEDLINE]

139: Adachi-Akahane S, Kurachi Y.   Related Articles, Links

New era for translational research in cardiac arrhythmias.
Circ Res. 2001 Jun 8;88(11):1095-6. No abstract available.
PMID: 11397771 [PubMed - indexed for MEDLINE]

140: Li F, Hayes JK, Wong KC.   Related Articles, Links

Gene therapy: a novel method for the treatment of myocardial ischemia and reperfusion injury--mini-review.
Acta Anaesthesiol Sin. 2000 Dec;38(4):207-15. Review.
PMID: 11392069 [PubMed - indexed for MEDLINE]

141: Morin D, Hauet T, Spedding M, Tillement J.   Related Articles, Links

Mitochondria as target for antiischemic drugs.
Adv Drug Deliv Rev. 2001 Jul 2;49(1-2):151-74. Review.

PMID: 11377809 [PubMed - indexed for MEDLINE]

142: Shigekawa M, Iwamoto T.   Related Articles, Links

Cardiac Na(+)-Ca(2+) exchange: molecular and pharmacological aspects.
Circ Res. 2001 May 11;88(9):864-76. Review.
PMID: 11348995 [PubMed - indexed for MEDLINE]

143: Muller-Ehmsen J, Wang J, Schwinger RH, McDonough AA.   Related Articles, Links

Region specific regulation of sodium pump isoform and Na,Ca-exchanger
expression in the failing human heart--right atrium vs left ventricle.
Cell Mol Biol (Noisy-le-grand). 2001 Mar;47(2):373-81.
PMID: 11357898 [PubMed - indexed for MEDLINE]

144: Szerencsei RT, Prinsen CF, Schnetkamp PP.   Related Articles, Links

Stoichiometry of the retinal cone Na/Ca-K exchanger heterologously
expressed in insect cells: comparison with the bovine heart Na/Ca
exchanger.
Biochemistry. 2001 May 22;40(20):6009-15.
PMID: 11352736 [PubMed - indexed for MEDLINE]

145: Terracciano CM, MacLeod KT.   Related Articles, Links

Overexpression of the Na/Ca exchanger and reduced SERCa function.
Cardiovasc Res. 2001 Apr;50(1):167-9. No abstract available.
PMID: 11345943 [PubMed - indexed for MEDLINE]

146: Reddy PR, Patni A, Sharma A, Gupta S, Tiwary AK.   Related Articles, Links

Effect of 2',4'-dichlorobenzamil hydrochloride, a Na(+)-Ca(2+) exchange
inhibitor, on human spermatozoa.
Eur J Pharmacol. 2001 Apr 20;418(1-2):153-5.
PMID: 11334878 [PubMed - indexed for MEDLINE]

147: Bhattacharjee AK, Nagashima T, Kondoh T, Tamaki N.   Related Articles, Links

The effects of the Na(+)/Ca(++) exchange blocker on osmotic blood-brain
barrier disruption.
Brain Res. 2001 May 11;900(2):157-62.
PMID: 11334793 [PubMed - indexed for MEDLINE]

148: Kraev A, Quednau BD, Leach S, Li XF, Dong H, Winkfein R,
Perizzolo M, Cai X, Yang R, Philipson KD, Lytton J.   Related Articles, Links

Molecular cloning of a third member of the potassium-dependent sodium-
calcium exchanger gene family, NCKX3.
J Biol Chem. 2001 Jun 22;276(25):23161-72. Epub 2001 Apr 09.
PMID: 11294880 [PubMed - indexed for MEDLINE]

149: Takano S, Kimura J, Ono T.   Related Articles, Links

Inhibition of aggregation of rabbit and human platelets induced by
adrenaline and 5-hydroxytryptamine by KB-R7943, a Na(+)/Ca(2+)
exchange inhibitor.
Br J Pharmacol. 2001 Apr;132(7):1383-8.
PMID: 11264230 [PubMed - indexed for MEDLINE]

150: Li Y, Woo V, Bose R.   Related Articles, Links

Platelet hyperactivity and abnormal Ca(2+) homeostasis in diabetes
mellitus.
Am J Physiol Heart Circ Physiol. 2001 Apr;280(4):H1480-9.
PMID: 11247757 [PubMed - indexed for MEDLINE]

151: Van Eylen F, Bollen A, Herchuelz A.   Related Articles, Links

NCX1 Na/Ca exchanger splice variants in pancreatic islet cells.
J Endocrinol. 2001 Mar;168(3):517-26.
PMID: 11241183 [PubMed - indexed for MEDLINE]

152: Kim JA, Kang YY, Lee YS.   Related Articles, Links

Activation of Na(+), K(+), Cl(-)-cotransport mediates intracellular Ca(2+) increase and apoptosis induced by Pinacidil in HepG2 human hepatoblastoma cells.
Biochem Biophys Res Commun. 2001 Feb 23;281(2):511-9.
PMID: 11181077 [PubMed - indexed for MEDLINE]

153: Gabellini N.   Related Articles, Links

A polymorphic GT repeat from the human cardiac Na+Ca2+ exchanger intron 2 activates splicing.
Eur J Biochem. 2001 Feb;268(4):1076-83.
PMID: 11179974 [PubMed - indexed for MEDLINE]

154: Brown RE, Stevens DR, Haas HL.   Related Articles, Links

The physiology of brain histamine.
Prog Neurobiol. 2001 Apr;63(6):637-72. Review.
PMID: 11164999 [PubMed - indexed for MEDLINE]

155: Poon S, Leach S, Li XF, Tucker JE, Schnetkamp PP, Lytton J.   Related Articles, Links

Alternatively spliced isoforms of the rat eye sodium/calcium+potassium exchanger NCKX1.
Am J Physiol Cell Physiol. 2000 Apr;278(4):C651-60.
PMID: 10751314 [PubMed - indexed for MEDLINE]

156: Ren X, Kasir J, Rahamimoff H.   Related Articles, Links

The transport activity of the Na+-Ca2+ exchanger NCX1 expressed in HEK 293 cells is sensitive to covalent modification of intracellular cysteine residues by sulfhydryl reagents.
J Biol Chem. 2001 Mar 23;276(12):9572-9. Epub 2000 Dec 27.
PMID: 11134012 [PubMed - indexed for MEDLINE]

157: Isenberg G.   Related Articles, Links

How can overexpression of Na(+),Ca(2+)-exchanger compensate the negative inotropic effects of downregulated SERCA?
Cardiovasc Res. 2001 Jan;49(1):1-6. Review. No abstract available.
PMID: 11121788 [PubMed - indexed for MEDLINE]

158: Nattel S.   Related Articles, Links

Acquired delayed rectifier channelopathies: how heart disease and antiarrhythmic drugs mimic potentially-lethal congenital cardiac disorders.
Cardiovasc Res. 2000 Nov;48(2):188-90. No abstract available.
PMID: 11054465 [PubMed - indexed for MEDLINE]

159: Qiu Z, Nicoll DA, Philipson KD.   Related Articles, Links

Helix packing of functionally important regions of the cardiac Na(+)-Ca(2+) exchanger.
J Biol Chem. 2001 Jan 5;276(1):194-9.
PMID: 11035002 [PubMed - indexed for MEDLINE]

160: Pogwizd SM.   Related Articles, Links

Increased Na(+)-Ca(2+) exchanger in the failing heart.
Circ Res. 2000 Oct 13;87(8):641-3. No abstract available.

PMID: 11029397 [PubMed - indexed for MEDLINE]

☐ **161:** Sheng JZ, Prinsen CF, Clark RB, Giles WR, Schnetkamp PP.   Related Articles, Links

Na(+)-Ca(2+)-K(+) currents measured in insect cells transfected with the retinal cone or rod Na(+)-Ca(2+)-K(+) exchanger cDNA.
Biophys J. 2000 Oct;79(4):1945-53.
PMID: 11023899 [PubMed - indexed for MEDLINE]

☐ **162:** Piper C, Bilger J, Henrichs EM, Wudel E, Schultheiss HP,   Related Articles, Links
Horstkotte D, Dorner A.

[Is Na+Ca(2+) exchanger expression altered in the endomyocardium of patients with chronic heart valve diseases parallel to myocardial dysfunction?]
Z Kardiol. 2000 Aug;89(8):682-90. German.
PMID: 11013973 [PubMed - indexed for MEDLINE]

☐ **163:** Schillinger W, Janssen PM, Emami S, Henderson SA, Ross RS,   Related Articles, Links
Teucher N, Zeitz O, Philipson KD, Prestle J, Hasenfuss G.

Impaired contractile performance of cultured rabbit ventricular myocytes after adenoviral gene transfer of Na(+)-Ca(2+) exchanger.
Circ Res. 2000 Sep 29;87(7):581-7.
PMID: 11009563 [PubMed - indexed for MEDLINE]

☐ **164:** Barry WH.   Related Articles, Links

Na(+)-Ca(2+) exchange in failing myocardium: friend or foe?
Circ Res. 2000 Sep 29;87(7):529-31. No abstract available.
PMID: 11009553 [PubMed - indexed for MEDLINE]

☐ **165:** Kim JA, Kang YS, Lee SH, Lee YS.   Related Articles, Links

Inhibitors of Na+/Ca2+ exchanger prevent oxidant-induced intracellular Ca2+ increase and apoptosis in a human hepatoma cell line.
Free Radic Res. 2000 Sep;33(3):267-77.
PMID: 10993480 [PubMed - indexed for MEDLINE]

☐ **166:** Stengl M, Pucelik P.   Related Articles, Links

[Na+/Ca+ exchange: structure, mechanism, regulation and function]
Cesk Fysiol. 2000 May;49(2):73-90. Review. Czech.
PMID: 10953508 [PubMed - indexed for MEDLINE]

☐ **167:** Schaffer SW, Lombardini JB, Azuma J.   Related Articles, Links

Interaction between the actions of taurine and angiotensin II.
Amino Acids. 2000;18(4):305-18. Review.
PMID: 10949914 [PubMed - indexed for MEDLINE]

☐ **168:** Burkhoff D, Holmes JW, Madigan J, Barbone A, Oz MC.   Related Articles, Links

Left ventricular assist device-induced reverse ventricular remodeling.
Prog Cardiovasc Dis. 2000 Jul-Aug;43(1):19-26. Review.
PMID: 10935554 [PubMed - indexed for MEDLINE]

☐ **169:** McDonald RL, Colyer J, Harrison SM.   Related Articles, Links

Quantitative analysis of Na+-Ca2+ exchanger expression in guinea-pig heart.
Eur J Biochem. 2000 Aug;267(16):5142-8.
PMID: 10931198 [PubMed - indexed for MEDLINE]

☐ **170:** Lundquist P, Lundgren T, Gritli-Linde A, Linde A,   Related Articles, Links

Na+/Ca2+ exchanger isoforms of rat odontoblasts and osteoblasts.
Calcif Tissue Int. 2000 Jul;67(1):60-7.

h   cb   h g   e   e   e   fcg   e   ch   b   e

PMID: 10908415 [PubMed - indexed for MEDLINE]

□ **171:** Adam-Vizi V.   Related Articles, Links

[Neuroprotective effect of sodium channel blockers in ischemia: the pathomechanism of early ischemic dysfunction]
Orv Hetil. 2000 Jun 4;141(23):1279-86. Review. Hungarian.
PMID: 10905082 [PubMed - indexed for MEDLINE]

□ **172:** Wakimoto K, Kuro-O M, Yanaka N, Omori K, Komuro I, Imai   Related Articles, Links
Y, Nabeshima Y.

Isolation and characterization of Na+/Ca2+ exchanger gene and splicing isoforms in mice.
DNA Seq. 2000;11(1-2):75-81.
PMID: 10902911 [PubMed - indexed for MEDLINE]

□ **173:** Glendenning P, Ratajczak T, Dick IM, Prince RL.   Related Articles, Links

Calcitriol upregulates expression and activity of the 1b isoform of the plasma membrane calcium pump in immortalized distal kidney tubular cells.
Arch Biochem Biophys. 2000 Aug 1;380(1):126-32.
PMID: 10900141 [PubMed - indexed for MEDLINE]

□ **174:** Piper C, Bilger J, Henrichs EM, Schultheiss HP, Horstkotte D,   Related Articles, Links
Doerner A.

Is myocardial Na+/Ca2+ exchanger transcription a marker for different stages of myocardial dysfunction? Quantitative polymerase chain reaction of the messenger RNA in endomyocardial biopsies of patients with heart failure.
J Am Coll Cardiol. 2000 Jul;36(1):233-41.
PMID: 10898440 [PubMed - indexed for MEDLINE]

□ **175:** Philipson KD, Nicoll DA.   Related Articles, Links

Sodium-calcium exchange: a molecular perspective.
Annu Rev Physiol. 2000;62:111-33. Review.
PMID: 10845086 [PubMed - indexed for MEDLINE]

□ **176:** Nofer JR, Junker R, Seedorf U, Assmann G, Zidek W, Tepel M.   Related Articles, Links

D609-phosphatidylcholine-specific phospholipase C inhibitor attenuates thapsigargin-induced sodium influx in human lymphocytes.
Cell Signal. 2000 May;12(5):289-96.
PMID: 10822169 [PubMed - indexed for MEDLINE]

□ **177:** Paltauf-Doburzynska J, Frieden M, Spitaler M, Graier WF.   Related Articles, Links

Histamine-induced Ca2+ oscillations in a human endothelial cell line depend on transmembrane ion flux, ryanodine receptors and endoplasmic reticulum Ca2+-ATPase.
J Physiol. 2000 May 1;524 Pt 3:701-13.
PMID: 10790152 [PubMed - indexed for MEDLINE]

□ **178:** Seiler EP, Guerini D, Guidi F, Carafoli E.   Related Articles, Links

The N-terminal portion of the main cytosolic loop mediates K+ sensitivity in the retinal rod Na+/Ca2+-K+-exchanger.
Eur J Biochem. 2000 May;267(9):2461-72.
PMID: 10785365 [PubMed - indexed for MEDLINE]

□ **179:** Li L, Guerini D, Carafoli E.   Related Articles, Links

Calcineurin controls the transcription of Na+/Ca2+ exchanger isoforms in developing cerebellar neurons.

h   cb   h g   e   e   e   fcg   e   ch   b   e

J Biol Chem. 2000 Jul 7;275(27):20903-10.
PMID: 10767288 [PubMed - indexed for MEDLINE]

☐ **180:** Nakamura H, Kawasaki Y, Arakawa N, Saeki M, Maeda S,   Related Articles, Links
Koyama Y, Baba A, Matsuda T

The Na+-Ca2+ exchange inhibitor KB-R7943 inhibits high K+-induced
increases in intracellular Ca2+ concentration and [3H]noradrenaline
release in the human neuroblastoma SH-SY5Y.
Neurochem Res. 2000 Mar;25(3):385-7.
PMID: 10761983 [PubMed - indexed for MEDLINE]

☐ **181:** Qu Y, Ghatpande A, el-Sherif N, Boutjdir M.   Related Articles, Links

Gene expression of Na+/Ca2+ exchanger during development in human
heart.
Cardiovasc Res. 2000 Mar;45(4):866-73.
PMID: 10728412 [PubMed - indexed for MEDLINE]

☐ **182:** Kurosawa M, Numazawa S, Tani Y, Yoshida T.   Related Articles, Links

ERK signaling mediates the induction of inflammatory cytokines by
bufalin in human monocytic cells.
Am J Physiol Cell Physiol. 2000 Mar;278(3):C500-8.
PMID: 10712238 [PubMed - indexed for MEDLINE]

☐ **183:** Kiang JG, McClain DE.   Related Articles, Links

N(omega)-nitro-L-arginine decreases resting cytosolic [Ca2+] and
enhances heat stress-induced increase in cytosolic [Ca2+] in human colon
carcinoma T84 cells.
Chin J Physiol. 1999 Sep 30;42(3):153-9.
PMID: 10707889 [PubMed - indexed for MEDLINE]

☐ **184:** Bell PD, Mashburn N, Unlap MT.   Related Articles, Links

Renal sodium/calcium exchange; a vasodilator that is defective in salt-
sensitive hypertension.
Acta Physiol Scand. 2000 Jan;168(1):209-14. Review.
PMID: 10691802 [PubMed - indexed for MEDLINE]

☐ **185:** Prinsen CF, Szerencsei RT, Schnetkamp PP.   Related Articles, Links

Molecular cloning and functional expression of the potassium-dependent
sodium-calcium exchanger from human and chicken retinal cone
photoreceptors.
J Neurosci. 2000 Feb 15;20(4):1424-34.
PMID: 10662833 [PubMed - indexed for MEDLINE]

☐ **186:** McKiernan CJ, Friedlander M.   Related Articles, Links

The retinal rod Na(+)/Ca(2+),K(+) exchanger contains a noncleaved
signal sequence required for translocation of the N terminus.
J Biol Chem. 1999 Dec 31;274(53):38177-82.
PMID: 10608890 [PubMed - indexed for MEDLINE]

☐ **187:** Lehnart SE, Schillinger W, Pieske B, Prestle J, Just H, Hasenfuss   Related Articles, Links
G.

Sarcoplasmic reticulum proteins in heart failure.
Ann N Y Acad Sci. 1998 Sep 16;853:220-30. Review.
PMID: 10603950 [PubMed - indexed for MEDLINE]

☐ **188:** Goldhaber JI.   Related Articles, Links

Sodium-calcium exchange: the phantom menace.
Circ Res. 1999 Nov 26;85(11):982-4. No abstract available.

PMID: 10571527 [PubMed - indexed for MEDLINE]

☐ **189:** Prestle J, Dieterich S, Preuss M, Bieligk U, Hasenfuss G.   Related Articles, Links

Heterogeneous transmural gene expression of calcium-handling proteins and natriuretic peptides in the failing human heart.
Cardiovasc Res. 1999 Aug 1;43(2):323-31.
PMID: 10536662 [PubMed - indexed for MEDLINE]

☐ **190:** Brundel BJ, van Gelder IC, Henning RH, Tuinenburg AE,   Related Articles, Links
Deelman LE, Tieleman RG, Grandjean JG, van Gilst WH, Crijns
HJ.

Gene expression of proteins influencing the calcium homeostasis in patients with persistent and paroxysmal atrial fibrillation.
Cardiovasc Res. 1999 May;42(2):443-54.
PMID: 10533580 [PubMed - indexed for MEDLINE]

☐ **191:** Zacikova L, Krizanova O.   Related Articles, Links

[Structure and function of selected Ca(2+) transport systems in cardiac cells]
Cesk Fysiol. 1999 May;48(2):62-76. Review. Slovak.
PMID: 10510560 [PubMed - indexed for MEDLINE]

☐ **192:** Kimura M, Jeanclos EM, Donnelly RJ, Lytton J, Reeves JP, Aviv   Related Articles, Links
A.

Physiological and molecular characterization of the Na+/Ca2+ exchanger in human platelets.
Am J Physiol. 1999 Sep;277(3 Pt 2):H911-7.
PMID: 10484410 [PubMed - indexed for MEDLINE]

☐ **193:** Kasir J, Ren X, Furman I, Rahamimoff H.   Related Articles, Links

Truncation of the C terminus of the rat brain Na(+)-Ca(2+) exchanger RBE-1 (NCX1.4) impairs surface expression of the protein.
J Biol Chem. 1999 Aug 27;274(35):24873-80.
PMID: 10455160 [PubMed - indexed for MEDLINE]

☐ **194:** Gaughan JP, Furukawa S, Jeevanandam V, Hefner CA, Kubo H,   Related Articles, Links
Margulies KB, McGowan BS, Mattiello JA, Dipla K, Piacentino
V 3rd, Li S, Houser SR.

Sodium/calcium exchange contributes to contraction and relaxation in failed human ventricular myocytes.
Am J Physiol. 1999 Aug;277(2 Pt 2):H714-24.
PMID: 10444498 [PubMed - indexed for MEDLINE]

☐ **195:** Nofer JR, Pulawski E, Junker R, Seedorf U, Assmann G, Zidek   Related Articles, Links
W, Tepel M.

Na(+)/Ca(2+) exchange inhibitors modulate thapsigargin-induced Ca(2+) and Na(+) influx in human lymphocytes.
Int J Clin Lab Res. 1999;29(2):89-92.
PMID: 10436268 [PubMed - indexed for MEDLINE]

☐ **196:** Maixent JM, Lelievre L, Berrebi-Bertrand I.   Related Articles, Links

Mechanism underlying the strong positive inotropic effects of LND-623: specific inhibition of Na, K-ATPase isoforms and exclusion of cellular sites of contractile control.
Cardiovasc Drugs Ther. 1998 Dec;12(6):585-94.
PMID: 10410828 [PubMed - indexed for MEDLINE]

☐ **197:** Blaustein MP, Lederer WJ.   Related Articles, Links

Sodium/calcium exchange: its physiological implications.

h   cb   hg   e   e   e   fcg   e   ch   b   e

Physiol Rev. 1999 Jul;79(3):763-854. Review.
PMID: 10390518 [PubMed - indexed for MEDLINE]

198: Van Gelder IC, Brundel BJ, Henning RH, Tuinenburg AE, Tieleman RG, Deelman L, Grandjean JG, De Kam PJ, Van Gilst WH, Crijns HJ.   Related Articles, Links

Alterations in gene expression of proteins involved in the calcium handling in patients with atrial fibrillation.
J Cardiovasc Electrophysiol. 1999 Apr;10(4):552-60.
PMID: 10355697 [PubMed - indexed for MEDLINE]

199: Su Z, Bridge JH, Philipson KD, Spitzer KW, Barry WH.   Related Articles, Links

Quantitation of Na/Ca exchanger function in single ventricular myocytes.
J Mol Cell Cardiol. 1999 May;31(5):1125-35.
PMID: 10336850 [PubMed - indexed for MEDLINE]

200: Owen VJ, Burton PB, Michel MC, Zolk O, Bohm M, Pepper JR, Barton PJ, Yacoub MH, Harding SE.   Related Articles, Links

Myocardial dysfunction in donor hearts. A possible etiology.
Circulation. 1999 May 18;99(19):2565-70.
PMID: 10330389 [PubMed - indexed for MEDLINE]

201: Egger M, Ruknudin A, Niggli E, Lederer WJ, Schulze DH.   Related Articles, Links

Ni2+ transport by the human Na+/Ca2+ exchanger expressed in Sf9 cells.
Am J Physiol. 1999 May;276(5 Pt 1):C1184-92.
PMID: 10329968 [PubMed - indexed for MEDLINE]

202: Cooper CB, Winkfein RJ, Szerencsei RT, Schnetkamp PP.   Related Articles, Links

cDNA cloning and functional expression of the dolphin retinal rod Na-Ca+K exchanger NCKX1: comparison with the functionally silent bovine NCKX1.
Biochemistry. 1999 May 11;38(19):6276-83.
PMID: 10320357 [PubMed - indexed for MEDLINE]

203: Schwinger RH, Wang J, Frank K, Muller-Ehmsen J, Brixius K, McDonough AA, Erdmann E.   Related Articles, Links

Reduced sodium pump alpha1, alpha3, and beta1-isoform protein levels and Na+,K+-ATPase activity but unchanged Na+-Ca2+ exchanger protein levels in human heart failure.
Circulation. 1999 Apr 27;99(16):2105-12.
PMID: 10217649 [PubMed - indexed for MEDLINE]

204: Jornot L, Maechler P, Wollheim CB, Junod AF.   Related Articles, Links

Reactive oxygen metabolites increase mitochondrial calcium in endothelial cells: implication of the Ca2+/Na+ exchanger.
J Cell Sci. 1999 Apr;112 (Pt 7):1013-22.
PMID: 10198283 [PubMed - indexed for MEDLINE]

205: Egger M, Ruknudin A, Lipp P, Kofuji P, Lederer WJ, Schulze DH, Niggli E.   Related Articles, Links

Functional expression of the human cardiac Na+/Ca2+ exchanger in Sf9 cells: rapid and specific Ni2+ transport.
Cell Calcium. 1999 Jan;25(1):9-17.
PMID: 10191956 [PubMed - indexed for MEDLINE]

206: Guerini D.   Related Articles, Links

The Ca2+ pumps and the Na+/Ca2+ exchangers.
Biometals. 1998 Dec;11(4):319-30. Review.
PMID: 10191496 [PubMed - indexed for MEDLINE]

207: Iwamoto T, Nakamura TY, Pan Y, Uehara A, Imanaga I, Shigekawa M.
Related Articles, Links

Unique topology of the internal repeats in the cardiac Na+/Ca2+ exchanger.
FEBS Lett. 1999 Mar 12;446(2-3):264-8.
PMID: 10100855 [PubMed - indexed for MEDLINE]

208: Kim HS, Lee JH, Suh YH.
Related Articles, Links

C-terminal fragment of Alzheimer's amyloid precursor protein inhibits sodium/calcium exchanger activity in SK-N-SH cell.
Neuroreport. 1999 Jan 18;10(1):113-6.
PMID: 10094144 [PubMed - indexed for MEDLINE]

209: Mochizuki S, Jiang C.
Related Articles, Links

Na+/Ca++ exchanger and myocardial ischemia/reperfusion.
Jpn Heart J. 1998 Nov;39(6):707-14.
PMID: 10089932 [PubMed - indexed for MEDLINE]

210: Egger M, Niggli E.
Related Articles, Links

Regulatory function of Na-Ca exchange in the heart: milestones and outlook.
J Membr Biol. 1999 Mar 15;168(2):107-30. Review. No abstract available.
PMID: 10089232 [PubMed - indexed for MEDLINE]

211: DiPolo R, Beauge L.
Related Articles, Links

Metabolic pathways in the regulation of invertebrate and vertebrate Na+/Ca2+ exchange.
Biochim Biophys Acta. 1999 Feb 25;1422(1):57-71. Review. No abstract available.
PMID: 10082981 [PubMed - indexed for MEDLINE]

212: Winslow RL, Rice J, Jafri S, Marban E, O'Rourke B.
Related Articles, Links

Mechanisms of altered excitation-contraction coupling in canine tachycardia-induced heart failure, II: model studies.
Circ Res. 1999 Mar 19;84(5):571-86.
PMID: 10082479 [PubMed - indexed for MEDLINE]

213: O'Rourke B, Kass DA, Tomaselli GF, Kaab S, Tunin R, Marban E.
Related Articles, Links

Mechanisms of altered excitation-contraction coupling in canine tachycardia-induced heart failure, I: experimental studies.
Circ Res. 1999 Mar 19;84(5):562-70.
PMID: 10082478 [PubMed - indexed for MEDLINE]

214: Li XF, Lytton J.
Related Articles, Links

A circularized sodium-calcium exchanger exon 2 transcript.
J Biol Chem. 1999 Mar 19;274(12):8153-60.
PMID: 10075718 [PubMed - indexed for MEDLINE]

215: Marin J, Encabo A, Briones A, Garcia-Cohen EC, Alonso MJ.
Related Articles, Links

Mechanisms involved in the cellular calcium homeostasis in vascular smooth muscle: calcium pumps.
Life Sci. 1999;64(5):279-303. Review.
PMID: 10072189 [PubMed - indexed for MEDLINE]

216: Dipla K, Mattiello JA, Margulies KB, Jeevanandam V, Houser SR.
Related Articles, Links

The sarcoplasmic reticulum and the Na+/Ca2+ exchanger both contribute to the Ca2+ transient of failing human ventricular myocytes.

h   cb   h g   e   e   e   fcg   e   ch   b   e

Circ Res. 1999 Mar 5;84(4):435-44.
PMID: 10066678 [PubMed - indexed for MEDLINE]

217: Hasenfuss G, Schillinger W, Lehnart SE, Preuss M, Pieske B, Maier LS, Prestle J, Minami K, Just H.

Relationship between Na+-Ca2+-exchanger protein levels and diastolic function of failing human myocardium.
Circulation. 1999 Feb 9;99(5):641-8.
PMID: 9950661 [PubMed - indexed for MEDLINE]

218: Loeffler KU, Mangini NJ.

Immunohistochemical localization of Na+/Ca2+ exchanger in human retina and retinal pigment epithelium.
Graefes Arch Clin Exp Ophthalmol. 1998 Dec;236(12):929-33.
PMID: 9865624 [PubMed - indexed for MEDLINE]

219: Tucker JE, Winkfein RJ, Murthy SK, Friedman JS, Walter MA, Demetrick DJ, Schnetkamp PP.

Chromosomal localization and genomic organization of the human retinal rod Na-Ca+K exchanger.
Hum Genet. 1998 Oct;103(4):411-4.
PMID: 9856482 [PubMed - indexed for MEDLINE]

220: Tomiyama Y, Shiraga M, Kinoshita S, Ambo H, Kurata Y, Matsuzawa Y, Kunicki TJ.

A Glanzmann thrombasthenia-like phenotype caused by a defect in inside-out signaling through the integrin alpha(IIb)beta3.
Thromb Haemost. 1998 Nov;80(5):735-42.
PMID: 9843164 [PubMed - indexed for MEDLINE]

221: Schillinger W, Lehnart SE, Prestle J, Preuss M, Pieske B, Maier LS, Meyer M, Just H, Hasenfuss G.

Influence of SR Ca(2+)-ATPase and Na(+)-Ca(2+)-exchanger on the force-frequency relation.
Basic Res Cardiol. 1998;93 Suppl 1:38-45. Review.
PMID: 9833129 [PubMed - indexed for MEDLINE]

222: Horiguchi M, Kimura M, Skurnick J, Aviv A.

Parameters of lymphocyte Na+-Ca2+ regulation and blood pressure: the gender effect.
Hypertension. 1998 Nov;32(5):869-74.
PMID: 9822446 [PubMed - indexed for MEDLINE]

223: Shiraga M, Tomiyama Y, Honda S, Suzuki H, Kosugi S, Tadokoro S, Kanakura Y, Tanoue K, Kurata Y, Matsuzawa Y.

Involvement of Na+/Ca2+ exchanger in inside-out signaling through the platelet integrin IIbbeta3.
Blood. 1998 Nov 15;92(10):3710-20.
PMID: 9808565 [PubMed - indexed for MEDLINE]

224: Foster RH, Prat H, Rothman I.

Is ouabain produced by the adrenal gland?
Gen Pharmacol. 1998 Oct;31(4):499-501. Review.
PMID: 9792206 [PubMed - indexed for MEDLINE]

225: Mikoshiba K.

[Ca2+ mobilization and pumping out mechanism]
Tanpakushitsu Kakusan Koso. 1998 Sep;43(12 Suppl):1577-8. Review. Japanese. No abstract available.
PMID: 9788155 [PubMed - indexed for MEDLINE]

h   cb   h g   e   e   e   fcg   e   ch   b   e

226: Matsuoka S, Noma A.   Related Articles, Links

[Na(+)-Ca2+ exchange]
Tanpakushitsu Kakusan Koso. 1998 Sep;43(12 Suppl):155S-60. Review. Japanese. No
abstract available.
PMID: 9788152 [PubMed - indexed for MEDLINE]

227: Winslow RL, Rice J, Jafri S.   Related Articles, Links

Modeling the cellular basis of altered excitation-contraction coupling in
heart failure.
Prog Biophys Mol Biol. 1998;69(2-3):497-514. Review.
PMID: 9785953 [PubMed - indexed for MEDLINE]

228: Fukuba Y, Makino S, Takeda Y, Kawashima J, Murakami H,   Related Articles, Links
Miura A.

The effect of high-salt diet intake on muscular exercise ability in young
Japanese women.
Appl Human Sci. 1998 Jul;17(4):145-8.
PMID: 9757602 [PubMed - indexed for MEDLINE]

229: Fang Y, Rong M, He L, Zhou C.   Related Articles, Links

Mode-actions of the Na(+)-Ca2+ exchanger: from genes to mechanisms to
a new strategy in brain disorders.
Biomed Pharmacother. 1998;52(4):145-56.
PMID: 9755808 [PubMed - indexed for MEDLINE]

230: Courtemanche M, Ramirez RJ, Nattel S.   Related Articles, Links

Ionic mechanisms underlying human atrial action potential properties:
insights from a mathematical model.
Am J Physiol. 1998 Jul;275(1 Pt 2):H301-21.
PMID: 9688927 [PubMed - indexed for MEDLINE]

231: Iwamoto T, Shigekawa M.   Related Articles, Links

Differential inhibition of Na+/Ca2+ exchanger isoforms by divalent
cations and isothiourea derivative.
Am J Physiol. 1998 Aug;275(2 Pt 1):C423-30.
PMID: 9688596 [PubMed - indexed for MEDLINE]

232: Pieske B.   Related Articles, Links

[New aspects of the pathophysiology of heart failure]
Wien Med Wochenschr. 1998;148(5):108-20. Review. German.
PMID: 9654696 [PubMed - indexed for MEDLINE]

233: Itoh T, Itoh A, Horiuchi K, Pleasure D.   Related Articles, Links

AMPA receptor-mediated excitotoxicity in human NT2-N neurons results
from loss of intracellular Ca2+ homeostasis following marked elevation
of intracellular Na+.
J Neurochem. 1998 Jul;71(1):112-24.
PMID: 9648857 [PubMed - indexed for MEDLINE]

234: Priebe L, Beuckelmann DJ.   Related Articles, Links

Simulation study of cellular electric properties in heart failure.
Circ Res. 1998 Jun 15;82(11):1206-23.
PMID: 9633920 [PubMed - indexed for MEDLINE]

235: Carrillo C, Cafferata EG, Genovese J, O'Reilly M, Roberts AB,   Related Articles, Links
Santa-Coloma TA.

TGF-beta1 up-regulates the mRNA for the Na+/Ca2+ exchanger in
neonatal rat cardiac myocytes.

Cell Mol Biol (Noisy-le-grand). 1998 May;44(3):543-51.
PMID: 9620452 [PubMed - indexed for MEDLINE]

☐ **236:** Mattiello JA, Margulies KB, Jeevanandam V, Houser SR.   Related Articles, Links

Contribution of reverse-mode sodium-calcium exchange to contractions in failing human left ventricular myocytes.
Cardiovasc Res. 1998 Feb;37(2):424-31.
PMID: 9614497 [PubMed - indexed for MEDLINE]

☐ **237:** Cook O, Low W, Rahamimoff H.   Related Articles, Links

Membrane topology of the rat brain Na+-Ca2+ exchanger.
Biochim Biophys Acta. 1998 Apr 22;1371(1):40-52.
PMID: 9565655 [PubMed - indexed for MEDLINE]

☐ **238:** Endoh M.   Related Articles, Links

Changes in intracellular Ca2+ mobilization and Ca2+ sensitization as mechanisms of action of physiological interventions and inotropic agents in intact myocardial cells.
Jpn Heart J. 1998 Jan;39(1):1-44. Review.
PMID: 9601480 [PubMed - indexed for MEDLINE]

☐ **239:** Dyck C, Maxwell K, Buchko J, Trac M, Omelchenko A,   Related Articles, Links
Hnatowich M, Hryshko LV.

Structure-function analysis of CALX1.1, a Na+-Ca2+ exchanger from Drosophila. Mutagenesis of ionic regulatory sites.
J Biol Chem. 1998 May 22;273(21):12981-7.
PMID: 9582332 [PubMed - indexed for MEDLINE]

☐ **240:** Kiang JG, Ding XZ, McClain DE.   Related Articles, Links

Overexpression of HSP-70 attenuates increases in [Ca2+]i and protects human epidermoid A-431 cells after chemical hypoxia.
Toxicol Appl Pharmacol. 1998 Apr;149(2):185-94.
PMID: 9571987 [PubMed - indexed for MEDLINE]

☐ **241:** Friedman PA.   Related Articles, Links

Codependence of renal calcium and sodium transport.
Annu Rev Physiol. 1998;60:179-97. Review.
PMID: 9558460 [PubMed - indexed for MEDLINE]

☐ **242:** Matsuda T, Baba A.   Related Articles, Links

[Response of Na+/Ca2+ antiporter to ischemia and glial/neuronal death]
Nippon Yakurigaku Zasshi. 1998 Jan;111(1):13-9. Review. Japanese.
PMID: 9551468 [PubMed - indexed for MEDLINE]

☐ **243:** Scheller T, Kraev A, Skinner S, Carafoli E.   Related Articles, Links

Cloning of the multipartite promoter of the sodium-calcium exchanger gene NCX1 and characterization of its activity in vascular smooth muscle cells.
J Biol Chem. 1998 Mar 27;273(13):7643-9.
PMID: 9516469 [PubMed - indexed for MEDLINE]

☐ **244:** Berberian G, Hidalgo C, DiPolo R, Beauge L.   Related Articles, Links

ATP stimulation of Na+/Ca2+ exchange in cardiac sarcolemmal vesicles.
Am J Physiol. 1998 Mar;274(3 Pt 1):C724-33.
PMID: 9530104 [PubMed - indexed for MEDLINE]

☐ **245:** Satoh H, Sperelakis N.   Related Articles, Links

Review of some actions of taurine on ion channels of cardiac muscle cells

and others.
Gen Pharmacol. 1998 Apr;30(4):451-63. Review.
PMID: 9522160 [PubMed - indexed for MEDLINE]

246: Watano T, Kimura J.   Related Articles, Links

Calcium-dependent inhibition of the sodium-calcium exchange current by KB-R7943.
Can J Cardiol. 1998 Feb;14(2):259-62.
PMID: 9520863 [PubMed - indexed for MEDLINE]

247: Tucker JE, Winkfein RJ, Cooper CB, Schnetkamp PP.   Related Articles, Links

cDNA cloning of the human retinal rod Na-Ca + K exchanger: comparison with a revised bovine sequence.
Invest Ophthalmol Vis Sci. 1998 Feb;39(2):435-40.
PMID: 9478004 [PubMed - indexed for MEDLINE]

248: Mangini NJ, Haugh-Scheidt L, Valle JE, Cragoe EJ Jr, Ripps H,   Related Articles, Links
Kennedy BG.

Sodium-calcium exchanger in cultured human retinal pigment epithelium.
Exp Eye Res. 1997 Dec;65(6):821-34.
PMID: 9441706 [PubMed - indexed for MEDLINE]

249: Aviv A.   Related Articles, Links

Cellular calcium and sodium regulation, salt-sensitivity and essential hypertension in African Americans.
Ethn Health. 1996 Sep;1(3):275-81. Review.
PMID: 9395572 [PubMed - indexed for MEDLINE]

250: Schwinger RH, Brixius K, Bavendiek U, Hoischen S, Muller-   Related Articles, Links
Ehmsen J, Bolck B, Erdmann E.

Effect of cyclopiazonic acid on the force-frequency relationship in human nonfailing myocardium.
J Pharmacol Exp Ther. 1997 Oct;283(1):286-92.
PMID: 9336335 [PubMed - indexed for MEDLINE]

251: Morad M, Suzuki YJ.   Related Articles, Links

Ca(2+)-signaling in cardiac myocytes: evidence from evolutionary and transgenic models.
Adv Exp Med Biol. 1997;430:3-12. Review.
PMID: 9330714 [PubMed - indexed for MEDLINE]

252: Wu A, Derrico CA, Hatem L, Colvin RA.   Related Articles, Links

Alzheimer's amyloid-beta peptide inhibits sodium/calcium exchange measured in rat and human brain plasma membrane vesicles.
Neuroscience. 1997 Oct;80(3):675-84.
PMID: 9276485 [PubMed - indexed for MEDLINE]

253: Ruknudin A, Valdivia C, Kofuji P, Lederer WJ, Schulze DH.   Related Articles, Links

Na+/Ca2+ exchanger in Drosophila: cloning, expression, and transport differences.
Am J Physiol. 1997 Jul;273(1 Pt 1):C257-65.
PMID: 9252464 [PubMed - indexed for MEDLINE]

254: Navangione A, Rispoli G, Gabellini N, Carafoli E.   Related Articles, Links

Electrophysiological characterization of ionic transport by the retinal exchanger expressed in human embryonic kidney cells.
Biophys J. 1997 Jul;73(1):45-51.
PMID: 9199770 [PubMed - indexed for MEDLINE]

255: Levi AJ, Dalton GR, Hancox JC, Mitcheson JS, Issberner J, Bates Related Articles, Links
JA, Evans SJ, Howarth FC, Hobai IA, Jones JV.

Role of intracellular sodium overload in the genesis of cardiac
arrhythmias.
J Cardiovasc Electrophysiol. 1997 Jun;8(6):700-21. Review.
PMID: 9209972 [PubMed - indexed for MEDLINE]

256: Matsuda T, Takuma K, Baba A. Related Articles, Links

Na(+)-Ca2+ exchanger: physiology and pharmacology.
Jpn J Pharmacol. 1997 May;74(1):1-20. Review.
PMID: 9195292 [PubMed - indexed for MEDLINE]

257: Muller-Ehmsen J, Frank K, Brixius K, Schwinger RH. Related Articles, Links

Increase in force of contraction by activation of the Na+/Ca(2+)-
exchanger in human myocardium.
Br J Clin Pharmacol. 1997 Apr;43(4):399-405.
PMID: 9146852 [PubMed - indexed for MEDLINE]

258: LoPachin RM, Lehning EJ. Related Articles, Links

Mechanism of calcium entry during axon injury and degeneration.
Toxicol Appl Pharmacol. 1997 Apr;143(2):233-44. Review.
PMID: 9144441 [PubMed - indexed for MEDLINE]

259: Resendes MC, Kalogeros GC, Dixon SJ, Philp RB. Related Articles, Links

Nitrous oxide enhances Na+/Ca++ exchange in the neuroblastoma cell
line SK-N-SH.
J Pharmacol Exp Ther. 1997 Feb;280(2):795-801.
PMID: 9023293 [PubMed - indexed for MEDLINE]

260: Foey AD, Crawford A, Hall ND. Related Articles, Links

Modulation of cytokine production by human mononuclear cells
following impairment of Na, K-ATPase activity.
Biochim Biophys Acta. 1997 Jan 10;1355(1):43-9.
PMID: 9030200 [PubMed - indexed for MEDLINE]

261: Studer R, Reinecke H, Vetter R, Holtz J, Drexler H. Related Articles, Links

Expression and function of the cardiac Na+/Ca2+ exchanger in postnatal
development of the rat, in experimental-induced cardiac hypertrophy and
in the failing human heart.
Basic Res Cardiol. 1997;92 Suppl 1:53-8. Review.
PMID: 9202844 [PubMed - indexed for MEDLINE]

262: Hryshko LV, Philipson KD. Related Articles, Links

Sodium-calcium exchange: recent advances.
Basic Res Cardiol. 1997;92 Suppl 1:45-51. Review.
PMID: 9202843 [PubMed - indexed for MEDLINE]

263: Pitt A, Knox AJ. Related Articles, Links

Molecular characterization of the human airway smooth muscle
Na+/Ca2+ exchanger.
Am J Respir Cell Mol Biol. 1996 Dec;15(6):726-30.
PMID: 8969266 [PubMed - indexed for MEDLINE]

264: Brandenburger Y, Kennedy ED, Python CP, Rossier MF, Related Articles, Links
Vallotton MB, Wollheim CB, Capponi AM.

Possible role for mitochondrial calcium in angiotensin II- and potassium-
stimulated steroidogenesis in bovine adrenal glomerulosa cells.
Endocrinology. 1996 Dec;137(12):5544-51.

h   cb   hg   e   e   e   fcg   e   ch   b   e

PMID: 8940382 [PubMed - indexed for MEDLINE]

265: White KE, Gesek FA, Friedman PA.　　　　　Related Articles, Links

Na+/Ca2+ exchange in rat osteoblast-like UMR 106 cells.
J Bone Miner Res. 1996 Nov;11(11):1666-75.
PMID: 8915774 [PubMed - indexed for MEDLINE]

266: Kraev A, Chumakov I, Carafoli E.　　　　　Related Articles, Links

The organization of the human gene NCX1 encoding the sodium-calcium exchanger.
Genomics. 1996 Oct 1;37(1):105-12.
PMID: 8921376 [PubMed - indexed for MEDLINE]

267: Shiraga M, Tomiyama Y, Honda S, Kashiwagi H, Kosugi S,　　Related Articles, Links
Handa M, Ikeda Y, Kanakura Y, Kurata Y, Matsuzawa Y.

Affinity modulation of the platelet integrin alpha IIb beta 3 by alpha-chymotrypsin: a possible role for Na+/Ca2+ exchanger.
Blood. 1996 Oct 1;88(7):2594-602.
PMID: 8839852 [PubMed - indexed for MEDLINE]

268: Wang J, Schwinger RH, Frank K, Muller-Ehmsen J, Martin-　Related Articles, Links
Vasallo P, Pressley TA, Xiang A, Erdmann E, McDonough AA.

Regional expression of sodium pump subunits isoforms and Na+-Ca++ exchanger in the human heart.
J Clin Invest. 1996 Oct 1;98(7):1650-8.
PMID: 8833915 [PubMed - indexed for MEDLINE]

269: Benardeau A, Hatem SN, Rucker-Martin C, Le Grand B, Mace L, Related Articles, Links
Dervanian P, Mercadier JJ, Coraboeuf E.

Contribution of Na+/Ca2+ exchange to action potential of human atrial myocytes.
Am J Physiol. 1996 Sep;271(3 Pt 2):H1151-61.
PMID: 8853354 [PubMed - indexed for MEDLINE]

270: Flesch M, Schwinger RH, Schiffer F, Frank K, Sudkamp M,　　Related Articles, Links
Kuhn-Regnier F, Arnold G, Bohm M.

Evidence for functional relevance of an enhanced expression of the Na (+)-Ca2+ exchanger in failing human myocardium.
Circulation. 1996 Sep 1;94(5):992-1002.
PMID: 8790037 [PubMed - indexed for MEDLINE]

271: Gabellini N, Zatti A, Rispoli G, Navangione A, Carafoli E.　　Related Articles, Links

Expression of an active Na+/Ca2+ exchanger isoform lacking the six C-terminal transmembrane segments.
Eur J Biochem. 1996 Aug 1;239(3):897-904.
PMID: 8774741 [PubMed - indexed for MEDLINE]

272: Janvier NC, Boyett MR.　　　　　Related Articles, Links

The role of Na-Ca exchange current in the cardiac action potential.
Cardiovasc Res. 1996 Jul;32(1):69-84. Review.
PMID: 8776405 [PubMed - indexed for MEDLINE]

273: Lederer WJ, He S, Luo S, duBell W, Kofuji P, Kieval R,　　Related Articles, Links
Neubauer CF, Ruknudin A, Cheng H, Cannell MB, Rogers TB,
Schulze DH.

The molecular biology of the Na(+)-Ca2+ exchanger and its functional roles in heart, smooth muscle cells, neurons, glia, lymphocytes, and nonexcitable cells.
Ann N Y Acad Sci. 1996 Apr 15;779:7-17. Review. No abstract available.
PMID: 8659882 [PubMed - indexed for MEDLINE]

h　　　　cb　　　　hg　　e　　e　　e　　fcg　　　　e　　ch　　　　b　　e

274: Reinecke H, Studer R, Vetter R, Just H, Holtz J, Drexler H.   Related Articles, Links

Role of the cardiac sarcolemmal Na(+)-Ca2+ exchanger in end-stage human heart failure.
Ann N Y Acad Sci. 1996 Apr 15;779:543-5. No abstract available.
PMID: 8659875 [PubMed - indexed for MEDLINE]

275: Flesch M, Putz F, Schwinger RH, Bohm M.   Related Articles, Links

Functional relevance of an enhanced expression of the Na(+)-Ca2+ exchanger in the failing human heart.
Ann N Y Acad Sci. 1996 Apr 15;779:539-42. No abstract available.
PMID: 8659874 [PubMed - indexed for MEDLINE]

276: Li GR, Nattel S.   Related Articles, Links

Demonstration of an inward Na(+)-Ca2+ exchange current in adult human atrial myocytes.
Ann N Y Acad Sci. 1996 Apr 15;779:525-8. No abstract available.
PMID: 8659869 [PubMed - indexed for MEDLINE]

277: Gardner JP, Balasubramanyam M.   Related Articles, Links

Na-Ca exchange in circulating blood cells.
Ann N Y Acad Sci. 1996 Apr 15;779:502-14. Review.
PMID: 8659866 [PubMed - indexed for MEDLINE]

278: Schulze DH, Kofuji P, Valdivia C, He S, Luo S, Ruknudin A, Wisel S, Kirby MS, duBell W, Lederer WJ.   Related Articles, Links

Alternative splicing of the Na(+)-Ca2+ exchanger gene, NCX1.
Ann N Y Acad Sci. 1996 Apr 15;779:46-57. Review.
PMID: 8659862 [PubMed - indexed for MEDLINE]

279: Langer GA, Peskoff A.   Related Articles, Links

Calcium in the cardiac diadic cleft. Implications for sodium-calcium exchange.
Ann N Y Acad Sci. 1996 Apr 15;779:408-16. Review. No abstract available.
PMID: 8659857 [PubMed - indexed for MEDLINE]

280: Rahamimoff H, Low W, Cook O, Furman I, Kasir J, Vatashski R.   Related Articles, Links

The structural basis of Na(+)-Ca2+ exchange activity.
Ann N Y Acad Sci. 1996 Apr 15;779:29-36. Review. No abstract available.
PMID: 8659840 [PubMed - indexed for MEDLINE]

281: Gabellini N, Iwata T, Carafoli E.   Related Articles, Links

Expression of Na(+)-Ca2+ exchanger with modified C-terminal hydrophobic domains and enhanced activity.
Ann N Y Acad Sci. 1996 Apr 15;779:110-4. Review.
PMID: 8659816 [PubMed - indexed for MEDLINE]

282: Kraev A, Chumakov I, Carafoli E.   Related Articles, Links

Molecular biological studies of the cardiac sodium-calcium exchanger.
Ann N Y Acad Sci. 1996 Apr 15;779:103-9. Review.
PMID: 8659815 [PubMed - indexed for MEDLINE]

283: [No authors listed]   Related Articles, Links

3rd International Conference on Sodium-Calcium Exchange. Woods Hole, Massachusetts, April 23-26, 1995. Proceedings.
Ann N Y Acad Sci. 1996 Apr 15;779:1-589. No abstract available.
PMID: 8659814 [PubMed - indexed for MEDLINE]

284: Just H.   Related Articles, Links

h   cb   h g   e   e   e   fcg   e   ch   b   e

Pathophysiological targets for beta-blocker therapy in congestive heart failure.
Eur Heart J. 1996 Apr;17 Suppl B:2-7.
PMID: 8733064 [PubMed - indexed for MEDLINE]

285: Colvin RA, Walker JP, Schummers J, Davis N.   Related Articles, Links

Aging does not affect steady-state expression of the Na+/Ca2+ exchanger in rat brain.
Cell Mol Neurobiol. 1996 Feb;16(1):11-9.
PMID: 8714556 [PubMed - indexed for MEDLINE]

286: Drexler H.   Related Articles, Links

[Sympathetic nervous system in heart failure: effect of catecholamines and nitric oxide]
Z Kardiol. 1996;85 Suppl 6:247-52. Review. German.
PMID: 9064972 [PubMed - indexed for MEDLINE]

287: Capponi AM.   Related Articles, Links

Distribution and signal transduction of angiotensin II AT1 and AT2 receptors.
Blood Press Suppl. 1996;2:41-6. Review.
PMID: 8913539 [PubMed - indexed for MEDLINE]

288: Sham JS, Hatem SN, Morad M.   Related Articles, Links

Species differences in the activity of the Na(+)-Ca2+ exchanger in mammalian cardiac myocytes.
J Physiol. 1995 Nov 1;488 (Pt 3):623-31.
PMID: 8576853 [PubMed - indexed for MEDLINE]

289: Loo TW, Ho C, Clarke DM.   Related Articles, Links

Expression of a functionally active human renal sodium-calcium exchanger lacking a signal sequence.
J Biol Chem. 1995 Aug 18;270(33):19345-50.
PMID: 7642612 [PubMed - indexed for MEDLINE]

290: Furman I, Cook O, Kasir J, Low W, Rahamimoff H.   Related Articles, Links

The putative amino-terminal signal peptide of the cloned rat brain Na(+)-Ca2+ exchanger gene (RBE-1) is not mandatory for functional expression.
J Biol Chem. 1995 Aug 11;270(32):19120-7.
PMID: 7642578 [PubMed - indexed for MEDLINE]

291: Lipp P, Schwaller B, Niggli E.   Related Articles, Links

Specific inhibition of Na-Ca exchange function by antisense oligodeoxynucleotides.
FEBS Lett. 1995 May 8;364(2):198-202. Erratum in: FEBS Lett 1995 Aug 21;370 (3):280.
PMID: 7750570 [PubMed - indexed for MEDLINE]

292: Gabellini N, Iwata T, Carafoli E.   Related Articles, Links

An alternative splicing site modifies the carboxyl-terminal trans-membrane domains of the Na+/Ca2+ exchanger.
J Biol Chem. 1995 Mar 24;270(12):6917-24.
PMID: 7896841 [PubMed - indexed for MEDLINE]

293: Kordeli E, Lambert S, Bennett V.   Related Articles, Links

AnkyrinG. A new ankyrin gene with neural-specific isoforms localized at the axonal initial segment and node of Ranvier.

J Biol Chem. 1995 Feb 3;270(5):2352-9.
PMID: 7836469 [PubMed - indexed for MEDLINE]

294: Gatto C, Hale CC, Xu W, Milanick MA.   Related Articles, Links

Eosin, a potent inhibitor of the plasma membrane Ca pump, does not inhibit the cardiac Na-Ca exchanger.
Biochemistry. 1995 Jan 24;34(3):965-72.
PMID: 7530047 [PubMed - indexed for MEDLINE]

295: Morishita F, Kawarabayashi T, Sakamoto Y, Shirakawa K.   Related Articles, Links

Role of the sodium-calcium exchange mechanism and the effect of magnesium on sodium-free and high-potassium contractures in pregnant human myometrium.
Am J Obstet Gynecol. 1995 Jan;172(1 Pt 1):186-95.
PMID: 7847532 [PubMed - indexed for MEDLINE]

296: Fisher DJ.   Related Articles, Links

Recent insights into the regulation of cardiac Ca2+ flux during perinatal development and in cardiac failure.
Curr Opin Cardiol. 1995 Jan;10(1):44-51. Review.
PMID: 7787264 [PubMed - indexed for MEDLINE]

297: Michaelis ML.   Related Articles, Links

Ion transport systems and Ca2+ regulation in aging neurons.
Ann N Y Acad Sci. 1994 Dec 15;747:407-18. Review. No abstract available.
PMID: 7847687 [PubMed - indexed for MEDLINE]

298: Colvin RA, Davis N, Wu A, Murphy CA, Levengood J.   Related Articles, Links

Studies of the mechanism underlying increased Na+/Ca2+ exchange activity in Alzheimer's disease brain.
Brain Res. 1994 Dec 5;665(2):192-200.
PMID: 7895054 [PubMed - indexed for MEDLINE]

299: Wu A, Colvin RA.   Related Articles, Links

Characterization of exchange inhibitory peptide effects on Na+/Ca2+ exchange in rat and human brain plasma membrane vesicles.
J Neurochem. 1994 Dec;63(6):2136-43.
PMID: 7964733 [PubMed - indexed for MEDLINE]

300: Suleiman MS.   Related Articles, Links

New concepts in the cardioprotective action of magnesium and taurine during the calcium paradox and ischaemia of the heart.
Magnes Res. 1994 Dec;7(3-4):295-312. Review.
PMID: 7786694 [PubMed - indexed for MEDLINE]

301: Balasubramanyam M, Rohowsky-Kochan C, Reeves JP, Gardner   Related Articles, Links
JP.

Na+/Ca2+ exchange-mediated calcium entry in human lymphocytes.
J Clin Invest. 1994 Nov;94(5):2002-8.
PMID: 7962546 [PubMed - indexed for MEDLINE]

302: Reeves JP, Condrescu M, Chernaya G, Gardner JP.   Related Articles, Links

Na+/Ca2+ antiport in the mammalian heart.
J Exp Biol. 1994 Nov;196:375-88. Review.
PMID: 7823035 [PubMed - indexed for MEDLINE]

303: Grinstein S, Wieczorek H.   Related Articles, Links

Cation antiports of animal plasma membranes.

J Exp Biol. 1994 Nov;196:307-18. Review. No abstract available.
PMID: 7823030 [PubMed - indexed for MEDLINE]

304: Kim-Lee MH, Stokes BT, McDonald JS.   Related Articles, Links

Procaine, lidocaine, and hypothermia inhibit calcium paradox in glial cells.
Anesth Analg. 1994 Oct;79(4):728-33.
PMID: 7943783 [PubMed - indexed for MEDLINE]

305: Benders AA, Li J, Lock RA, Bindels RJ, Bonga SE, Veerkamp   Related Articles, Links
JH.

Copper toxicity in cultured human skeletal muscle cells: the involvement of Na+/K(+)-ATPase and the Na+/Ca(2+)-exchanger.
Pflugers Arch. 1994 Oct;428(5-6):461-7.
PMID: 7838667 [PubMed - indexed for MEDLINE]

306: Atsma DE, Bastiaanse EM, Ince C, van der Laarse A.   Related Articles, Links

A novel two-compartment culture dish allows microscopic evaluation of two different treatments in one cell culture simultaneously. Influence of external pH on Na+/Ca2+ exchanger activity in cultured rat cardiomyocytes.
Pflugers Arch. 1994 Oct;428(3-4):296-9.
PMID: 7816552 [PubMed - indexed for MEDLINE]

307: Studer R, Reinecke H, Bilger J, Eschenhagen T, Bohm M,   Related Articles, Links
Hasenfuss G, Just H, Holtz J, Drexler H.

Gene expression of the cardiac Na(+)-Ca2+ exchanger in end-stage human heart failure.
Circ Res. 1994 Sep;75(3):443-53.
PMID: 8062418 [PubMed - indexed for MEDLINE]

308: Harvey BJ.   Related Articles, Links

Crosstalk and epithelial ion transport.
Curr Opin Nephrol Hypertens. 1994 Sep;3(5):523-8.
PMID: 7804751 [PubMed - indexed for MEDLINE]

309: Kimura M, Cho JH, Reeves JP, Aviv A.   Related Articles, Links

Inhibition of Ca2+ entry by Ca2+ overloading of intracellular Ca2+ stores in human platelets.
J Physiol. 1994 Aug 15;479 (Pt 1):1-10.
PMID: 7527459 [PubMed - indexed for MEDLINE]

310: Lax D, Martinez-Zaguilan R, Gillies RJ.   Related Articles, Links

Furazolidone increases thapsigargin-sensitive Ca(2+)-ATPase in chick cardiac myocytes.
Am J Physiol. 1994 Aug;267(2 Pt 2):H734-41.
PMID: 8067429 [PubMed - indexed for MEDLINE]

311: Reithmeier RA.   Related Articles, Links

Mammalian exchangers and co-transporters.
Curr Opin Cell Biol. 1994 Aug;6(4):583-94. Review.
PMID: 7986536 [PubMed - indexed for MEDLINE]

312: Hoey A, Amos GJ, Ravens U.   Related Articles, Links

Comparison of the action potential prolonging and positive inotropic activity of DPI 201-106 and BDF 9148 in human ventricular myocardium.
J Mol Cell Cardiol. 1994 Aug;26(8):985-94.
PMID: 7799453 [PubMed - indexed for MEDLINE]

h   cb   hg   e   e   e   fcg   e   ch   b   e

313: Kiang JG, Smallridge RC. Related Articles, Links

Sodium cyanide increases cytosolic free calcium: evidence for activation of the reversed mode of the Na+/Ca2+ exchanger and Ca2+ mobilization from inositol trisphosphate-insensitive pools.
Toxicol Appl Pharmacol. 1994 Aug;127(2):173-81.
PMID: 7519371 [PubMed - indexed for MEDLINE]

314: Loo TW, Clarke DM. Related Articles, Links

Functional expression of human renal Na+/Ca2+ exchanger in insect cells.
Am J Physiol. 1994 Jul;267(1 Pt 2):F70-4.
PMID: 8048567 [PubMed - indexed for MEDLINE]

315: Li Z, Matsuoka S, Hryshko LV, Nicoll DA, Bersohn MM, Burke EP, Lifton RP, Philipson KD. Related Articles, Links

Cloning of the NCX2 isoform of the plasma membrane Na(+)-Ca2+ exchanger.
J Biol Chem. 1994 Jul 1;269(26):17434-9.
PMID: 8021246 [PubMed - indexed for MEDLINE]

316: Drexler H. Related Articles, Links

Heart failure: an update on pathophysiology.
Arch Mal Coeur Vaiss. 1994 Jun;87 Spec No 2:13-6.
PMID: 7864717 [PubMed - indexed for MEDLINE]

317: Macdonald RL, Weir BK. Related Articles, Links

Cerebral vasospasm and free radicals.
Free Radic Biol Med. 1994 May;16(5):633-43. Review.
PMID: 8026807 [PubMed - indexed for MEDLINE]

318: Kimura M, Cho JH, Lasker N, Aviv A. Related Articles, Links

Differences in platelet calcium regulation between African Americans and Caucasians: implications for the predisposition of African Americans to essential hypertension.
J Hypertens. 1994 Feb;12(2):199-207.
PMID: 8021471 [PubMed - indexed for MEDLINE]

319: Tepel M, Bauer S, Kegel M, Raffelsiefer A, Wischniowski H, Zidek W. Related Articles, Links

Increased cytosolic free sodium in platelets from patients with early-stage chronic renal failure.
Nephrol Dial Transplant. 1994;9(1):27-34.
PMID: 8177473 [PubMed - indexed for MEDLINE]

320: Levi AJ, Boyett MR, Lee CO. Related Articles, Links

The cellular actions of digitalis glycosides on the heart.
Prog Biophys Mol Biol. 1994;62(1):1-54. Review. No abstract available.
PMID: 8085015 [PubMed - indexed for MEDLINE]

321: Cox DA, Matlib MA. Related Articles, Links

Modulation of intramitochondrial free Ca2+ concentration by antagonists of Na(+)-Ca2+ exchange.
Trends Pharmacol Sci. 1993 Nov;14(11):408-13. Review.
PMID: 8296399 [PubMed - indexed for MEDLINE]

322: Schulze D, Kofuji P, Hadley R, Kirby MS, Kieval RS, Doering A, Niggli E, Lederer WJ. Related Articles, Links

Sodium/calcium exchanger in heart muscle: molecular biology, cellular function, and its special role in excitation-contraction coupling.

h   cb   hg   e   e   e   fcg   e   ch   b   e

Cardiovasc Res. 1993 Oct;27(10):1726-34. Review.
PMID: 8275517 [PubMed - indexed for MEDLINE]

☐ **323:** Noble D, Bett G.   Related Articles, Links

Reconstructing the heart: a challenge for integrative physiology.
Cardiovasc Res. 1993 Oct;27(10):1701-12. No abstract available.
PMID: 8275516 [PubMed - indexed for MEDLINE]

☐ **324:** Ishida T, Matsuura H, Ishida-Kainouchi M, Ozono R, Watanabe   Related Articles, Links
M, Kajiyama G, Oshima T.

Na(+)-Ca2+ exchange modulates Ca2+ handling of human platelets by
altering intracellular Ca2+ store size.
J Hypertens. 1993 Oct;11(10):1089-95.
PMID: 8258673 [PubMed - indexed for MEDLINE]

☐ **325:** Marlier LN, Zheng T, Tang J, Grayson DR.   Related Articles, Links

Regional distribution in the rat central nervous system of a mRNA
encoding a portion of the cardiac sodium/calcium exchanger isolated from
cerebellar granule neurons.
Brain Res Mol Brain Res. 1993 Oct;20(1-2):21-39.
PMID: 8255180 [PubMed - indexed for MEDLINE]

☐ **326:** Donnadieu E, Trautmann A.   Related Articles, Links

Is there a Na+/Ca2+ exchanger in macrophages and in lymphocytes?
Pflugers Arch. 1993 Sep;424(5-6):448-55.
PMID: 8255728 [PubMed - indexed for MEDLINE]

☐ **327:** Mene P, Pugliese F, Cinotti GA.   Related Articles, Links

Cyclic nucleotides inhibit Na+/Ca2+ exchange in cultured human
mesangial cells.
Exp Nephrol. 1993 Jul-Aug;1(4):245-52.
PMID: 7521769 [PubMed - indexed for MEDLINE]

☐ **328:** Barry WH.   Related Articles, Links

Is "fuzzy space" necessary for Ca2+ extrusion on the Na(+)-Ca+
exchanger in cardiac myocytes?
J Mol Cell Cardiol. 1993 Jun;25(6):641-3; discussion 645-6. No abstract available.
PMID: 8411189 [PubMed - indexed for MEDLINE]

☐ **329:** Langer GA, Peskoff A, Post JA.   Related Articles, Links

How does the Na(+)-Ca2+ exchanger work in the intact cardiac cell?
J Mol Cell Cardiol. 1993 Jun;25(6):637-9. No abstract available.
PMID: 8411188 [PubMed - indexed for MEDLINE]

☐ **330:** Katnik C, Nelson DJ.   Related Articles, Links

Platelet activating factor-induced increase in cytosolic calcium and
transmembrane current in human macrophages.
J Membr Biol. 1993 Jun;134(3):213-24.
PMID: 8411123 [PubMed - indexed for MEDLINE]

☐ **331:** Barry WH, Bridge JH.   Related Articles, Links

Intracellular calcium homeostasis in cardiac myocytes.
Circulation. 1993 Jun;87(6):1806-15. Review.
PMID: 8389258 [PubMed - indexed for MEDLINE]

☐ **332:** Kimura M, Aviv A, Reeves JP.   Related Articles, Links

K(+)-dependent Na+/Ca2+ exchange in human platelets.
J Biol Chem. 1993 Apr 5;268(10):6874-7.

h   cb   h g   e   e   e   fcg   e   ch   b   e   /

PMID: 8463216 [PubMed - indexed for MEDLINE]

☐ **333:** Pijuan V, Zhuang Y, Smith L, Kroupis C, Condrescu M, Aceto   Related Articles, Links
JF, Reeves JP, Smith JB.

Stable expression of the cardiac sodium-calcium exchanger in CHO cells.
Am J Physiol. 1993 Apr;264(4 Pt 1):C1066-74.
PMID: 8476012 [PubMed - indexed for MEDLINE]

☐ **334:** Furman I, Cook O, Kasir J, Rahamimoff H.   Related Articles, Links

Cloning of two isoforms of the rat brain Na(+)-Ca2+ exchanger gene and
their functional expression in HeLa cells.
FEBS Lett. 1993 Mar 15;319(1-2):105-9.
PMID: 8454039 [PubMed - indexed for MEDLINE]

☐ **335:** Wacholtz MC, Cragoe EJ Jr, Lipsky PE.   Related Articles, Links

Delineation of the role of a Na+/Ca2+ exchanger in regulating
intracellular Ca2+ in T cells.
Cell Immunol. 1993 Mar;147(1):95-109.
PMID: 8462115 [PubMed - indexed for MEDLINE]

☐ **336:** Kimura M, Aviv A.   Related Articles, Links

Regulation of the cytosolic pH set point for activation of the Na+/H+
antiport in human platelets: the roles of the Na+/Ca2+ exchange, the Na
(+)-K(+)-2Cl- cotransport and cellular volume.
Pflugers Arch. 1993 Mar;422(6):585-90.
PMID: 8385772 [PubMed - indexed for MEDLINE]

☐ **337:** Waxman SG, Ritchie JM.   Related Articles, Links

Molecular dissection of the myelinated axon.
Ann Neurol. 1993 Feb;33(2):121-36. Review.
PMID: 7679565 [PubMed - indexed for MEDLINE]

☐ **338:** Low W, Kasir J, Rahamimoff H.   Related Articles, Links

Cloning of the rat heart Na(+)-Ca2+ exchanger and its functional
expression in HeLa cells.
FEBS Lett. 1993 Jan 18;316(1):63-7.
PMID: 8422940 [PubMed - indexed for MEDLINE]

☐ **339:** McDaniel LD, Lederer WJ, Kofuji P, Schulze DH, Kieval R,   Related Articles, Links
Schultz RA.

Mapping of the human cardiac Na+/Ca2+ exchanger gene (NCX1) by
fluorescent in situ hybridization to chromosome region 2p22-->p23.
Cytogenet Cell Genet. 1993;63(3):192-3.
PMID: 8485996 [PubMed - indexed for MEDLINE]

☐ **340:** Ransom BR, Waxman SG, Stys PK.   Related Articles, Links

Anoxic injury of central myelinated axons: ionic mechanisms and
pharmacology.
Res Publ Assoc Res Nerv Ment Dis. 1993;71:121-51. Review. No abstract available.
PMID: 8417464 [PubMed - indexed for MEDLINE]

☐ **341:** Ponce-Hornos JE, Bonazzola P, Taquini AC.   Related Articles, Links

[Energetics of ionic behavior in heart muscle contraction. Physiologic and
physiopathologic aspects]
Medicina (B Aires). 1993;53(5):445-58. Review. Spanish.
PMID: 8201934 [PubMed - indexed for MEDLINE]

☐ **342:** Decollogne S, Bertrand IB, Ascensio M, Drubaix I, Lelievre LG.   Related Articles, Links

Na+, K(+)-ATPase and Na+/Ca2+ exchange isoforms: physiological and physiopathological relevance.
J Cardiovasc Pharmacol. 1993;22 Suppl 2:S96-8. Review.
PMID: 7508043 [PubMed - indexed for MEDLINE]

□ 343: Kofuji P, Hadley RW, Kieval RS, Lederer WJ, Schulze DH.   Related Articles, Links

Expression of the Na-Ca exchanger in diverse tissues: a study using the cloned human cardiac Na-Ca exchanger.
Am J Physiol. 1992 Dec;263(6 Pt 1):C1241-9.
PMID: 1476165 [PubMed - indexed for MEDLINE]

□ 344: Valant PA, Adjei PN, Haynes DH.   Related Articles, Links

Rapid Ca2+ extrusion via the Na+/Ca2+ exchanger of the human platelet.
J Membr Biol. 1992 Oct;130(1):63-82.
PMID: 1469706 [PubMed - indexed for MEDLINE]

□ 345: Wacholtz MC, Cragoe EJ Jr, Lipsky PE.   Related Articles, Links

A Na(+)-dependent Ca2+ exchanger generates the sustained increase in intracellular Ca2+ required for T cell activation.
J Immunol. 1992 Sep 15;149(6):1912-20.
PMID: 1387665 [PubMed - indexed for MEDLINE]

□ 346: Varro A, Papp JG.   Related Articles, Links

The impact of single cell voltage clamp on the understanding of the cardiac ventricular action potential.
Cardioscience. 1992 Sep;3(3):131-44. Review.
PMID: 1384746 [PubMed - indexed for MEDLINE]

□ 347: Philipson KD, Nicoll DA.   Related Articles, Links

Sodium-calcium exchange.
Curr Opin Cell Biol. 1992 Aug;4(4):678-83. Review.
PMID: 1419049 [PubMed - indexed for MEDLINE]

□ 348: Kiang JG, Koenig ML, Smallridge RC.   Related Articles, Links

Heat shock increases cytosolic free Ca2+ concentration via Na(+)-Ca2+ exchange in human epidermoid A 431 cells.
Am J Physiol. 1992 Jul;263(1 Pt 1):C30-8.
PMID: 1636682 [PubMed - indexed for MEDLINE]

□ 349: Komuro I, Wenninger KE, Philipson KD, Izumo S   Related Articles, Links

Molecular cloning and characterization of the human cardiac Na+/Ca2+ exchanger cDNA.
Proc Natl Acad Sci U S A. 1992 May 15;89(10):4769-73.
PMID: 1374913 [PubMed - indexed for MEDLINE]

□ 350: Smith TF, Sanchez-Legrand F, McKean LP, Kutner MH, Cragoe   Related Articles, Links
EJ Jr, Eaton DC.

Role of sodium in mediator release from human basophils.
J Allergy Clin Immunol. 1992 May;89(5):978-86.
PMID: 1374773 [PubMed - indexed for MEDLINE]

□ 351: Shieh BH, Xia Y, Sparkes RS, Klisak I, Lusis AJ, Nicoll DA,   Related Articles, Links
Philipson KD.

Mapping of the gene for the cardiac sarcolemmal Na(+)-Ca2+ exchanger to human chromosome 2p21-p23.
Genomics. 1992 Mar;12(3):616-7.
PMID: 1559714 [PubMed - indexed for MEDLINE]

□ 352: Kim-Lee MH, Stokes BT, Yates AJ.   Related Articles, Links

h   cb   h g   e   e   e   fcg   e   ch   b   e

Reperfusion paradox: a novel mode of glial cell injury.
Glia. 1992;5(1):56-64.
PMID: 1531810 [PubMed - indexed for MEDLINE]

353: Blaustein MP, Ambesi A, Bloch RJ, Goldman WF, Juhaszova M, Related Articles, Links
Lindenmayer GE, Weiss DN.

Regulation of vascular smooth muscle contractility: roles of the
sarcoplasmic reticulum (SR) and the sodium/calcium exchanger.
Jpn J Pharmacol. 1992;58 Suppl 2:107P-114P. Review. No abstract available.
PMID: 1507528 [PubMed - indexed for MEDLINE]

354: Michaelis EK, Michaelis ML.   Related Articles, Links

Molecular aspects of glutamate receptors and sodium-calcium exchange
carriers in mammalian brain: implications for neuronal development and
degeneration.
Neurochem Res. 1992 Jan;17(1):29-34. Review.
PMID: 1371600 [PubMed - indexed for MEDLINE]

355: Holubarsch C.   Related Articles, Links

[Biochemical changes and disorders of electromechanical coupling in
chronic heart failure]
Z Kardiol. 1992;81 Suppl 4:17-21. Review. German.
PMID: 1290294 [PubMed - indexed for MEDLINE]

356: Lafond J, Leclerc M, Brunette MG.   Related Articles, Links

Characterization of calcium transport by basal plasma membranes from
human placental syncytiotrophoblast.
J Cell Physiol. 1991 Jul;148(1):17-23.
PMID: 1650372 [PubMed - indexed for MEDLINE]

357: Colvin RA, Bennett JW, Colvin SL, Allen RA, Martinez J, Miner Related Articles, Links
GD.

Na+/Ca2+ exchange activity is increased in Alzheimer's disease brain
tissues.
Brain Res. 1991 Mar 8;543(1):139-47.
PMID: 1647256 [PubMed - indexed for MEDLINE]

358: Williams JM, Abramovich DR, Dacke CG, Mayhew TM, Page Related Articles, Links
KR.

Inhibitor action on placental calcium transport.
Calcif Tissue Int. 1991 Jan;48(1):7-12.
PMID: 1826093 [PubMed - indexed for MEDLINE]

359: Mullins LJ.   Related Articles, Links

Is stoichiometry constant in Na-Ca exchange?
Ann N Y Acad Sci. 1991;639:96-8. No abstract available.
PMID: 1785898 [PubMed - indexed for MEDLINE]

360: Khananshvili D.   Related Articles, Links

Mechanism of partial reactions in the cardiac Na(+)-Ca2+ exchange
system.
Ann N Y Acad Sci. 1991;639:85-95. Review. No abstract available.
PMID: 1785897 [PubMed - indexed for MEDLINE]

361: Hoenig M, Culberson LH, Wheeler CA, Ferguson DC.   Related Articles, Links

Characterization of Na(+)-Ca2+ exchange in the beta cell.
Ann N Y Acad Sci. 1991;639:657-9. Review. No abstract available.
PMID: 1785893 [PubMed - indexed for MEDLINE]

h   cb   h g   e   e   e   fcg   e   ch   b   e

362: Herchuelz A, Plasman PO.   Related Articles, Links

Sodium-calcium exchange in the pancreatic B cell.
Ann N Y Acad Sci. 1991;639:642-56. Review. No abstract available.
PMID: 1785892 [PubMed - indexed for MEDLINE]

363: Haynes DH, Valant PA, Adjei PN.   Related Articles, Links

Calcium extrusion by the sodium-calcium exchanger of the human
platelet.
Ann N Y Acad Sci. 1991;639:592-603. No abstract available.
PMID: 1785888 [PubMed - indexed for MEDLINE]

364: Windhager EE, Frindt G, Milovanovic S.   Related Articles, Links

The role of Na-Ca exchange in renal epithelia. An overview.
Ann N Y Acad Sci. 1991;639:577-91. Review. No abstract available.
PMID: 1785887 [PubMed - indexed for MEDLINE]

365: Matlib MA.   Related Articles, Links

Role of sarcolemmal membrane sodium-calcium exchange in vascular
smooth muscle tension.
Ann N Y Acad Sci. 1991;639:531-42. Review.
PMID: 1785880 [PubMed - indexed for MEDLINE]

366: Aaronson PI, Poston L, Woolfson RG, Smirnov SV.   Related Articles, Links

Evidence for Na-Ca exchange in human resistance arteries.
Ann N Y Acad Sci. 1991;639:521-30. No abstract available.
PMID: 1785879 [PubMed - indexed for MEDLINE]

367: Smith JB, Lyu RM, Smith L.   Related Articles, Links

Sodium-calcium exchange in aortic myocytes and renal epithelial cells.
Dependence on metabolic energy and intracellular sodium.
Ann N Y Acad Sci. 1991;639:505-20. Review. No abstract available.
PMID: 1785878 [PubMed - indexed for MEDLINE]

368: Colvin RA, Bennett JW, Colvin SL.   Related Articles, Links

Na(+)-Ca2+ exchange activity is increased in Alzheimer's disease brain
tissues.
Ann N Y Acad Sci. 1991;639:325-7. No abstract available.
PMID: 1785858 [PubMed - indexed for MEDLINE]

369: Mills LR.   Related Articles, Links

Neuron-specific and state-specific differences in calcium regulation. Their
role in the development of neuronal architecture.
Ann N Y Acad Sci. 1991;639:312-24. Review. No abstract available.
PMID: 1785857 [PubMed - indexed for MEDLINE]

370: Yau KW, Nakatani K, Tamura T.   Related Articles, Links

Sodium-calcium exchange and phototransduction in retinal
photoreceptors.
Ann N Y Acad Sci. 1991;639:275-84. Review. No abstract available.
PMID: 1785854 [PubMed - indexed for MEDLINE]

371: DiPolo R, Beauge L.   Related Articles, Links

Regulation of Na-Ca exchange. An overview.
Ann N Y Acad Sci. 1991;639:100-11. Review. No abstract available.
PMID: 1785834 [PubMed - indexed for MEDLINE]

372: Dale WE, Simchowitz L.   Related Articles, Links

h   cb   hg   e   e   e   fcg   e   ch   b   e

The role of Na(+)-Ca2+ exchange in human neutrophil function.
Ann N Y Acad Sci. 1991;639:616-30. Review. No abstract available.
PMID: 1664709 [PubMed - indexed for MEDLINE]

☐ **373:** Mene P, Pugliese F, Faraggiana T, Cinotti GA.   Related Articles, Links

Identification and characteristics of a Na+/Ca2+ exchanger in cultured human mesangial cells.
Kidney Int. 1990 Dec;38(6):1199-205.
PMID: 2074662 [PubMed - indexed for MEDLINE]

☐ **374:** Hoel G, Michaelis ML, Freed WJ, Kleinman JE.   Related Articles, Links

Characterization of Na(+)-Ca2+ exchange activity in plasma membrane vesicles from postmortem human brain.
Neurochem Res. 1990 Sep;15(9):881-7.
PMID: 1703282 [PubMed - indexed for MEDLINE]

☐ **375:** Strehler EE.   Related Articles, Links

Plasma membrane Ca2+ pumps and Na+/Ca2+ exchangers.
Semin Cell Biol. 1990 Aug;1(4):283-95. Review.
PMID: 2151738 [PubMed - indexed for MEDLINE]

☐ **376:** [No authors listed]   Related Articles, Links

Na(+)-Ca2+ exchanger and cardiac contraction.
Lancet. 1990 Jul 28;336(8709):219-20. No abstract available.
PMID: 1973777 [PubMed - indexed for MEDLINE]

☐ **377:** Gruver CL, Katz AM, Messineo FC.   Related Articles, Links

Canine cardiac sarcolemmal vesicles demonstrate rapid initial Na(+)-Ca2+ exchange activity.
Circ Res. 1990 May;66(5):1171-7.
PMID: 2335019 [PubMed - indexed for MEDLINE]

☐ **378:** Chapman R.   Related Articles, Links

A rise in intracellular sodium would seem to predispose the heart to the calcium paradox.
J Mol Cell Cardiol. 1990 May;22(5):503-5. No abstract available.
PMID: 2167385 [PubMed - indexed for MEDLINE]

☐ **379:** Ruigrok TJ.   Related Articles, Links

Is an increase of intracellular Na+ during Ca2+ depletion essential for the occurrence of the calcium paradox?
J Mol Cell Cardiol. 1990 May;22(5):499-501. No abstract available.
PMID: 2167384 [PubMed - indexed for MEDLINE]

☐ **380:** Philipson KD.   Related Articles, Links

The cardiac Na(+)-Ca2+ exchanger: dependence on membrane environment.
Cell Biol Int Rep. 1990 Apr;14(4):305-9. Review. No abstract available.
PMID: 2191788 [PubMed - indexed for MEDLINE]

☐ **381:** Heilmann C, Spamer C, Gerok W.   Related Articles, Links

Aspects of hepatic calcium metabolism.
Prog Liver Dis. 1990;9:261-79. Review. No abstract available.
PMID: 2156295 [PubMed - indexed for MEDLINE]

☐ **382:** Smith JB, Zheng T, Smith L.   Related Articles, Links

Relationship between cytosolic free Ca2+ and Na+-Ca2+ exchange in

h   cb   hg   e   e   e   fcg   e   ch   b   e

aortic muscle cells.
Am J Physiol. 1989 Jan;256(1 Pt 1):C147-54.
PMID: 2912132 [PubMed - indexed for MEDLINE]

☐ **383:** Parker JC.   Related Articles, Links

Sodium-calcium and sodium-proton exchangers in red blood cells.
Methods Enzymol. 1989;173:292-300. No abstract available.
PMID: 2550727 [PubMed - indexed for MEDLINE]

☐ **384:** Rengasamy A, Feinberg H.   Related Articles, Links

Sodium-calcium exchange in platelet plasma membrane vesicles.
Adv Exp Med Biol. 1988;232:105-8. No abstract available.
PMID: 3213678 [PubMed - indexed for MEDLINE]

☐ **385:** Hermsmeyer RK.   Related Articles, Links

Vascular muscle membrane cation mechanisms and total peripheral
resistance.
Hypertension. 1987 Nov;10(5 Pt 2):I20-2. Review.
PMID: 2445679 [PubMed - indexed for MEDLINE]

☐ **386:** Letarte M, Quackenbush EJ, Baumal R, Michalak M.   Related Articles, Links

Correlations between the 44D7 antigenic complex and the plasma
membrane Na+-Ca2+ exchanger.
Biochem Cell Biol. 1986 Nov;64(11):1160-9.
PMID: 3828108 [PubMed - indexed for MEDLINE]

☐ **387:** Michalak M, Quackenbush EJ, Letarte M.   Related Articles, Links

Inhibition of Na+/Ca2+ exchanger activity in cardiac and skeletal muscle
sarcolemmal vesicles by monoclonal antibody 44D7.
J Biol Chem. 1986 Jan 5;261(1):92-5.
PMID: 2416754 [PubMed - indexed for MEDLINE]

☐ **388:** Carafoli E.   Related Articles, Links

The homeostasis of calcium in heart cells.
J Mol Cell Cardiol. 1985 Mar;17(3):203-12.
PMID: 2943901 [PubMed - indexed for MEDLINE]

☐ **389:** Philipson KD.   Related Articles, Links

Sodium-calcium exchange in plasma membrane vesicles.
Annu Rev Physiol. 1985;47:561-71. Review. No abstract available.
PMID: 3888080 [PubMed - indexed for MEDLINE]

☐ **390:** Garrick R, Ziyadeh FN, Jorkasky D, Goldfarb S.   Related Articles, Links

Bartter's syndrome: a unifying hypothesis.
Am J Nephrol. 1985;5(5):379-84. Review.
PMID: 2998188 [PubMed - indexed for MEDLINE]

☐ **391:** Shamoo AE, Ambudkar IS.   Related Articles, Links

Regulation of calcium transport in cardiac cells.
Can J Physiol Pharmacol. 1984 Jan;62(1):9-22. Review.
PMID: 6143603 [PubMed - indexed for MEDLINE]

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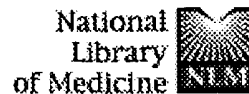
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☐ **1:** Gabellini N.   Related Articles, Links

Transcriptional regulation by cAMP and Ca2+ links the na+/ca2+ exchanger 3 to memory and sensory pathways.
Mol Neurobiol. 2004 Aug;30(1):91-116.
PMID: 15247490 [PubMed - in process]

☐ **2:** Gabellini N, Bortoluzzi S, Danieli GA, Carafoli E.   Related Articles, Links

Control of the Na+/Ca2+ exchanger 3 promoter by cyclic adenosine monophosphate and Ca2+ in differentiating neurons.
J Neurochem. 2003 Jan;84(2):282-93.
PMID: 12558991 [PubMed - indexed for MEDLINE]

☐ **3:** Gabellini N, Bortoluzzi S, Danieli GA, Carafoli E.   Related Articles, Links

The gene promoter of human Na+/Ca2+ exchanger isoform 3 (SLC8A3) is controlled by cAMP and calcium.
Ann N Y Acad Sci. 2002 Nov;976:282-4. No abstract available.
PMID: 12502570 [PubMed - indexed for MEDLINE]

☐ **4:** Gabellini N, Bortoluzzi S, Danieli GA, Carafoli E.   Related Articles, Links

The human SLC8A3 gene and the tissue-specific Na+/Ca2+ exchanger 3 isoforms.
Gene. 2002 Sep 18;298(1):1-7.
PMID: 12406570 [PubMed - indexed for MEDLINE]

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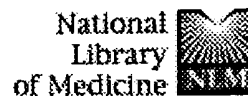
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☐ 1: Viola G, Bressanini M, Gabellini N, Vedaldi D, Dall'Acqua F, Ihmels H   Related Articles, Links

Naphthoquinolizinium derivatives as a novel platform for DNA-binding and DNA-photodamaging chromophores.
Photochem Photobiol Sci. 2002 Nov;1(11):882-9.
PMID: 12659528 [PubMed - indexed for MEDLINE]

☐ 2: Gabellini N, Bortoluzzi S, Danieli GA, Carafoli E.   Related Articles, Links

The gene promoter of human Na+/Ca2+ exchanger isoform 3 (SLC8A3) is controlled by cAMP and calcium.
Ann N Y Acad Sci. 2002 Nov;976:282-4. No abstract available.
PMID: 12502570 [PubMed - indexed for MEDLINE]

☐ 3: Gabellini N, Bortoluzzi S, Danieli GA, Carafoli E.   Related Articles, Links

The human SLC8A3 gene and the tissue-specific Na+/Ca2+ exchanger 3 isoforms.
Gene. 2002 Sep 18;298(1):1-7.
PMID: 12406570 [PubMed - indexed for MEDLINE]

☐ 4: Viola G, Dall'Acqua F, Gabellini N, Moro S, Vedaldi D, Ihmels H   Related Articles, Links

Indolo[2,3-b]-quinolizinium bromide: an efficient intercalator with DNA-photodamaging properties.
Chembiochem. 2002 Jun 3;3(6):550-8.
PMID: 12325011 [PubMed - indexed for MEDLINE]

☐ 5: Gabellini D, Green MR, Tupler R.   Related Articles, Links

Inappropriate gene activation in FSHD: a repressor complex binds a chromosomal repeat deleted in dystrophic muscle.
Cell. 2002 Aug 9;110(3):339-48.
PMID: 12176321 [PubMed - indexed for MEDLINE]

☐ 6: Calado RT, Falcao RP, Garcia AB, Gabellini SM, Zago MA, Franco RF   Related Articles, Links

Influence of functional MDR1 gene polymorphisms on P-glycoprotein activity in CD34+ hematopoietic stem cells.
Haematologica. 2002 Jun;87(6):564-8.
PMID: 12031911 [PubMed - indexed for MEDLINE]

☐ 7: Targa L, Conti G, Gabellini A, Bergamo S, Rossetto A, Corbara F.   Related Articles, Links

[Carcinoid heart disease and primary ovarian tumor]
Ital Heart J. 2002 Apr;3(4 Suppl):450-3. Review. Italian.
PMID: 12025391 [PubMed - indexed for MEDLINE]

☐ 8: Franco RF, Simoes BP, Tone LG, Gabellini SM, Zago MA, Falcao RP.   Related Articles, Links

The methylenetetrahydrofolate reductase C677T gene polymorphism decreases the risk of childhood acute lymphocytic leukaemia.

Br J Haematol. 2001 Dec;115(3):616-8.
PMID: 11736945 [PubMed - indexed for MEDLINE]

9: Anelli PL, Lattuada L, Gabellini M, Recanati P.   Related Articles, Links

DOTA tris(phenylmethyl) ester: a new useful synthon for the synthesis of
DOTA monoamides containing acid-labile bonds.
Bioconjug Chem. 2001 Nov-Dec;12(6):1081-4.
PMID: 11716703 [PubMed - indexed for MEDLINE]

10: Ihmels H, Faulhaber K, Sturm C, Bringmann G, Messer K,   Related Articles, Links
Gabellini N, Vedaldi D, Viola G.

Acridizinium salts as a novel class of DNA-binding and site-selective
DNA-photodamaging chromophores.
Photochem Photobiol. 2001 Oct;74(4):505-11.
PMID: 11683029 [PubMed - indexed for MEDLINE]

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   19 FILES SEARCHED...
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L4    ANSWER 1 OF 473   ADISCTI COPYRIGHT (C) 2004 Adis Data Information BV on
      STN
AN    1997:43605   ADISCTI
DN    800540795
TI    Positive inotropic effect of the novel Na+ -channel modulator BDF 9198 on
        ***human***    non-failing and failing myocardium.
      ADIS TITLE: BDF 9148 vs BDF 9198: pharmacodynamics.
      Positive inotropic effects
      In vitro study.
AU    Muller Ehmsen J; Frank K; Brixius K; Schwinger R H G.
CS    Klinik III fur Innere Medizin der Universitat zu Koln, Germany.
SO    2nd International Meeting of the Working Group on Heart Failure (May 24,
      1997), pp. 78
DT    Study
RE    Heart Failure
FS    Summary
LA    English
WC    242


L4    ANSWER 2 OF 473   BIOSIS  COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN    2003:400914   BIOSIS
DN    PREV200300400914
TI    ***Human***    genes for K+-dependent Na/Ca-exchangers, NCKX1, NCKX2 and
      NCKX3; genomic structure, comparative analysis of promoter regions and
      expression patterns.
AU    Reigo, A. [Reprint Author]; Metspalu, A. [Reprint Author]
CS    Tartu University Institute of Molecular and Cell Biology, Tartu, Estonia
      3pusa2susa@hot.ee; 3pusa2susa@hot.ee
SO    European Journal of Human Genetics, (2001) Vol. 9, No. Supplement 1, pp.
      P0756. print.
      Meeting Info.: 10th International Congress of Human Genetics. Vienna,
      Austria. May 15-19, 2001. International Federation of Human Genetics
      Societies.
      ISSN: 1018-4813.
DT    Conference; (Meeting)
      Conference; Abstract; (Meeting Abstract)
LA    English
ED    Entered STN: 3 Sep 2003
      Last Updated on STN: 3 Sep 2003

L4    ANSWER 3 OF 473   BIOSIS  COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
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TI   Changes in sarcolemmal Ca entry and sarcoplasmic reticulum (SR) Ca content in isolated ventricular myocytes from patients with end-stage heart failure following left ventricular assist device support.

AU   Terracciano, Cesare Mn. [Reprint author]; Koban, Maren [Reprint author]; Harding, Sian E. [Reprint author]; Tansley, Patrick [Reprint author]; Birks, Emma J. [Reprint author]; Yacoub, Magdi H. [Reprint author]
CS   Imperial Coll Sch of Med, London, UK

TI   Calcium influx via INCX is favored in failing   ***human***   ventricular myocytes.

AU   Weber, Christopher R. [Reprint author]; Piacentino, Valentino; Margulies, Kenneth B.; Bers, Donald M.; Houser, Steven R.
CS   Loyola Univ, Maywood, IL, USA

TI   Annexin VI and the Na/Ca exchanger are residents of caveolae microdomains in the   ***human***   heart.

AU   Matteo, Rosalia G. [Reprint author]; Moravec, Christine S. [Reprint author]
CS   Cleveland Clin Fdn, Cleveland, OH, USA

TI   Very low dose of the Na+/Ca2+ exchange inhibitor, KB-R7943, protects ischemic reperfused aged Fischer 344 rat hearts: Considerable strain difference in the sensitivity to KB-R7943.

AU   Yamamura, Ken [Reprint author]; Tani, Masato; Hasegawa, Hiroshi; Gen, Wen
CS   Department of Geriatrics, Keio University School of Medicine, 35 Shinanomachi, Shinjuku-ku, Tokyo, 160-8582, Japan
      yamamura@sc.itc.keio.ac.jp

L4   ANSWER 7 OF 473   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   2002:71595   BIOSIS
DN   PREV200200071595
TI   Novel inhibitors of the   ***sodium***   -   ***calcium***
     exchanger   : Benzene ring analogues of N-guanidino substituted
     amiloride derivatives.
AU   Rogister, Francoise; Laeckmann, Didier; Plasman, Pierre-Olivier; Van
     Eylen, Francoise; Ghyoot, Marianne; Maggetto, Carine; Liegeois,
     Jean-Francois; Geczy, Joseph; Herchuelz, Andre; Delarge, Jacques;
     Masereel, Bernard [Reprint author]
CS   Department of Pharmacy, University of Namur, 61 Rue de Bruxelles, B-5000,
     Namur, Belgium
     bernard.masereel@fundp.ac.be
SO   European Journal of Medicinal Chemistry, (July-August, 2001) Vol. 36, No.
     7-8, pp. 597-614. print.
     CODEN: EJMCA5. ISSN: 0223-5234.
DT   Article
LA   English
ED   Entered STN: 16 Jan 2002
     Last Updated on STN: 25 Feb 2002

L4   ANSWER 8 OF 473   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   2002:69723   BIOSIS
DN   PREV200200069723
TI   Chronic atrial fibrillation in   ***humans***   is associated with reduced
     SERCA2a expression and depressed force-frequency response.
AU   Schmidt-Schweda, S. H. [Reprint author]; Schaller, C. [Reprint author];
     Pieske, B. [Reprint author]
CS   Kardiologie and Pneumologie, Universitaet Goettingen, Goettingen, Germany
SO   European Heart Journal, (September, 2001) Vol. 22, No. Abstract
     Supplement, pp. 37. print.
     Meeting Info.: XXIII Congress of the European Society of Cardiology
     together with the 36th Annual General Meeting of the Association for
     European Paediatric Cardiology. Stockholm, Sweden. September 01-05, 2001.
     CODEN: EHJODF. ISSN: 0195-668X.
DT   Conference; (Meeting)
     Conference; Abstract; (Meeting Abstract)
LA   English
ED   Entered STN: 16 Jan 2002
     Last Updated on STN: 25 Feb 2002

L4   ANSWER 9 OF 473   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   2001:558807   BIOSIS
DN   PREV200100558807
TI   Genome search for QTL controlling pulse pressure: A practical application
     of the unified Haseman-Elston algorithm.
AU   Li, J. [Reprint author]; Niu, T. [Reprint author]; Rogus, J.; Yang, J.;
     Schork, N. [Reprint author]; Fang, Z.; Xu, X. [Reprint author]
CS   Prog Population Genetics, Harvard Sch Public Health, Boston, MA, USA
SO   American Journal of Human Genetics, (October, 2001) Vol. 69, No. 4
     Supplement, pp. 510. print.
     Meeting Info.: 51st Annual Meeting of the American Society of Human
     Genetics. San Diego, California, USA. October 12-16, 2001.
     CODEN: AJHGAG. ISSN: 0002-9297.
DT   Conference; (Meeting)
     Conference; Abstract; (Meeting Abstract)
     Conference; (Meeting Poster)
LA   English
ED   Entered STN: 5 Dec 2001
     Last Updated on STN: 25 Feb 2002

L4   ANSWER 10 OF 473   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   2001:552622   BIOSIS
DN   PREV200100552622
TI   Gender influences (Ca2+)i during metabolic inhibition in myocytes
     overexpressing the Na+-Ca2+ exchanger.
AU   Sugishita, Kazuro; Su, Zhi; Li, Fenghua; Philipson, Kenneth D.; Barry,
     William H. [Reprint author]
CS   Division of Cardiology, University of Utah Health Sciences Center, 50 N
     Medical Dr, Salt Lake City, UT, 84132, USA
     whbarry@med.utah.edu
SO   Circulation, (October 23, 2001) Vol. 104, No. 17, pp. 2101-2106. print.
     CODEN: CIRCAZ. ISSN: 0009-7322.

AN   2001:441286 BIOSIS
DN   PREV200100441286
TI   A new Na/Ca exchanger splicing pattern identified in situ leads to a
       functionally active 70 kDa NH2-terminal protein.
AU   Van Eylen, F.; Kamagate, A.; Herchuelz, A. [Reprint author]
CS   Laboratoire de Pharmacodynamie et de Therapeutique, Faculte de Medecine,
       Universite Libre de Bruxelles, Route de Lennik, 808, Batiment GE, B-1070,
       Bruxelles, Belgium
       herchu@ulb.ac.be
SO   Cell Calcium, (September, 2001) Vol. 30, No. 3, pp. 191-198. print.
       CODEN: CECADV. ISSN: 0143-4160.
DT   Article
LA   English
ED   Entered STN: 19 Sep 2001
       Last Updated on STN: 22 Feb 2002

AN   2001:384901 BIOSIS
DN   PREV200100384901
TI   Molecular cloning of a third member of the potassium-dependent
         sodium - ***calcium*** ***exchanger*** gene family, NCKX3.
AU   Kraev, Alexander; Quednau, Beate D.; Leach, Stephen; Li, Xiao-Fang; Dong,
       Hui; Winkfein, Robert; Perizzolo, Marco; Cai, Xinjiang; Yang, RuoMei;
       Philipson, Kenneth D.; Lytton, Jonathan [Reprint author]
CS   University of Calgary Health Sciences Center, 3330 Hospital Dr. NW,
       Calgary, AB, T2N 4N1, Canada
       jlytton@ucalgary.ca
SO   Journal of Biological Chemistry, (June 22, 2001) Vol. 276, No. 25, pp.
       23161-23172. print.
       CODEN: JBCHA3. ISSN: 0021-9258.
DT   Article
LA   English
OS   Genbank-AF169257; Genbank-AF288087; Genbank-AF314821; Genbank-AF314822;
       Genbank-AY009158
ED   Entered STN: 15 Aug 2001
       Last Updated on STN: 23 Feb 2002

AN   2001:358275 BIOSIS
DN   PREV200100358275
TI   ***Sodium*** - ***calcium*** ***exchanger*** (NCX-1) and calcium
       modulation: NCX protein expression patterns and regulation of early heart
       development.
AU   Linask, Kersti K. [Reprint author]; Han, Ming-Da; Artman, Michael; Ludwig,
       Cheryl A.
CS   Dept. of Cell Biology, UMDNJ-SOM, 2 Medical Center Drive, Stratford, NJ,
       08084, USA
       linaskkk@umdnj.edu
SO   Developmental Dynamics, (July, 2001) Vol. 221, No. 3, pp. 249-264. print.
       CODEN: DEDYEI. ISSN: 1058-8388.
DT   Article
LA   English
ED   Entered STN: 2 Aug 2001
       Last Updated on STN: 19 Feb 2002

AN   2001:301835 BIOSIS
DN   PREV200100301835
TI   Region specific regulation of sodium pump isoform and Na,Ca-exchanger
       expression in the failing ***human*** heart: Right atrium vs left
       ventricle.
AU   Mueller-Ehmsen, Jochen; Wang, Jiangnan; Schwinger, Robert H. G.;
       McDonough, Alicia A. [Reprint author]
CS   Department of Physiology and Biophysics, University of Southern California
       Keck School of Medicine, 1333 San Pablo Street, Los Angeles, CA, 90033,
       USA
       mcdonoug@hsc.usc.edu
SO   Cellular and Molecular Biology (Noisy-Le-Grand), (March, 2001) Vol. 47,
       No. 2, pp. 373-381. print.
       CODEN: CMBID4. ISSN: 0145-5680.

L4   ANSWER 15 OF 473 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   2001:299602 BIOSIS
DN   PREV200100299602
TI   Targeted inactivation of the   ***sodium*** - ***calcium***
       exchanger   (Ncx1) results in the lack of a heartbeat and abnormal
       myofibrillar organization.
AU   Conway, Simon J. [Reprint author]; Koushik, Srinagesh [Reprint author];
       Wang, Jian [Reprint author]; Rogers, Rhonda [Reprint author]; Creazzo,
       Tony [Reprint author]
CS   Medical College of Georgia, 1120 15th Street, Augusta, GA, 30912, USA
SO   FASEB Journal, (March 7, 2001) Vol. 15, No. 4, pp. A377. print.
       Meeting Info.: Annual Meeting of the Federation of American Societies for
       Experimental Biology on Experimental Biology 2001. Orlando, Florida, USA.
       March 31-April 04, 2001.
       CODEN: FAJOEC. ISSN: 0892-6638.
DT   Conference; (Meeting)
       Conference; Abstract; (Meeting Abstract)
LA   English
ED   Entered STN: 20 Jun 2001
       Last Updated on STN: 19 Feb 2002

L4   ANSWER 16 OF 473 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   2001:290988 BIOSIS
DN   PREV200100290988
TI   Stoichiometry of the retinal cone Na/Ca-K exchanger heterologously
       expressed in insect cells: Comparison with the bovine heart Na/Ca
       exchanger.
AU   Szerencsei, Robert T.; Prinsen, Clemens F. M.; Schnetkamp, Paul P. M.
       [Reprint author]
CS   Department of Physiology and Biophysics, Faculty of Medicine, University
       of Calgary, 3330 Hospital Dr., NW, Calgary, AB, T2N 4N1, Canada
       pschnetk@ucalgary.ca
SO   Biochemistry, (May 22, 2001) Vol. 40, No. 20, pp. 6009-6015. print.
       CODEN: BICHAW. ISSN: 0006-2960.
DT   Article
LA   English
ED   Entered STN: 20 Jun 2001
       Last Updated on STN: 19 Feb 2002

L4   ANSWER 17 OF 473 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   2001:242468 BIOSIS
DN   PREV200100242468
TI   Overexpression of the Na/Ca exchanger and reduced SERCa function.
AU   Terracciano, Cesare M. N. [Reprint author]; MacLeod, Kenneth T.
CS   Department of Cardiac Medicine, National Heart and Lung Institute,
       Imperial College, Dovehouse Street, London, SW3 6LY, UK
SO   Cardiovascular Research, (April, 2001) Vol. 50, No. 1, pp. 167-169. print.
       CODEN: CVREAU. ISSN: 0008-6363.
DT   Letter
LA   English
ED   Entered STN: 16 May 2001
       Last Updated on STN: 19 Feb 2002

L4   ANSWER 18 OF 473 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   2001:189134 BIOSIS
DN   PREV200100189134
TI   NCX1 Na/Ca exchanger splice variants in pancreatic islet cells.
AU   Van Eylen, F.; Bollen, A.; Herchuelz, A. [Reprint author]
CS   Laboratoire de Pharmacodynamie et de Therapeutique, Faculte de Medecine,
       Universite Libre de Bruxelles, Route de Lennik, 808-Batiment GE, B-1070,
       Bruxelles, Belgium
       herchu@ulb.ac.be
SO   Journal of Endocrinology, (March, 2001) Vol. 168, No. 3, pp. 517-526.
       print.
       CODEN: JOENAK. ISSN: 0022-0795.
DT   Article
LA   English
ED   Entered STN: 20 Apr 2001
       Last Updated on STN: 18 Feb 2002

L4   ANSWER 19 OF 473 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN

DN   PREV200100172359
TI   Is Na+Ca2+-exchanger-expression altered parallel to myocardial dysfunction
      in the endomyocardium of patients with valvular heart disease?.
      Original Title: Aendert sich die Na+Ca2+-Exchanger-Expression im
      Endomyokard von Patienten mit chronischen Herzklappenfehlern parallel zur
      Stoerung der myokardialen Pumpfunktion?.
AU   Piper, C. [Reprint author]; Bilger, J.; Henrichs, E.-M.; Wudel, E.;
      Schultheiss, H. P.; Horstkotte, D.; Doerner, A.
CS   Kardiologische Klinik, Herzzentrum Nordrhein-Westfalen, Ruhr-Universitaet
      Bochum, Georgstr. 11, D-32545, Bad Oeynhausen, Germany
      cpiper@hdz.nrw.ruhr-uni-bochum.de
SO   Zeitschrift fuer Kardiologie, (August, 2000) Vol. 89, No. 8, pp. 682-690.
      print.
      CODEN: ZKRDAX. ISSN: 0300-5860.
DT   Article
LA   German
ED   Entered STN: 4 Apr 2001
      Last Updated on STN: 18 Feb 2002

L4   ANSWER 20 OF 473   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   2001:164162   BIOSIS
DN   PREV200100164162
TI   Activation of Na+, K+, Cl--cotransport mediates intracellular Ca2+
      increase and apoptosis induced by Pinacidil in HepG2   ***human***
      hepatoblastoma cells.
AU   Kim, Jung-Ae; Kang, Young Shin; Lee, Yong Soo [Reprint author]
CS   Department of Physiology, College of Medicine, Kwandong University,
      Kangnung, 210-701, South Korea
      yslee@mail.kwandong.ac.kr
SO   Biochemical and Biophysical Research Communications, (February 23, 2001)
      Vol. 281, No. 2, pp. 511-519. print.
      CODEN: BBRCA9. ISSN: 0006-291X.
DT   Article
LA   English
ED   Entered STN: 4 Apr 2001
      Last Updated on STN: 15 Feb 2002

L4   ANSWER 21 OF 473   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   2001:139518   BIOSIS
DN   PREV200100139518
TI   Stoichiometry of the rat brain K-dependent Na/Ca exchanger, NCKX2.
AU   Lytton, Jonathan [Reprint author]; Dong, Hui [Reprint author]
CS   University of Calgary, Calgary, AB, T2N 4N1, Canada
SO   Biophysical Journal, (January, 2001) Vol. 80, No. 1 Part 2, pp. 18a.
      print.
      Meeting Info.: 45th Annual Meeting of the Biophysical Society. Boston,
      Massachusetts, USA. February 17-21, 2001. Biophysical Society.
      CODEN: BIOJAU. ISSN: 0006-3495.
DT   Conference; (Meeting)
      Conference; Abstract; (Meeting Abstract)
LA   English
ED   Entered STN: 21 Mar 2001
      Last Updated on STN: 15 Feb 2002

L4   ANSWER 22 OF 473   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   2001:128287   BIOSIS
DN   PREV200100128287
TI   Altered Ca2+ transport and signal transduction in diabetes mellitus.
AU   Balasubramanyam, M. [Reprint author]; Premanand, C. [Reprint author];
      Mohan, V. [Reprint author]
CS   Madras Diabetes Research Foundation, Chennai, India
SO   Cell Biology International, (2000) Vol. 24, No. 12, pp. 921. print.
      Meeting Info.: 7th International Congress of Cell Biology. Gold Coast,
      Queensland, Australia. September 24-28, 2000. International Federation for
      Cell Biology; Australia and New Zealand Society for Cell and Developmental
      Biology.
      ISSN: 1065-6995.
DT   Conference; (Meeting)
      Conference; Abstract; (Meeting Abstract)
LA   English
ED   Entered STN: 14 Mar 2001
      Last Updated on STN: 15 Feb 2002

L4   ANSWER 23 OF 473   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   2001:124102   BIOSIS

TI   Hiv-1 TAT transgenically targeted to ventricular cardiac myocytes alters
      mitochondrial structure as the mice age.
AU   Raidel, Scott M. [Reprint author]; Haase, Chad P. [Reprint author];
      Samarel, Allen M.; Lewis, William
CS   Emory Univ Sch of Medicine, Atlanta, GA, USA
SO   Circulation, (October 31, 2000) Vol. 102, No. 18 Supplement, pp. II.136.
      print.
      Meeting Info.: Abstracts from American Heart Association Scientific
      Sessions 2000. New Orleans, Louisiana, USA. November 12-15, 2000. American
      Heart Association.
      CODEN: CIRCAZ. ISSN: 0009-7322.
DT   Conference; (Meeting)
      Conference; Abstract; (Meeting Abstract)
LA   English
ED   Entered STN: 7 Mar 2001
      Last Updated on STN: 15 Feb 2002

L4   ANSWER 24 OF 473   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   2001:112282   BIOSIS
DN   PREV200100112282
TI   Does Ca influx during the action potential plateau via reverse-mode Na/Ca
      exchange slow the decay of the Ca transient of failing   ***human***
      myocytes?.
AU   Weisser, Jutta [Reprint author]; Piacentino, Valentino; Margulies, Kenneth
      B.; Houser, Steven R.
CS   Temple Univ Sch of Medicine, Philadelphia, PA, USA
SO   Circulation, (October 31, 2000) Vol. 102, No. 18 Supplement, pp. II.295.
      print.
      Meeting Info.: Abstracts from American Heart Association Scientific
      Sessions 2000. New Orleans, Louisiana, USA. November 12-15, 2000. American
      Heart Association.
      CODEN: CIRCAZ. ISSN: 0009-7322.
DT   Conference; (Meeting)
      Conference; Abstract; (Meeting Abstract)
LA   English
ED   Entered STN: 28 Feb 2001
      Last Updated on STN: 15 Feb 2002

L4   ANSWER 25 OF 473   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   2001:110845   BIOSIS
DN   PREV200100110845
TI   Pharmacological regulation of mitochondrial permeability in cultured
      neuroblastoma cells.
AU   Woollacott, A. J. [Reprint author]; Simpson, P. B. [Reprint author]
CS   MSD, NRC, Terlings Park, Harlow, CM20 2QR, UK
SO   Biochemical Society Transactions, (October, 2000) Vol. 28, No. 5, pp.
      A205. print.
      Meeting Info.: 18th International Congress of Biochemistry and Molecular
      Biology. Birmingham, UK. July 16-20, 2000. International Union of
      Biochemistry and Molecular Biology; Federation of European Biochemical
      Societies; Biochemical Society.
      CODEN: BCSTB5. ISSN: 0300-5127.
DT   Conference; (Meeting)
      Conference; Abstract; (Meeting Abstract)
LA   English
ED   Entered STN: 28 Feb 2001
      Last Updated on STN: 15 Feb 2002

L4   ANSWER 26 OF 473   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   2001:108240   BIOSIS
DN   PREV200100108240
TI   An orphan G-protein coupled receptor with multiple Na+/Ca2+ exchanger
      calcium binding domain repeats: NCGR-1.
AU   Dietrich, P. S. [Reprint author]; Wisotzky, R.; Abel, K.; Johnson, C.;
      Catalano, S. M.; Ilnicka, M.; Sangameswaran, L.
CS   Roche Bioscience, Palo Alto, CA, USA
SO   Society for Neuroscience Abstracts, (2000) Vol. 26, No. 1-2, pp. Abstract
      No.-537.15. print.
      Meeting Info.: 30th Annual Meeting of the Society of Neuroscience. New
      Orleans, LA, USA. November 04-09, 2000. Society for Neuroscience.
      ISSN: 0190-5295.
DT   Conference; (Meeting)
      Conference; Abstract; (Meeting Abstract)
LA   English
ED   Entered STN: 28 Feb 2001

AN   2001:59764   BIOSIS
DN   PREV200100059764
TI   Gene expression analysis by transcriptional profiling in the left
      ventricle of patients pre- and post-LVAD support.
AU   Rodrigue-Way, Amelie C. [Reprint author]; Pollman, Matthew J. [Reprint
      author]; Tang, Nga K. [Reprint author]; Jeyaseelan, Raju [Reprint author];
      Rigotti, Attilio [Reprint author]; Golden, Serge [Reprint author];
      Donoghue, Mary A. [Reprint author]; Houser, Steven R.; Marks, Andrew R.;
      Burkhoff, Daniel; Breitbart, Roger E.; Acton, Susan
CS   Millennium Pharmaceuticals Inc, Cambridge, MA, USA
SO   Circulation, (October 31, 2000) Vol. 102, No. 18 Supplement, pp. II.266.
      print.
      Meeting Info.: Abstracts from American Heart Association Scientific
      Sessions 2000. New Orleans, Louisiana, USA. November 12-15, 2000. American
      Heart Association.
      CODEN: CIRCAZ. ISSN: 0009-7322.
DT   Conference; (Meeting)
      Conference; Abstract; (Meeting Abstract)
LA   English
ED   Entered STN: 31 Jan 2001
      Last Updated on STN: 12 Feb 2002

AN   2000:534982   BIOSIS
DN   PREV200000534982
TI   ***Human***   distal nephron: Distribution of transport proteins.
AU   Lagger, H. [Reprint author]; Arpin-Bott, M. P.; Loffing-Cueni, D. [Reprint
      author]; Loffing, J. [Reprint author]; Knepper, M.; Kaissling, B. [Reprint
      author]
CS   Anatomical Department, University Zurich, Zurich, Switzerland
SO   Kidney and Blood Pressure Research, (2000) Vol. 23, No. 3-5, pp. 222.
      print.
      Meeting Info.: Congress of Nephrology 2000. Vienna, Austria. September
      02-05, 2000. Gesellschaft fuer Nephrologie.
      ISSN: 1420-4096.
DT   Conference; (Meeting)
      Conference; Abstract; (Meeting Abstract)
LA   English
ED   Entered STN: 13 Dec 2000
      Last Updated on STN: 11 Jan 2002

AN   2000:519978   BIOSIS
DN   PREV200000519978
TI   Activation of Na+/Ca2+ exchanger in kinin B1 receptor-stimulated
         human   fibroblast is associated with collagen production.
AU   Romero, Jose R. [Reprint author]; Ricupero, Dennis A.; Rivera, Alicia;
      Goldstein, Ronald H.; Conlin, Paul R.
CS   Brigham and Women's Hosp, Harvard Medical Sch, Boston, MA, USA
SO   Hypertension (Baltimore), (October, 2000) Vol. 36, No. 4, pp. 720. print.
      Meeting Info.: 54th Annual Fall Conference and Scientific Sessions of the
      Council for High Blood Pressure Research. Washington, DC, USA. November
      24-27, 2000.
      CODEN: HPRTDN. ISSN: 0194-911X.
DT   Conference; (Meeting)
      Conference; Abstract; (Meeting Abstract)
      Conference; (Meeting Poster)
LA   English
ED   Entered STN: 29 Nov 2000
      Last Updated on STN: 11 Jan 2002

AN   2000:501794   BIOSIS
DN   PREV200000501915
TI   Increased Na+-Ca2+ exchanger in the failing heart.
AU   Pogwizd, Steven M. [Reprint author]
CS   Department of Medicine, Section of Cardiology, University of Illinois at
      Chicago, 840 S Wood St, Chicago, IL, 60612-7323, USA
SO   Circulation Research, (October 13, 2000) Vol. 87, No. 8, pp. 641-643.
      print.
      CODEN: CIRUAL. ISSN: 0009-7330.
DT   Article
      Editorial

L4   ANSWER 31 OF 473 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   2000:456471 BIOSIS
DN   PREV200000456471
TI   Abnormalities of calcium cycling in the hypertrophied and failing heart.
AU   Houser, Steven R. [Reprint author]; Piacentino, Valentino, III; Weisser,
        Jutta
CS   Temple University School of Medicine, 3400 North Broad Street,
        Philadelphia, PA, 19140, USA
SO   Journal of Molecular and Cellular Cardiology, (September, 2000) Vol. 32,
        No. 9, pp. 1595-1607. print.
        CODEN: JMCDAY. ISSN: 0022-2828.
DT   Article
        General Review; (Literature Review)
LA   English
ED   Entered STN: 25 Oct 2000
        Last Updated on STN: 10 Jan 2002

L4   ANSWER 32 OF 473 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   2000:403066 BIOSIS
DN   PREV200000403066
TI   Calcineurin controls the transcription of Na+/Ca2+ exchanger isoforms in
        developing cerebellar neurons.
AU   Li, Lei; Guerini, Danilo; Carafoli, Ernesto [Reprint author]
CS   Institute of Biochemistry, Swiss Federal Institute of Technology, 8092,
        Zurich, Switzerland
SO   Journal of Biological Chemistry, (July 7, 2000) Vol. 275, No. 27, pp.
        20903-20910. print.
        CODEN: JBCHA3. ISSN: 0021-9258.
DT   Article
LA   English
ED   Entered STN: 20 Sep 2000
        Last Updated on STN: 8 Jan 2002

L4   ANSWER 33 OF 473 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   2000:397751 BIOSIS
DN   PREV200000397751
TI   Quantitative analysis of Na+-Ca2+ exchanger expression in guinea-pig
        heart.
AU   McDonald, Ruth L.; Colyer, John; Harrison, Simon M. [Reprint author]
CS   School of Biomedical Sciences, University of Leeds, Worsley Building,
        Leeds, LS2 9NQ, UK
SO   European Journal of Biochemistry, (August, 2000) Vol. 267, No. 16, pp.
        5142-5148. print.
        CODEN: EJBCAI. ISSN: 0014-2956.
DT   Article
LA   English
ED   Entered STN: 20 Sep 2000
        Last Updated on STN: 8 Jan 2002

L4   ANSWER 34 OF 473 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   2000:361429 BIOSIS
DN   PREV200000361429
TI   Helix packing of the cardiac ***sodium*** - ***calcium***
        exchanger : Proximity of transmembrane segments 2, 3, and 7.
AU   Qiu, Zhiyong [Reprint author]; Nicoll, Debora A. [Reprint author];
        Philipson, Kenneth D. [Reprint author]
CS   Department of Physiology, University of California at Los Angeles, Los
        Angeles, CA, USA
SO   Journal of General Physiology, (July, 2000) Vol. 116, No. 1, pp. 17a.
        print.
        Meeting Info.: Fifty-fourth Annual Meeting of the Society of General
        Physiologists. Woods Hole, Massachusetts, USA. September 07-09, 2000.
        Society of General Physiologists.
        CODEN: JGPLAD. ISSN: 0022-1295.
DT   Conference; (Meeting)
        Conference; Abstract; (Meeting Abstract)
        Conference; (Meeting Poster)
LA   English
ED   Entered STN: 23 Aug 2000
        Last Updated on STN: 8 Jan 2002

L4   ANSWER 35 OF 473 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN

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DN    PREV200000263063
TI    Molecular cloning and functional expression of the potassium-dependent
        ***sodium*** - ***calcium***    ***exchanger*** from    ***human***
      and chicken retinal cone photoreceptors.
AU    Prinsen, Clemens F. M.; Szerencsei, Robert T.; Schnetkamp, Paul P. M.
      [Reprint author]
CS    Faculty of Medicine, University of Calgary, 3330 Hospital Drive N.W.,
      Calgary, AB, T2N 4N1, Canada
SO    Journal of Neuroscience, (Feb. 15, 2000) Vol. 20, No. 4, pp. 1424-1434.
      print.
      CODEN: JNRSDS. ISSN: 0270-6474.
DT    Article
LA    English
ED    Entered STN: 21 Jun 2000
      Last Updated on STN: 5 Jan 2002

L4    ANSWER 36 OF 473  BIOSIS  COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN    2000:181934  BIOSIS
DN    PREV200000181934
TI    Cardiac dysfunction occurs in the HIV-1 transgenic mouse treated with
      zidovudine.
AU    Lewis, William [Reprint author]; Grupp, Ingrid L.; Grupp, Gunter; Hoit,
      Brian; Morris, Randal; Samarel, Allen M.; Bruggeman, Leslie; Klotman, Paul
CS    Department of Pathology, Emory University School of Medicine ML 529, 1639
      Pierce Drive, 7117 Woodruff Memorial Building, Atlanta, GA, 30322, USA
SO    Laboratory Investigation, (Feb., 2000) Vol. 80, No. 2, pp. 187-197. print.
      CODEN: LAINAW. ISSN: 0023-6837.
DT    Article
LA    English
ED    Entered STN: 11 May 2000
      Last Updated on STN: 4 Jan 2002

L4    ANSWER 37 OF 473  BIOSIS  COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN    2000:137081  BIOSIS
DN    PREV200000137081
TI    Functional characterization of a "split" Na+-Ca2+ exchanger.
AU    Ottolia, Michela [Reprint author]; Qiu, Zhiyong [Reprint author];
      Philipson, Kenneth D. [Reprint author]
CS    Dept. of Physiology, UCLA, Los Angeles, CA, USA
SO    Biophysical Journal, (Jan., 2000) Vol. 78, No. 1 Part 2, pp. 54A. print.
      Meeting Info.: 44th Annual Meeting of the Biophysical Society. New
      Orleans, Louisiana, USA. February 12-16, 2000.
      CODEN: BIOJAU. ISSN: 0006-3495.
DT    Conference; (Meeting)
      Conference; Abstract; (Meeting Abstract)
LA    English
ED    Entered STN: 19 Apr 2000
      Last Updated on STN: 4 Jan 2002

L4    ANSWER 38 OF 473  BIOSIS  COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN    2000:24570  BIOSIS
DN    PREV200000024570
TI    Molecular and ultrastructural features of cardiomyopathy occur in AIDS
      transgenic (TG) mice treated with zidovudine.
AU    Lewis, William [Reprint author]; Samarel, Allen M.
CS    Univ of Cincinnati Coll of Medicine, Cincinnati, OH, USA
SO    Circulation, (Nov. 2, 1999) Vol. 100, No. 18 SUPPL., pp. I.269. print.
      Meeting Info.: 72nd Scientific Sessions of the American Heart Association.
      Atlanta, Georgia, USA. November 7-10, 1999.
      CODEN: CIRCAZ. ISSN: 0009-7322.
DT    Conference; (Meeting)
      Conference; Abstract; (Meeting Abstract)
LA    English
ED    Entered STN: 29 Dec 1999
      Last Updated on STN: 31 Dec 2001

L4    ANSWER 39 OF 473  BIOSIS  COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN    1999:494502  BIOSIS
DN    PREV199900494502
TI    Physiological and molecular characterization of the Na+/Ca2+ exchanger in
        ***human***   platelets.
AU    Kimura, Masayuki [Reprint author]; Jeanclos, Elisabeth M.; Donnelly,
      Robert J.; Lytton, Jonathan; Reeves, John P.; Aviv, Abraham
CS    Hypertension Research Center, Univ. of Medicine and Dentistry of New
      Jersey, 185 South Orange Ave., MSB Rm. F-464, Newark, NJ, 07103, USA
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        H911-H917. print.
        CODEN: AJPHAP. ISSN: 0002-9513.
DT      Article
LA      English
ED      Entered STN: 16 Nov 1999
        Last Updated on STN: 16 Nov 1999


L4      ANSWER 40 OF 473   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN      1999:482343   BIOSIS
DN      PREV199900482343
TI      Exposure of N-formyl-L-methionyl-L-leucyl-L-phenylalanine-activated
          ***human***    neutrophils to the Pseudomonas aeruginosa-derived pigment
        1-hydroxyphenazine is associated with impaired calcium efflux and
        potentiation of primary granule enzyme release.
AU      Ramafi, Grace; Anderson, Ronald [Reprint author]; Theron, Annette;
        Feldman, Charles; Taylor, Graham W.; Wilson, Robert; Cole, Peter J.
CS      Institute for Pathology, Pretoria, South Africa
SO      Infection and Immunity, (Oct., 1999) Vol. 67, No. 10, pp. 5157-5162.
        print.
        CODEN: INFIBR. ISSN: 0019-9567.
DT      Article
LA      English
ED      Entered STN: 16 Nov 1999
        Last Updated on STN: 16 Nov 1999


L4      ANSWER 41 OF 473   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN      1999:479932   BIOSIS
DN      PREV199900479932
TI      Quantitative assessment of the myocardial Na+/Ca+2 exchanger transcription
        in inflamed heart tissue.
AU      Doerner, A. [Reprint author]; Bilger, J. [Reprint author]; Piper, C.
        [Reprint author]; Henrichs, E. [Reprint author]; Kuehl, U. [Reprint
        author]; Horstkotte, D. [Reprint author]; Schultheiss, H.-P. [Reprint
        author]
CS      Department of Cardiology, Benjamin Franklin Hospital, Free University of
        Berlin, Berlin, Germany
SO      European Heart Journal, (Aug., 1999) Vol. 20, No. ABSTR. SUPPL., pp. 620.
        print.
        Meeting Info.: XXIst Congress of the European Society of Cardiology.
        Barcelona, Spain. August 28-September 1, 1999. European Society of
        Cardiology.
        CODEN: EHJODF. ISSN: 0195-668X.
DT      Conference; (Meeting)
        Conference; Abstract; (Meeting Abstract)
        Conference; (Meeting Poster)
LA      English
ED      Entered STN: 9 Nov 1999
        Last Updated on STN: 9 Nov 1999

L4      ANSWER 42 OF 473   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN      1999:479608   BIOSIS
DN      PREV199900479608
TI      Regional dependent differences in the activity of the Na+/Ca2+-exchanger
        in   ***human***    non-failing myocardium.
AU      Diedrichs, H. [Reprint author]; Mueller-Ehmsen, J.; Zobel, C. [Reprint
        author]; Mc Donough, A. A.; Schwinger, R. H. G. [Reprint author]
CS      Klinik III fuer Innere Medizin der Universitaet zu Cologne, Cologne,
        Germany
SO      European Heart Journal, (Aug., 1999) Vol. 20, No. ABSTR. SUPPL., pp. 44.
        print.
        Meeting Info.: XXIst Congress of the European Society of Cardiology.
        Barcelona, Spain. August 28-September 1, 1999. European Society of
        Cardiology.
        CODEN: EHJODF. ISSN: 0195-668X.
DT      Conference; (Meeting)
        Conference; Abstract; (Meeting Abstract)
        Conference; (Meeting Poster)
LA      English
ED      Entered STN: 9 Nov 1999
        Last Updated on STN: 9 Nov 1999


L4      ANSWER 43 OF 473   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN      1999:472218   BIOSIS
DN      PREV199900472218
TI      Upregulation of the sarcolemmal Na+/Ca2+-exchanger in patients with
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AU   Schotten, U. [Reprint author]; van Helden, M.; Benke, D.; Stellbrink, C.;
      Schoendube, F.; Hanrath, P.; Allessie, M.
CS   Dept. of Cardiology, University Hospital Aachen, Aachen, Germany
SO   European Heart Journal, (Aug., 1999) Vol. 20, No. ABSTR. SUPPL., pp. 573.
      print.
      Meeting Info.: XXIst Congress of the European Society of Cardiology.
      Barcelona, Spain. August 28-September 1, 1999. European Society of
      Cardiology.
      CODEN: EHJODF. ISSN: 0195-668X.
DT   Conference; (Meeting)
      Conference; Abstract; (Meeting Abstract)
      Conference; (Meeting Poster)
LA   English
ED   Entered STN: 9 Nov 1999
      Last Updated on STN: 9 Nov 1999

L4   ANSWER 44 OF 473   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1999:458986   BIOSIS
DN   PREV199900458986
TI   Elevated plasma norepinephrine levels in endstage heart failure are
      significantly correlated to upregulation of Na+/Ca2+ exchanger protein
      levels.
AU   Schillinger, W. [Reprint author]; Schneider, H.; El-Armouche, A.; Ferrari,
      R.; Hasenfuss, G. [Reprint author]
CS   Kardiologie und Pneumologie, Georg-August-Universitaet Goettingen,
      Goettingen, Germany
SO   European Heart Journal, (Aug., 1999) Vol. 20, No. ABSTR. SUPPL., pp. 323.
      print.
      Meeting Info.: XXIst Congress of the European Society of Cardiology.
      Barcelona, Spain. August 28-September 1, 1999. European Society of
      Cardiology.
      CODEN: EHJODF. ISSN: 0195-668X.
DT   Conference; (Meeting)
      Conference; Abstract; (Meeting Abstract)
      Conference; (Meeting Poster)
LA   English
ED   Entered STN: 1 Nov 1999
      Last Updated on STN: 3 May 2000

L4   ANSWER 45 OF 473   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1999:442974   BIOSIS
DN   PREV199900442974
TI   Truncation of the C terminus of the rat brain Na+-Ca2+ exchanger RBE-1
      (NCX1.4) impairs surface expression of the protein.
AU   Kasir, Judith; Ren, Xiaoyan; Furman, Ian; Rahamimoff, Hannah [Reprint
      author]
CS   Department of Biochemistry, Hebrew University Hadassah Medical School
      Jerusalem, 91120, Jerusalem, Israel
SO   Journal of Biological Chemistry, (Aug. 27, 1999) Vol. 274, No. 35, pp.
      24873-24880. print.
      CODEN: JBCHA3. ISSN: 0021-9258.
DT   Article
LA   English
ED   Entered STN: 26 Oct 1999
      Last Updated on STN: 26 Oct 1999

L4   ANSWER 46 OF 473   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1999:428012   BIOSIS
DN   PREV199900428012
TI   Sodium/calcium exchange contributes to contraction and relaxation in
      failed   ***human***   ventricular myocytes.
AU   Gaughan, John P. [Reprint author]; Furukawa, Satoshi [Reprint author];
      Jeevanandam, Valluvan [Reprint author]; Hefner, Colleen A. [Reprint
      author]; Kubo, Hajime [Reprint author]; Margulies, Kenneth B. [Reprint
      author]; McGowan, Brian S. [Reprint author]; Mattiello, Julian A. [Reprint
      author]; Dipla, Konstantina [Reprint author]; Piacentino, Valentino, III
      [Reprint author]; Li, Siyun [Reprint author]; Houser, Steven R. [Reprint
      author]
CS   Departments of Physiology and Cardio-Thoracic Surgery, Temple University
      School of Medicine, Philadelphia, PA, 19140, USA
SO   American Journal of Physiology, (Aug., 1999) Vol. 277, No. 2 PART 2, pp.
      H714-H724. print.
      CODEN: AJPHAP. ISSN: 0002-9513.
DT   Article
LA   English

L4   ANSWER 47 OF 473   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1999:406435   BIOSIS
DN   PREV199900406435
TI   Changes in Ca2+ transport proteins in   ***human***   atrial fibrillation.
AU   Schotten, Ulrich [Reprint author]; Stellbrink, Christoph; Hanrath, Peter;
      Allessie, Maurits
CS   University Hospital Aachen, Aachen, Germany
SO   Journal of Molecular and Cellular Cardiology, (June, 1999) Vol. 31, No. 6,
      pp. A63. print.
      Meeting Info.: Abstracts of the XXth Meeting of the International Society
      for Heart Research, European Section. Maastricht, The Netherlands. June
      20-30, 1999.
      CODEN: JMCDAY. ISSN: 0022-2828.
DT   Conference; (Meeting)
      Conference; Abstract; (Meeting Abstract)
LA   English
ED   Entered STN: 8 Oct 1999
      Last Updated on STN: 8 Oct 1999

L4   ANSWER 48 OF 473   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1999:376958   BIOSIS
DN   PREV199900376958
TI   Ni2+ transport by the   ***human***   Na+/Ca2+ exchanger expressed in Sf9
      cells.
AU   Egger, M.; Ruknudin, A.; Niggli, E.; Lederer, W. J.; Schulze, D. H.
      [Reprint author]
CS   Dept. of Microbiology and Immunology, University of Maryland, 655 W.
      Baltimore St., Baltimore, MD, 21201, USA
SO   American Journal of Physiology, (May, 1999) Vol. 276, No. 5 PART 1, pp.
      C1184-C1192. print.
      CODEN: AJPHAP. ISSN: 0002-9513.
DT   Article
LA   English
ED   Entered STN: 13 Sep 1999
      Last Updated on STN: 13 Sep 1999

L4   ANSWER 49 OF 473   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1999:305800   BIOSIS
DN   PREV199900305800
TI   C-terminal fragment of Alzheimer's amyloid precursor protein inhibits
      sodium / ***calcium***   ***exchanger***   activity in SK-N-SH
      cell.
AU   Kim, Hye-Sun; Lee, Jun-Ho; Suh, Yoo-Hun [Reprint author]
CS   Department of Pharmacology, College of Medicine and Department of
      Molecular Pharmacology, Neuroscience Research Institute, Seoul National
      University, Seoul, 110-799, South Korea
SO   Neuroreport, (Jan. 18, 1999) Vol. 10, No. 1, pp. 113-116. print.
      CODEN: NERPEZ. ISSN: 0959-4965.
DT   Article
LA   English
ED   Entered STN: 12 Aug 1999
      Last Updated on STN: 12 Aug 1999

L4   ANSWER 50 OF 473   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1999:302785   BIOSIS
DN   PREV199900302785
TI   Gene expression of proteins influencing the calcium homeostasis in
      patients with persistent and paroxysmal atrial fibrillation.
AU   Brundel, Bianca J. J. M.; Van Gelder, Isabelle C. [Reprint author];
      Henning, Robert H.; Tuinenburg, Anton E.; Deelman, Leo E.; Tieleman,
      Robert G.; Grandjean, Jan G.; Van Gilst, Wiek H.; Crijns, Harry J. G. M.
CS   Department of Cardiology, Thoraxcenter, University Hospital Groningen,
      9700 RB, Groningen, Netherlands
SO   Cardiovascular Research, (May, 1999) Vol. 42, No. 2, pp. 443-454. print.
      CODEN: CVREAU. ISSN: 0008-6363.
DT   Article
LA   English
ED   Entered STN: 12 Aug 1999
      Last Updated on STN: 12 Aug 1999

L4   ANSWER 51 OF 473   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1999:289153   BIOSIS
DN   PREV199900289153

AU Su, Zhi; Bridge, John H.B.; Philipson, Kenneth D.; Spitzer, Kenneth W.;
    Barry, William H. [Reprint author]
CS Division of Cardiology, University of Utah Health Sciences Center, 50
    North Medical Drive, Salt Lake City, UT, 84132, USA

AN 1999:266056 BIOSIS
DN PREV199900266056
TI Myocardial dysfunction in donor hearts: A possible etiology.
AU Owen, Virginia J. [Reprint author]; Burton, Paul B. J.; Michel, Martin C.;
    Zolk, Oliver; Boehm, Michael; Pepper, John R.; Barton, Paul J. R.; Yacoub,
    Magdi H.; Harding, Sian E.
CS Cardiothoracic Surgery, National Heart and Lung Institute at Imperial
    College School of Medicine, Dovehouse St, London, SW3 6LY, UK

AN 1999:265910 BIOSIS
DN PREV199900265910
TI Alterations in gene expression of proteins involved in the calcium
    handling in patients with atrial fibrillation.
AU Van Gelder, Isabelle C. [Reprint author]; Brundel, Bianca J. J. M.;
    Henning, Robert H.; Tuinenburg, Anton E.; Tieleman, Robert G.; Deelman,
    Leo; Grandjean, Jan G.; De Kam, Pieter Jan; Van Gilst, Wiek H.; Crijns,
    Harry J. G. M.
CS Department of Cardiology, Thoraxcenter, University Hospital Groningen,
    9700 RB, Groningen, Netherlands

AN 1999:263444 BIOSIS
DN PREV199900263444
TI Na+/Ca2+ exchanger isoforms expressed in cultured   ***human***   retinal
    pigment epithedial cells.
AU Mangini, N. J. [Reprint author]; Chen, W. [Reprint author]; Kennedy, B.
    G.; Wang, Q. [Reprint author]
CS Department of Ophthalmology and Visual Sciences, University Illinois at
    Chicago College of Medicine, Chicago, IL, USA

AN 1999:219115 BIOSIS
DN PREV199900219115
TI A circularized   ***sodium*** - ***calcium***   ***exchanger***   exon
    2 transcript.
AU Li, Xiao-Fang; Lytton, Jonathan [Reprint author]
CS Dept. of Biochemistry and Molecular Biology, University of Calgary Health
    Sciences Centre, 3330 Hospital Dr. NW, Calgary, AB, T2N 4N1, Canada

DT   Article
LA   English
ED   Entered STN: 7 Jun 1999
      Last Updated on STN: 7 Jun 1999

L4   ANSWER 56 OF 473   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1999:217932   BIOSIS
DN   PREV199900217932
TI   Mechanisms of altered excitation-contraction coupling in canine
      tachycardia-induced heart failure, II: Model studies.
AU   Winslow, Raimond L. [Reprint author]; Rice, Jeremy; Jafri, Saleet; Marban,
      Eduardo; O'Rourke, Brian
CS   Department of Biomedical Engineering, Johns Hopkins University School of
      Medicine, 720 Rutland Ave, 411 Traylor Research Bldg, Baltimore, MD,
      21205, USA
SO   Circulation Research, (March 19, 1999) Vol. 84, No. 5, pp. 571-586. print.
      CODEN: CIRUAL. ISSN: 0009-7330.
DT   Article
LA   English
ED   Entered STN: 26 May 1999
      Last Updated on STN: 26 May 1999

L4   ANSWER 57 OF 473   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1999:217931   BIOSIS
DN   PREV199900217931
TI   Mechanisms of altered excitation-contraction coupling in canine
      tachycardia-induced heart failure, I: Experimental studies.
AU   O'Rourke, Brian [Reprint author]; Kass, David A.; Tomaselli, Gordon F.;
      Kaab, Stefan; Tunin, Richard; Marban, Eduardo
CS   Division of Cardiology, Department of Medicine, Johns Hopkins University,
      720 Rutland Avenue, 844 Ross Building, Baltimore, MD, 21205, USA
SO   Circulation Research, (March 19, 1999) Vol. 84, No. 5, pp. 562-570. print.
      CODEN: CIRUAL. ISSN: 0009-7330.
DT   Article
LA   English
ED   Entered STN: 26 May 1999
      Last Updated on STN: 26 May 1999

L4   ANSWER 58 OF 473   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1999:194919   BIOSIS
DN   PREV199900194919
TI   Gene expression of Na/Ca exchanger during development in   ***human***
      fetal heart.
AU   Qu, Y. [Reprint author]; Ghatpande, A. [Reprint author]; El-Sherif, N.
      [Reprint author]; Boutjdir, M. [Reprint author]
CS   V.A. Medical and SUNY/HS Centers, Brooklyn, NY, 11209, USA
SO   Biophysical Journal, (Jan., 1999) Vol. 76, No. 1 PART 2, pp. A300. print.
      Meeting Info.: Forty-third Annual Meeting of the Biophysical Society.
      Baltimore, Maryland, USA. February 13-17, 1999.
      CODEN: BIOJAU. ISSN: 0006-3495.
DT   Conference; (Meeting)
      Conference; Abstract; (Meeting Abstract)
      Conference; (Meeting Poster)
LA   English
ED   Entered STN: 25 May 1999
      Last Updated on STN: 25 May 1999

L4   ANSWER 59 OF 473   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1999:193611   BIOSIS
DN   PREV199900193611
TI   Helix packing of the cardiac Na+-Ca2+ exchanger: Proximity of TMS 3 and
      TMS 8.
AU   Qiu, Z. [Reprint author]; Nicoll, D. A. [Reprint author]; Philipson, K. D.
      [Reprint author]
CS   Dept. of Physiology, UCLA, Los Angeles, CA, USA
SO   Biophysical Journal, (Jan., 1999) Vol. 76, No. 1 PART 2, pp. A252. print.
      Meeting Info.: Forty-third Annual Meeting of the Biophysical Society.
      Baltimore, Maryland, USA. February 13-17, 1999.
      CODEN: BIOJAU. ISSN: 0006-3495.
DT   Conference; (Meeting)
      Conference; Abstract; (Meeting Abstract)
      Conference; (Meeting Poster)
LA   English

L4   ANSWER 60 OF 473 BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1999:192379 BIOSIS
DN   PREV199900192379
TI   Relaxation is a voltage-dependent process in failed   ***human***
      ventricular myocytes.
AU   Gaughan, John P. [Reprint author]; Jeevanandam, Valluvan [Reprint author];
      Houser, Steven R. [Reprint author]
CS   Temple University School of Medicine, 3420 North Broad St., Philadelphia,
      PA, 19140, USA
SO   Biophysical Journal, (Jan., 1999) Vol. 76, No. 1 PART 2, pp. A366. print.
      Meeting Info.: Forty-third Annual Meeting of the Biophysical Society.
      Baltimore, Maryland, USA. February 13-17, 1999.
      CODEN: BIOJAU. ISSN: 0006-3495.
DT   Conference; (Meeting)
      Conference; Abstract; (Meeting Abstract)
      Conference; (Meeting Poster)
LA   English
ED   Entered STN: 5 May 1999
      Last Updated on STN: 5 May 1999

L4   ANSWER 61 OF 473 BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1999:123171 BIOSIS
DN   PREV199900123171
TI   Relationship between Na+-Ca2+-exchanger protein levels and diastolic
      function of failing   ***human***   myocardium.
AU   Hasenfuss, Gerd [Reprint author]; Schillinger, Wolfgang; Lehnart, Stephan
      E.; Preuss, Michael; Pieske, Burkert; Maier, Lars S.; Prestle, Juergen;
      Minami, Kazutomo; Just, Hanjoerg
CS   Universitaet Goettingen, Zentrum Innere Medizin, Abteilung Kardiologie
      Pneumologie, Robert-Koch-Strasse 40, 37075 Goettingen, Germany
SO   Circulation, (Feb. 9, 1999) Vol. 99, No. 5, pp. 641-648. print.
      CODEN: CIRCAZ. ISSN: 0009-7322.
DT   Article
LA   English
ED   Entered STN: 12 Mar 1999
      Last Updated on STN: 12 Mar 1999

L4   ANSWER 62 OF 473 BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1999:123039 BIOSIS
DN   PREV199900123039
TI   Characterization of a (Ca2+)i-dependent current in   ***human***   atrial
      and ventricular cardiomyocytes in the absence of Na+ and K+.
AU   Koester, Olaf F. [Reprint author]; Szigeti, Gyula P.; Beuckelmann, Dirk J.
CS   Dep. Internal Med. III, Univ. Cologne, Joseph-Stetzmann-Strasse 9, 50924
      Cologne, Germany
SO   Cardiovascular Research, (Jan., 1999) Vol. 41, No. 1, pp. 175-187. print.
      CODEN: CVREAU. ISSN: 0008-6363.
DT   Article
LA   English
ED   Entered STN: 12 Mar 1999
      Last Updated on STN: 12 Mar 1999

L4   ANSWER 63 OF 473 BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1999:94560 BIOSIS
DN   PREV199900094560
TI   Sarcoplasmic reticulum proteins in heart failure.
AU   Lehnart, Stephan E.; Schillinger, Wolfgang; Pieske, Burkert; Prestle,
      Jurgen; Just, Hanjorg; Hasenfuss, Gerd [Reprint author]
CS   Abteilung Kardiologie Pneumologie, Univ. Goettingen, Robert-Koch-Str. 40,
      37075 Goettingen, Germany
SO   Johnson, R. G., Jr. [Editor]; Kranias, E. G. [Editor]. Ann. N. Y. Acad.
      Sci., (1998) pp. 220-230. Annals of the New York Academy of Sciences;
      Cardiac sarcoplasmic reticulum function and regulation of contractility.
      print.
      Publisher: New York Academy of Sciences, 2 East 63rd Street, New York, New
      York 10021, USA. Series: Annals of the New York Academy of Sciences.
      Meeting Info.: Conference. Washington, D.C., USA. September 27-30, 1997.
      New York Academy of Sciences.
      CODEN: ANYAA9. ISSN: 0077-8923. ISBN: 1-57331-130-8 (paper), 1-57331-129-4
      (cloth).
DT   Book
      Conference; (Meeting)
      Book; (Book Chapter)

AN   1999:34332 BIOSIS
DN   PREV199900034332
TI   Parameters of lymphocyte Na+-Ca2+ regulation and blood pressure: The
      gender effect.
AU   Horiguchi, Makoto; Kimura, Masayuki; Skurnick, Joan; Aviv, Abraham
      [Reprint author]
CS   Hypertension Res. Cent., Univ. Med. Dent. NJ, New Jersey Med. Sch., 185 S
      Orange Avenue, Room F-464, Newark, NJ 07103, USA
SO   Hypertension (Dallas), (Nov., 1998) Vol. 32, No. 5, pp. 869-874. print.
      CODEN: HPRTDN. ISSN: 0194-911X.
DT   Article
LA   English
ED   Entered STN: 3 Feb 1999
      Last Updated on STN: 3 Feb 1999

AN   1999:14766 BIOSIS
DN   PREV199900014766
TI   Influence of SR Ca2+-ATPase and Na+-Ca2+-exchanger on the force-frequency
      relation.
AU   Schillinger, W.; Lehnart, S. E.; Prestle, J.; Preuss, M.; Pieske, B.;
      Maier, L. S.; Meyer, M.; Just, H.; Hasenfuss, G. [Reprint author]
CS   Universitaetsklin. Goettingen, Zent. Innere Med. Kardiol. Pneumol.,
      Robert-Koch-Str. 40, 37075 Goettingen, Germany
SO   Basic Research in Cardiology, (1998) Vol. 93, No. SUPPL. 1, pp. 38-45.
      print.
      CODEN: BRCAB7. ISSN: 0300-8428.
DT   Article
LA   English
ED   Entered STN: 11 Jan 1999
      Last Updated on STN: 11 Jan 1999

AN   1999:14765 BIOSIS
DN   PREV199900014765
TI   Post-rest contraction amplitude in myocytes from failing   ***human***
      ventricle.
AU   Davia, K.; Harding, S. E. [Reprint author]
CS   Imperial Coll. Sci. Technol. Med., Royal Brompton Campus, Dovehouse St.,
      London SW3 6LY, UK
SO   Basic Research in Cardiology, (1998) Vol. 93, No. SUPPL. 1, pp. 33-37.
      print.
      CODEN: BRCAB7. ISSN: 0300-8428.
DT   Article
LA   English
ED   Entered STN: 11 Jan 1999
      Last Updated on STN: 11 Jan 1999

AN   1998:523863 BIOSIS
DN   PREV199800523863
TI   Decreased protein level and activity of the Na+, K+-ATPase but unchanged
      abundance and activity of the Na+, Ca2+-exchanger in the failing
      human   myocardium.
AU   Mueller-Ehmsen, J. H. [Reprint author]; Diedriches, H. [Reprint author];
      Thompson, C. B.; Wang, J.; Frank, K.; McDonough, A. A.; Schwinger, R. H.
      G. [Reprint author]
CS   Klinik II Innere Medizin Universitaet Koeln, Cologne, Germany
SO   European Heart Journal, (Aug., 1998) Vol. 19, No. ABST. SUPPL., pp. 407.
      print.
      Meeting Info.: XXth Congress of the European Society of Cardiology.
      Vienna, Austria. August 22-26, 1998. European Society of Cardiology.
      CODEN: EHJODF. ISSN: 0195-668X.
DT   Conference; (Meeting)
      Conference; Abstract; (Meeting Abstract)
      Conference; (Meeting Poster)
LA   English
ED   Entered STN: 22 Dec 1998
      Last Updated on STN: 22 Dec 1998

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AN    1998:523860  BIOSIS
DN    PREV199800523860
TI    SR Ca2+-ATPase and Na+ Ca2+-exchange differently contribute to myocardial
      relaxation in end-stage failing compared to nonfailing   ***human***
      myocardium.
AU    Maier, Lars S. [Reprint author]; Bers, Donald M.; Weber, Thomas [Reprint
      author]; Hasenfuss, Gerd [Reprint author]; Pieske, Burket [Reprint author]
CS    Medizinische Klinik III, Albert-Ludwigs-Universitaet, Freiburg, Germany
SO    European Heart Journal, (Aug., 1998) Vol. 19, No. ABST. SUPPL., pp. 406.
      print.
      Meeting Info.: XXth Congress of the European Society of Cardiology.
      Vienna, Austria. August 22-26, 1998. European Society of Cardiology.
      CODEN: EHJODF. ISSN: 0195-668X.
DT    Conference; (Meeting)
      Conference; Abstract; (Meeting Abstract)
      Conference; (Meeting Poster)
LA    English
ED    Entered STN: 22 Dec 1998
      Last Updated on STN: 22 Dec 1998


L4    ANSWER 69 OF 473  BIOSIS  COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN    1998:481956  BIOSIS
DN    PREV199800481956
TI    The effect of high-salt diet intake on muscular exercise ability in young
      Japanese women.
AU    Fukuba, Yoshiyuki [Reprint author]; Makino, Shiho; Takeda, Yuko;
      Kawashima, Junko; Murakami, Haruka; Miura, Akira
CS    Dep. Exercise Sci. Physiol., Sch. Health Sci., Hiroshima Women's Univ.,
      1-1-7 Ujina-higashi, Minami-ku, Hiroshima 734-8558, Japan
SO    Applied Human Science, (July, 1998) Vol. 17, No. 4, pp. 145-148. print.
      ISSN: 1341-3473.
DT    Article
LA    English
ED    Entered STN: 5 Nov 1998
      Last Updated on STN: 5 Nov 1998


L4    ANSWER 70 OF 473  BIOSIS  COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN    1998:420277  BIOSIS
DN    PREV199800420277
TI    SR and Na/Ca exchange contribute to the Cai2+ transient of failing
       ***human***   ventricular myocytes.
AU    Dipla, Konstantina; Jeevanandam, Valluvan; Margulies, Kenneth B.; Houser,
      Steven R.
CS    Dep. Physiol., Temple U. Sch. Med., Philadelphia, PA, USA
SO    Journal of Molecular and Cellular Cardiology, (June, 1998) Vol. 30, No. 6,
      pp. A90. print.
      Meeting Info.: XVI World Congress of the International Society for Heart
      Research: Cardiovascular Biology and Medicine into the 21st Century.
      CODEN: JMCDAY. ISSN: 0022-2828.
DT    Conference; (Meeting)
      Conference; Abstract; (Meeting Abstract)
LA    English
ED    Entered STN: 2 Oct 1998
      Last Updated on STN: 5 Nov 1998


L4    ANSWER 71 OF 473  BIOSIS  COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN    1998:415199  BIOSIS
DN    PREV199800415199
TI    Characterization of the plasma membrane calcium pump in T cells:
      Modulation and memory.
AU    Bautista, Diana M.; Hoth, Markus; Lewis, Ricahrd S.
CS    Dep. Molecular and Cellular Physiol., Stanford Univ., Stanford, CA, USA
SO    Journal of General Physiology, (July, 1998) Vol. 112, No. 1, pp. 22A.
      print.
      Meeting Info.: Fifty-second Annual Meeting of the Society of General
      Physiologists. Woods Hole, Massachusetts, USA. September 10-12, 1998.
      CODEN: JGPLAD. ISSN: 0022-1295.
DT    Conference; (Meeting)
      Conference; Abstract; (Meeting Abstract)
LA    English
ED    Entered STN: 2 Oct 1998
      Last Updated on STN: 2 Oct 1998


L4    ANSWER 72 OF 473  BIOSIS  COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN    1998:387930  BIOSIS
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TI   Summary of studies of changes in vascular reactivity caused by natriuretic
       hormones.
AU   Purdy, R. E. [Reprint author]
CS   Dep. Pharmacol., Univ. Calif. Irvine, Irvine, CA 92697-4625, USA
SO   Clinical and Experimental Hypertension, (July-Aug., 1998) Vol. 20, No.
       5-6, pp. 705-716. print.
       ISSN: 1064-1963.
DT   Article
LA   English
ED   Entered STN: 10 Sep 1998
       Last Updated on STN: 10 Sep 1998

L4   ANSWER 73 OF 473 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1998:350378 BIOSIS
DN   PREV199800350378
TI   AMPA receptor-mediated excitotoxicity in   ***human***   NT2-N neurons
       results from loss of intracellular Ca2+ homeostasis following marked
       elevation of intracellular Na+.
AU   Itoh, Takayuki; Itoh, Aki; Horiuchi, Kazumi; Pleasure, David [Reprint
       author]
CS   Div. Neurol. Res., Child. Hosp. Phila., 34th St. and Civic Cent. Blvd.,
       Philadelphia, PA 19104, USA
SO   Journal of Neurochemistry, (July, 1998) Vol. 71, No. 1, pp. 112-124.
       print.
       CODEN: JONRA9. ISSN: 0022-3042.
DT   Article
LA   English
ED   Entered STN: 13 Aug 1998
       Last Updated on STN: 10 Sep 1998

L4   ANSWER 74 OF 473 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1998:334986 BIOSIS
DN   PREV199800334986
TI   Cloning and sequence analysis of a new, Na/Ca exchanger-related protein
       from   ***human***   heart.
AU   Quednau, B. D.; Philipson, K. D.
CS   Cardiovascular Res. Lab., UCLA Sch. Med., Los Angeles, CA 90095-1760, USA
SO   Biophysical Journal, (Feb., 1998) Vol. 74, No. 2 PART 2, pp. A197. print.
       Meeting Info.: Forty-second Annual Meeting of the Biophysical Society.
       Kansas City, Missouri, USA. February 22-26, 1998.
       CODEN: BIOJAU. ISSN: 0006-3495.
DT   Conference; (Meeting)
       Conference; Abstract; (Meeting Abstract)
       Conference; (Meeting Poster)
LA   English
ED   Entered STN: 12 Aug 1998
       Last Updated on STN: 12 Aug 1998

L4   ANSWER 75 OF 473 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1998:334958 BIOSIS
DN   PREV199800334958
TI   A circularized exon 2 transcript of the Na-Ca exchanger.
AU   Li, X.-F.; Lytton, J.
CS   Dep. Med. Biochem., Univ. Calgary, Calgary, AB T2N 4N1, Canada
SO   Biophysical Journal, (Feb., 1998) Vol. 74, No. 2 PART 2, pp. A193. print.
       Meeting Info.: Forty-second Annual Meeting of the Biophysical Society.
       Kansas City, Missouri, USA. February 22-26, 1998.
       CODEN: BIOJAU. ISSN: 0006-3495.
DT   Conference; (Meeting)
       Conference; Abstract; (Meeting Abstract)
       Conference; (Meeting Poster)
LA   English
ED   Entered STN: 12 Aug 1998
       Last Updated on STN: 10 Sep 1998

L4   ANSWER 76 OF 473 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1998:260790 BIOSIS
DN   PREV199800260790
TI   Membrane topology of the rat brain Na+-Ca2+ exchanger.
AU   Cook, Orna; Low, Walter; Rahamimoff, Hannah [Reprint author]
CS   Dep. Biochem., Hebrew Univ.-Hadassah Med. Sch., Jerusalem, Israel
SO   Biochimica et Biophysica Acta, (April 22, 1998) Vol. 1371, No. 1, pp.
       40-52. print.
       CODEN: BBACAQ. ISSN: 0006-3002.
DT   Article

L4   ANSWER 77 OF 473 BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1998:243845 BIOSIS
DN   PREV199800243845
TI   Immunohistochemical localization of the Na+/Ca2+ exchanger in
      human   retina and RPE.
AU   Loeffler, K. U. [Reprint author]; Chen, W.; Mangini, N. J.
CS   Dep. Ophthalmol., Bonn Univ., Bonn, Germany
SO   IOVS, (March 15, 1998) Vol. 39, No. 4, pp. S1052. print.
      Meeting Info.: Annual Meeting of the Association for Research in Vision
      and Ophthalmology. Fort Lauderdale, Florida, USA. May 10-15, 1998.
      Association for Research in Vision and Ophthalmology.
DT   Conference; (Meeting)
      Conference; Abstract; (Meeting Abstract)
      Conference; (Meeting Poster)
LA   English
ED   Entered STN: 4 Jun 1998
      Last Updated on STN: 4 Jun 1998

L4   ANSWER 78 OF 473 BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1998:224375 BIOSIS
DN   PREV199800224375
TI   Cloning of the multipartite promoter of the   ***sodium***   -
      calcium   ***exchanger***   gene NCX1 and characterization of its
      activity in vascular smooth muscle cells.
AU   Scheller, Timo; Kraev, Alexander; Skinner, Sven; Carafoli, Ernesto
      [Reprint author]
CS   Lab. Biochemistry III, Swiss Federal Inst. Technol., Universitaetsstrasse
      16, CH-8092 Zurich, Switzerland
SO   Journal of Biological Chemistry, (March 27, 1998) Vol. 273, No. 13, pp.
      7643-7649. print.
      CODEN: JBCHA3. ISSN: 0021-9258.
DT   Article
LA   English
OS   Genbank-Y12878; Genbank-Y12885; Genbank-Y13032; Genbank-Y13033;
      Genbank-Y13034; Genbank-Y13035; Genbank-Y13036; Genbank-Y13037
ED   Entered STN: 20 May 1998
      Last Updated on STN: 20 May 1998

L4   ANSWER 79 OF 473 BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1998:202509 BIOSIS
DN   PREV199800202509
TI   Contribution of sodium-calcium exchange to contraction and relaxation in
      developing   ***human***   cardiac myocytes.
AU   Chin, T. [Reprint author]; Morgan, T.; Kasmarek, T.; Chen, Q.; Ward, K.
CS   East Tenn. State Univ., Johnson City, TN 37614, USA
SO   FASEB Journal, (March 20, 1998) Vol. 12, No. 5, pp. A710. print.
      Meeting Info.: Annual Meeting of the Professional Research Scientists on
      Experimental Biology 98, Part II. San Francisco, California, USA. April
      18-22, 1998. Federation of American Societies for Experimental Biology.
      CODEN: FAJOEC. ISSN: 0892-6638.
DT   Conference; (Meeting)
      Conference; Abstract; (Meeting Abstract)
LA   English
ED   Entered STN: 4 May 1998
      Last Updated on STN: 12 Aug 1998

L4   ANSWER 80 OF 473 BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1998:191065 BIOSIS
DN   PREV199800191065
TI   AMPA glutamate receptor-mediated toxicity in NT2-N neurons is primarily
      caused by excessive sodium loading.
AU   Itoh, Takayuki [Reprint author]; Itoh, Aki [Reprint author]; Horiuchi,
      Kazumi; Pleasure, David [Reprint author]
CS   Div. Neurology Res., Children's Hosp.-Phila., Philadelphia, PA 19104, USA
SO   Journal of Neurochemistry, (1998) Vol. 70, No. SUPPL. 1, pp. S13. print.
      Meeting Info.: 29th Annual Meeting of the American Society for
      Neurochemistry. Denver, Colorado, USA. March 7-11, 1998. American Society
      for Neurochemistry.
      CODEN: JONRA9. ISSN: 0022-3042.
DT   Conference; (Meeting)
      Conference; Abstract; (Meeting Abstract)
LA   English

L4   ANSWER 81 OF 473 BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1998:155097 BIOSIS
DN   PREV199800155097
TI   Transoesophageal echocardiographic assessment of cardiac donors -molecular
      and cellular correlates.
AU   Burton, P. B. J.; Owen, V. J.; Tadgkarimi, S.; Harding, S. E.; Yacoub, M.
      H.
CS   NHLI, Imperial Coll., London, UK
SO   Journal of Heart and Lung Transplantation, (Jan., 1998) Vol. 17, No. 1,
      pp. 46. print.
      Meeting Info.: Eighteenth Annual Meeting and Scientific Sessions of the
      International Society for Heart and Lung Transplantation. Chicago,
      Illinois, USA. April 15-18, 1998. International Society for Heart and Lung
      Transplantation.
      ISSN: 1053-2498.
DT   Conference; (Meeting)
      Conference; Abstract; (Meeting Abstract)
LA   English
ED   Entered STN: 31 Mar 1998
      Last Updated on STN: 31 Mar 1998

L4   ANSWER 82 OF 473 BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1998:73451 BIOSIS
DN   PREV199800073451
TI   ***Sodium***   - ***calcium***   ***exchanger***   in cultured
      human   retinal pigment epithelium.
AU   Mangini, Nancy J. [Reprint author]; Haugh-Scheidt, Laura; Valle, Jason E.;
      Cragoe, Edward J., Jr.; Ripps, Harris; Kennedy, Brian G.
CS   UIC, Dep. Ophthalmol. Visual Sci., 1855 W. Taylor St., Chicago, IL 60612,
      USA
SO   Experimental Eye Research, (Dec., 1997) Vol. 65, No. 6, pp. 821-834.
      print.
      CODEN: EXERA6. ISSN: 0014-4835.
DT   Article
LA   English
ED   Entered STN: 24 Feb 1998
      Last Updated on STN: 20 Mar 1998

L4   ANSWER 83 OF 473 BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1998:43653 BIOSIS
DN   PREV199800043653
TI   Correction of PREVIEWS 99606099. Alteration of excitation-contraction
      coupling in the failing   ***human***   heart. Correction of title from
      Calcium handling proteins in the failing   ***human***   heart. Erratum
      published in Basic Research in Cardiology Vol. 92. Iss. 4. 1997. p. 287.
AU   Hasenfuss, G. [Reprint author]; Meyer, M.; Schillinger, W.; Preuss, M.;
      Pieske, B.; Just, H.
CS   Medizinische Klinik III, Univ. Freiburg, Hugstetter Str. 55, 79106
      Freiburg, Germany
SO   Basic Research in Cardiology, (Aug., 1997) Vol. 92, No. 4, pp. 87-93.
      print.
      CODEN: BRCAB7. ISSN: 0300-8428.
DT   Article
      Errata
      Errata
      General Review; (Literature Review)
LA   English
ED   Entered STN: 27 Jan 1998
      Last Updated on STN: 27 Jan 1998

L4   ANSWER 84 OF 473 BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1998:37437 BIOSIS
DN   PREV199800037437
TI   Molecular biology of calcium channels in the cardiovascular system.
AU   Katz, Arnold M. [Reprint author]
CS   Cardiol. Div., Univ. Connecticut Health Cent., 263 Farmington Ave.,
      Farmington, CT 06030-1305, USA
SO   American Journal of Cardiology, (Nov. 6, 1997) Vol. 80, No. 9A, pp.
      17I-22I. print.
      CODEN: AJCDAG. ISSN: 0002-9149.
DT   Article
LA   English
ED   Entered STN: 14 Jan 1998

AN   1998:16162   BIOSIS
DN   PREV199800016162
TI   Frequency-dependent changes in intracellular Na+-concentration in isolated
      human   myocardium.
AU   Maier, Lars S.; Hasenfuss, Gerd; Pieske, Burkert [Reprint author]
CS   Albert Ludwigs Univ., Freiburg, Germany
SO   Circulation, (10/21/97) Vol. 96, No. 8 SUPPL., pp. I178. print.
      Meeting Info.: 70th Scientific Sessions of the American Heart Association.
      Orlando, Florida, USA. November 9-12, 1997.
      CODEN: CIRCAZ. ISSN: 0009-7322.
DT   Conference; (Meeting)
      Conference; Abstract; (Meeting Abstract)
LA   English
ED   Entered STN: 5 Jan 1998
      Last Updated on STN: 24 Feb 1998

AN   1997:480517   BIOSIS
DN   PREV199799779720
TI   Frequency-dependent changes of intracellular Na+-concentration in isolated
      human   myocardium.
AU   Pieske, B. [Reprint author]; Maier, L. [Reprint author]; Minami, K.; Just,
      H. [Reprint author]; Hasenfuss, G. [Reprint author]
CS   Med. Klin. III, Albert-Ludwigs-Univ. Freiburg, Freiburg, Germany
SO   European Heart Journal, (1997) Vol. 18, No. ABSTR. SUPPL., pp. 484.
      Meeting Info.: XIXth Congress of the European Society of Cardiology
      together with the 32nd Annual General Meeting of the Association of
      European Paediatric Cardiologists (AEPC). Stockholm, Sweden. August 24-28,
      1997.
      CODEN: EHJODF. ISSN: 0195-668X.
DT   Conference; (Meeting)
      Conference; Abstract; (Meeting Abstract)
      Conference; (Meeting Poster)
LA   English
ED   Entered STN: 4 Nov 1997
      Last Updated on STN: 10 Dec 1997

AN   1997:467335   BIOSIS
DN   PREV199799766538
TI   ***Human***   brain does not express rat brain   ***sodium***   -
      calcium   ***exchanger***   NCX2 homolog.
AU   Yu, L.; Colvin, R. A.
CS   Program Neurobiol., Dep. Biol. Sci., Ohio Univ. Coll. Osteopathic Med.,
      Athens, OH 45701, USA
SO   Society for Neuroscience Abstracts, (1997) Vol. 23, No. 1-2, pp. 136.
      Meeting Info.: 27th Annual Meeting of the Society for Neuroscience, Part
      1. New Orleans, Louisiana, USA. October 25-30, 1997.
      ISSN: 0190-5295.
DT   Conference; (Meeting)
      Conference; Abstract; (Meeting Abstract)
      Conference; (Meeting Poster)
LA   English
ED   Entered STN: 4 Nov 1997
      Last Updated on STN: 10 Dec 1997

AN   1997:414485   BIOSIS
DN   PREV199799706528
TI   Na+/Ca-2+ exchanger in Drosophila: Cloning, expression and transport
      differences.
AU   Ruknudin, Abdul; Valdivia, Carmen; Kofuji, Paulo; Leiderer, W. J.;
      Schulze, Dan H. [Reprint author]
CS   Dep. Microbiol. Immunol., 655 W. Baltimore St., Baltimore, MD 21201, USA
SO   American Journal of Physiology, (1997) Vol. 273, No. 1 PART 1, pp.
      C257-C265.
      CODEN: AJPHAP. ISSN: 0002-9513.
DT   Article
LA   English
ED   Entered STN: 24 Sep 1997
      Last Updated on STN: 24 Sep 1997

DN PREV199799606099
TI Calcium handling proteins in the failing   ***human***   heart.
AU Hasenfuss, G. [Reprint author]; Meyer, M.; Schillinger, W.; Preuss, M.;
    Pieske, B.; Just, H.
CS Medizinische Klinik III, Univ. Freiburg, Hugstetter Str. 55, 79106
    Freiburg, Germany
SO Basic Research in Cardiology, (1997) Vol. 92, No. SUPPL. 1, pp. 87-93.
    CODEN: BRCAB7. ISSN: 0300-8428.
DT Article
    General Review; (Literature Review)
LA English
ED Entered STN: 26 Jul 1997
    Last Updated on STN: 4 Sep 1997

L4 ANSWER 90 OF 473 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1997:315608 BIOSIS
DN PREV199799606096
TI Expression and function of the cardiac Na+/Ca-2+ exchanger in postnatal
    development of the rat, in experimental-induced cardiac hypertrophy and in
    the failing   ***human***   heart.
AU Studer, R. [Reprint author]; Reinecke, H.; Vetter, R.; Holtz, J.; Drexler,
    H.
CS Hans Reinecke, Helmut Drexler Universitaetsklinik, Innere Medizin III,
    Kardiologie und Angiologie, Breisacher Str. 33, 79106 Freiburg, Germany
SO Basic Research in Cardiology, (1997) Vol. 92, No. SUPPL. 1, pp. 53-58.
    CODEN: BRCAB7. ISSN: 0300-8428.
DT Article
LA English
ED Entered STN: 26 Jul 1997
    Last Updated on STN: 4 Sep 1997

L4 ANSWER 91 OF 473 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1997:255100 BIOSIS
DN PREV199799554303
TI Increase in force of contraction by activation of the Na+/Ca-2+-exchanger
    in   ***human***   myocardium.
AU Mueller-Ehmsen, Jochen; Frank, Konrad; Brixius, Klara; Schwinger, Robert
    H. G. [Reprint author]
CS Klinik III fuer Innere Medizin der Univ. zu Koeln, Joseph-Stelzmann-
    Strasse 9, 50924 Koeln, Germany
SO British Journal of Clinical Pharmacology, (1997) Vol. 43, No. 4, pp.
    399-405.
    CODEN: BCPHBM. ISSN: 0306-5251.
DT Article
LA English
ED Entered STN: 13 Jun 1997
    Last Updated on STN: 9 Jul 1997

L4 ANSWER 92 OF 473 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1997:142474 BIOSIS
DN PREV199799441677
TI Novel functional difference between Drosophila and   ***human***
    Na+/Ca-2+ exchangers.
AU Ruknudin, A. [Reprint author]; Lederer, W. J.; Schulze, D. H. [Reprint
    author]
CS Dep. Microbiol. and Immunol., Univ. Md. at Baltimore, MD 21201, USA
SO Biophysical Journal, (1997) Vol. 72, No. 2 PART 2, pp. A247.
    Meeting Info.: 41st Annual Meeting of the Biophysical Society. New
    Orleans, Louisiana, USA. March 2-6, 1997.
    CODEN: BIOJAU. ISSN: 0006-3495.
DT Conference; (Meeting)
    Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 2 Apr 1997
    Last Updated on STN: 2 May 1997

L4 ANSWER 93 OF 473 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1997:142006 BIOSIS
DN PREV199799441209
TI Ni-2+ uptake mediated by the   ***human***   cardiac Na-Ca exchanger.
AU Egger, M.; Ruknudin, A.; Niggli, E. [Reprint author]; Schuzle, D. H.;
    Lederer, W. J.
CS Dep. Physiol., Univ. Bern, Bern, Switzerland
SO Biophysical Journal, (1997) Vol. 72, No. 2 PART 2, pp. A164.
    Meeting Info.: 41st Annual Meeting of the Biophysical Society. New

DT   Conference; (Meeting)
      Conference; Abstract; (Meeting Abstract)
      Conference; (Meeting Poster)
LA   English
ED   Entered STN: 2 Apr 1997
      Last Updated on STN: 2 May 1997

L4   ANSWER 94 OF 473 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1997:141435 BIOSIS
DN   PREV199799440638
TI   Deletion of the alternatively spliced region of the Na+/Ca-2+ exchanger,
      NCX1, reduces functional activity.
AU   Luo, S. [Reprint author]; Neubauer, C. F.; Ruknudin, A. [Reprint author];
      He, S. [Reprint author]; Lederer, W. J.; Schulze, D. H. [Reprint author]
CS   Univ. Md., Dep. Microbiology Immunology, Baltimore, MD 21201, USA
SO   Biophysical Journal, (1997) Vol. 72, No. 2 PART 2, pp. A64.
      Meeting Info.: 41st Annual Meeting of the Biophysical Society. New
      Orleans, Louisiana, USA. March 2-6, 1997.
      CODEN: BIOJAU. ISSN: 0006-3495.
DT   Conference; (Meeting)
      Conference; Abstract; (Meeting Abstract)
      Conference; (Meeting Poster)
LA   English
ED   Entered STN: 2 Apr 1997
      Last Updated on STN: 2 May 1997

L4   ANSWER 95 OF 473 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1997:83448 BIOSIS
DN   PREV199799375161
TI   The sympathetic nervous system in heart failure: Modulation of cardiac
      function.
AU   Drexler, H.
CS   Med. Hochschule Hannover, Konstanty-Gutschowstr. 8, 30625 Hannover,
      Germany
SO   Zeitschrift fuer Kardiologie, (1996) Vol. 85, No. SUPPL. 6, pp. 247-252.
      CODEN: ZKRDAX. ISSN: 0300-5860.
DT   Article
LA   German
ED   Entered STN: 26 Feb 1997
      Last Updated on STN: 26 Feb 1997

L4   ANSWER 96 OF 473 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1997:72869 BIOSIS
DN   PREV199799372072
TI   Molecular characterization of the   ***human***   airway smooth muscle
      Na+/Ca-2+ exchanger.
AU   Pitt, Anthony [Reprint author]; Knox, Alan J.
CS   Dep. Respiratory Med., City Hosp., Nottingham NG5 1PB, UK
SO   American Journal of Respiratory Cell and Molecular Biology, (1996) Vol.
      15, No. 6, pp. 726-730.
      CODEN: AJRBEL. ISSN: 1044-1549.
DT   Article
LA   English
OS   EMBL-X91815
ED   Entered STN: 11 Feb 1997
      Last Updated on STN: 25 Mar 1997

L4   ANSWER 97 OF 473 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1997:4573 BIOSIS
DN   PREV199799303776
TI   Relationship between diastolic function and protein levels of
      sodium - ***calcium*** - ***exchanger*** in end-stage failing
      human hearts.
AU   Hasenfuss, Gerd; Preuss, Michael; Lehnart, Stephan; Prestle, Juergen;
      Meyer, Markus; Just, Hanjoerg
CS   Univ. Freiburg, Freiburg, Germany
SO   Circulation, (1996) Vol. 94, No. 8 SUPPL., pp. I433.
      Meeting Info.: 69th Scientific Sessions of the American Heart Association.
      New Orleans, Louisiana, USA. November 10-13, 1996.
      CODEN: CIRCAZ. ISSN: 0009-7322.
DT   Conference; (Meeting)
      Conference; Abstract; (Meeting Abstract)
LA   English
ED   Entered STN: 7 Jan 1997

AN   1997:2187 BIOSIS
DN   PREV199799301390
TI   Increased sensitivity of   ***human***   heart to inotropic stimulation
      with Na channel activator or cardiac glycosides associated with decreased
      expression of sodium pump isoforms.
AU   McDonough, Alicia A. [Reprint author]; Wang, Jiangnan; Frank, Konrad;
      Muller-Ehmsen, Jochen; Schwinger, Robert H. G.
CS   Univ. Southern Calif., Los Angeles, CA, USA
SO   Circulation, (1996) Vol. 94, No. 8 SUPPL., pp. I24.
      Meeting Info.: 69th Scientific Sessions of the American Heart Association.
      New Orleans, Louisiana, USA. November 10-13, 1996.
      CODEN: CIRCAZ. ISSN: 0009-7322.
DT   Conference; (Meeting)
      Conference; Abstract; (Meeting Abstract)
LA   English
ED   Entered STN: 7 Jan 1997
      Last Updated on STN: 7 Jan 1997

AN   1996:520901 BIOSIS
DN   PREV199699243257
TI   Distribution and signal transduction of angiotensin II AT-1 and AT-2
      receptors.
AU   Capponi, Alessandro M.
CS   Div. Endocrinol., Univ. Hosp., Rue Micheli-du-Crest 24, CH-1211 Geneva 14,
      Switzerland
SO   Blood Pressure, (1996) Vol. 5, No. SUPPL. 2, pp. 41-46.
      ISSN: 0803-7051.
DT   Article
      General Review; (Literature Review)
LA   English
ED   Entered STN: 22 Nov 1996
      Last Updated on STN: 23 Nov 1996

AN   1996:520830 BIOSIS
DN   PREV199699243186
TI   Regional expression of sodium pump subunit isoforms and Na+-Ca++ exchanger
      in the   ***human***   heart.
AU   Wang, Jiangnan; Schwinger, Robert H. G.; Frank, Konrad; Mueller-Ehmsen,
      Jochen; Martin-Vasallo, Pablo; Pressley, Thomas A.; Xiang, Anny; Erdmann,
      Erland; McDonough, Alicia A. [Reprint author]
CS   Dep. Physiol. Biophysics, Univ. Southern California Sch. Med., 1333 San
      Pablo St., Los Angeles, CA 90033, USA
SO   Journal of Clinical Investigation, (1996) Vol. 98, No. 7, pp. 1650-1658.
      CODEN: JCINAO. ISSN: 0021-9738.
DT   Article
LA   English
ED   Entered STN: 22 Nov 1996
      Last Updated on STN: 23 Jan 1997

AN   1996:508833 BIOSIS
DN   PREV199699231189
TI   The organization of the   ***human***   gene NCX1 encoding the
      sodium - ***calcium***   ***exchanger*** .
AU   Kraev, Alexander; Chumakov, Ilya; Carafoli, Ernesto [Reprint author]
CS   Lab. Biochem. III, Swiss Federal Inst. Technol., Universitaetsstr. 16,
      CH-8092 Zurich, Switzerland
SO   Genomics, (1996) Vol. 37, No. 1, pp. 105-112.
      CODEN: GNMCEP. ISSN: 0888-7543.
DT   Article
LA   English
OS   EMBL-X91213; EMBL-X91214; EMBL-X91215; EMBL-X91216; EMBL-X91217;
      EMBL-X91221; EMBL-X91614; EMBL-X91647; EMBL-X91963; EMBL-X92368;
      Genbank-X91213; Genbank-X91214; Genbank-X91215; Genbank-X91216;
      Genbank-X91217; Genbank-X91221; Genbank-X91614; Genbank-X91647;
      Genbank-X91963; Genbank-X92368
ED   Entered STN: 14 Nov 1996
      Last Updated on STN: 10 Dec 1996

AN   1996:454219 BIOSIS

TI   Hyperventilation induces two vasoconstrictory periods.
AU   Wojtowicz, D. [Reprint author]; Engelmann, L.
CS   Inst. Physiol. II, Univ. Jena, Teichgraben 8, 07743 Jena, Germany
SO   Pfluegers Archiv European Journal of Physiology, (1996) Vol. 432, No. 3
      SUPPL., pp. R132.
      Meeting Info.: Carl-Ludwig-Symposium. Leipzig, Germany. May 18-20, 1995.
      CODEN: PFLABK. ISSN: 0031-6768.
DT   Conference; (Meeting)
      Conference; Abstract; (Meeting Abstract)
LA   English
ED   Entered STN: 7 Oct 1996
      Last Updated on STN: 5 Nov 1996

L4   ANSWER 103 OF 473   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1996:409006   BIOSIS
DN   PREV199699131362
TI   Expression of an active Na+/Ca-2+ exchanger isoform lacking the six
      C-terminal transmembrane segments.
AU   Gabellini, Nadia [Reprint author]; Zatti, Alessandra; Rispoli, Giorgio;
      Navangione, Anacleto; Carafoli, Ernesto
CS   Dipartimento di Chimica Biologica, Univ. degli studi di Padova, Via
      Trieste, 75, I-35121 Padova, Italy
SO   European Journal of Biochemistry, (1996) Vol. 239, No. 3, pp. 897-904.
      CODEN: EJBCAI. ISSN: 0014-2956.
DT   Article
LA   English
ED   Entered STN: 10 Sep 1996
      Last Updated on STN: 10 Sep 1996

L4   ANSWER 104 OF 473   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1996:391960   BIOSIS
DN   PREV199699114316
TI   Molecular biological studies of the cardiac   ***sodium***   -
         calcium   ***exchanger***   .
AU   Kraev, Alexander; Chumakov, Ilya; Carafoli, Ernesto [Reprint author]
CS   Lab. Biochem. III, Swiss Fed. Inst. Technol., Universitatsstr. 16, CH-8092
      Zurich, Switzerland
SO   Hilgemann, D. W. [Editor]; Philipson, K. D. [Editor]; Vassort, G.
      [Editor]. Ann. N. Y. Acad. Sci., (1996) pp. 103-109. Annals of the New
      York Academy of Sciences; Sodium-calcium exchange.
      Publisher: New York Academy of Sciences, 2 East 63rd Street, New York, New
      York 10021, USA. Series: Annals of the New York Academy of Sciences.
      Meeting Info.: Third International Conference. Woods Hole, Massachusetts,
      USA. April 23-26, 1995.
      CODEN: ANYAA9. ISSN: 0077-8923. ISBN: 1-57331-001-8 (paper), 1-57331-000-X
      (cloth).
DT   Book
      Conference; (Meeting)
      Book; (Book Chapter)
      Conference; (Meeting Paper)
LA   English
ED   Entered STN: 3 Sep 1996
      Last Updated on STN: 11 Oct 1996

L4   ANSWER 105 OF 473   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1996:343445   BIOSIS
DN   PREV199699065801
TI   Vascular smooth muscle.
AU   Siegel, G.
CS   Inst. Physiol., Freien Univ. Berlin, Fachbereich Natur
      Sozialwissenschaftliche Grundlagenmedizin Med. Oekol., Arnimallee 22,
      14195 Berlin, Germany
SO   Greger, R. [Editor]; Windhorst, U. [Editor]. (1996) pp. 1941-1964.
      Comprehensive human physiology: From cellular mechanisms to integration,
      Vols. 1 and 2.
      Publisher: Springer-Verlag, Heidelberger Platz 3, D-1000 Berlin, Germany;
      Springer-Verlag New York, Inc., 175 Fifth Avenue, New York, New York
      10010, USA.
      ISBN: 3-540-58109-X.
DT   Book
      Book; (Book Chapter)
LA   English
ED   Entered STN: 5 Aug 1996
      Last Updated on STN: 26 Sep 1996

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AN      1996:343442  BIOSIS
DN      PREV199699065798
TI      Calcium-mediated control of cardiac contractility at the cellular level.
AU      Langer, G. A.
CS      UCLA Sch. Med., Cardiovasc. Res. Lab., Dep. Physiol., Macdonald Res. Lab.
        Build., 675 Circle Dr. S., Los Angeles, CA 90095, USA
SO      Greger, R. [Editor]; Windhorst, U. [Editor]. (1996) pp. 1857-1864.
        Comprehensive human physiology: From cellular mechanisms to integration,
        Vols. 1 and 2.
        Publisher: Springer-Verlag, Heidelberger Platz 3, D-1000 Berlin, Germany;
        Springer-Verlag New York, Inc., 175 Fifth Avenue, New York, New York
        10010, USA.
        ISBN: 3-540-58109-X.
DT      Book
        Book; (Book Chapter)
LA      English
ED      Entered STN: 5 Aug 1996
        Last Updated on STN: 26 Sep 1996

L4      ANSWER 107 OF 473  BIOSIS  COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN      1996:312577  BIOSIS
DN      PREV199699034933
TI      Pathophysiological targets for beta-blocker therapy in congestive heart
        failure.
AU      Just, H.
CS      Med. Universitaetsklin. Freiburg im Breisgau, Abt. Innere Med.
        III/Kardiol., Angiologie, 79016 Freiburg im Breisgau, Hugstetterstr. 55,
        Germany
SO      European Heart Journal, (1996) Vol. 17, No. SUPPL. B, pp. 2-7.
        CODEN: EHJODF. ISSN: 0195-668X.
DT      Article
LA      English
ED      Entered STN: 11 Jul 1996
        Last Updated on STN: 11 Jul 1996

L4      ANSWER 108 OF 473  BIOSIS  COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN      1996:239069  BIOSIS
DN      PREV199698787198
TI      Annexin VI overexpression targeted to heart alters cardiomyocyte function
        in transgenic mice.
AU      Gunteski-Hamblin, Ann-Marie [Reprint author]; Song, Guojie; Walsh, Richard
        A.; Frenzke, Marie; Boivin, Gregory P.; Dorn, Gerald W. Ii; Kaetzel,
        Marcia A.; Horseman, Nelson D.; Dedman, John R.
CS      Mol. Cellular Phaysiol., Univ. Cincinnati, PO Box 670576, Cincinnati, OH
        45267-0576, USA
SO      American Journal of Physiology, (1996) Vol. 270, No. 3 PART 2, pp.
        H1091-H1100.
        CODEN: AJPHAP. ISSN: 0002-9513.
DT      Article
LA      English
ED      Entered STN: 28 May 1996
        Last Updated on STN: 28 May 1996

L4      ANSWER 109 OF 473  BIOSIS  COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN      1996:159600  BIOSIS
DN      PREV199698731735
TI      Aging does not affect steady-state expression of the Na+/Ca-2+ exchanger
        in rat brain.
AU      Colvin, Robert A. [Reprint author]; Walker, Jon P.; Schummers, James;
        Davis, Nancy
CS      Dep. Biol. Sci., Ohio Univ., Athens, OH 45701, USA
SO      Cellular and Molecular Neurobiology, (1996) Vol. 16, No. 1, pp. 11-19.
        CODEN: CMNEDI. ISSN: 0272-4340.
DT      Article
LA      English
ED      Entered STN: 11 Apr 1996
        Last Updated on STN: 11 Apr 1996

L4      ANSWER 110 OF 473  BIOSIS  COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN      1996:141021  BIOSIS
DN      PREV199698713156
TI      Sodium/calcium exchange activities in cultured lymphocyte and monocyte
        cell lines.
AU      Balasubramanyam, M.; Condrescu, M.; Reeves, J. P.; Gardner, J. P.
CS      UMDNJ-New Jersey Med. Sch., Newark, NJ 07103, USA
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DT   Conference; (Meeting)
      Conference; Abstract; (Meeting Abstract)
LA   English
ED   Entered STN: 3 Apr 1996
      Last Updated on STN: 2 May 1996

L4   ANSWER 111 OF 473   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1996:141007 BIOSIS
DN   PREV199698713142
TI   Characterization and expression of the Drosophila Na+/Ca-2+ exchanger cDNA in Xenopus oocytes.
AU   Ruknudin, A. [Reprint author]; Wisel, S.; Valdivia, C.; Kofuji, P.; Lederer, W. J.; Schulze, D. H.
CS   Dep. Microbiol./Immunology, Univ. Maryland Sch. Med., Baltimore, MD 21201, USA
SO   Biophysical Journal, (1996) Vol. 70, No. 2 PART 2, pp. A202.
      Meeting Info.: 40th Annual Meeting of the Biophysical Society. Baltimore, Maryland, USA. February 17-21, 1996.
      CODEN: BIOJAU. ISSN: 0006-3495.
DT   Conference; (Meeting)
      Conference; Abstract; (Meeting Abstract)
LA   English
ED   Entered STN: 3 Apr 1996
      Last Updated on STN: 2 May 1996

L4   ANSWER 112 OF 473   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1996:141000 BIOSIS
DN   PREV199698713135
TI   Functional analysis of the   ***human***   cardiac Na/Ca exchanger expressed in SF9 cells.
AU   Egger, M. [Reprint author]; Lipp, P. [Reprint author]; Schwaller, B.; Lederer, W. J.; Schulze, D. H.; Niggli, E. [Reprint author]
CS   Dep. Physiol., Univ. Bern, Bern, Switzerland
SO   Biophysical Journal, (1996) Vol. 70, No. 2 PART 2, pp. A201.
      Meeting Info.: 40th Annual Meeting of the Biophysical Society. Baltimore, Maryland, USA. February 17-21, 1996.
      CODEN: BIOJAU. ISSN: 0006-3495.
DT   Conference; (Meeting)
      Conference; Abstract; (Meeting Abstract)
LA   English
ED   Entered STN: 3 Apr 1996
      Last Updated on STN: 2 May 1996

L4   ANSWER 113 OF 473   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1996:138802 BIOSIS
DN   PREV199698710937
TI   NA-CA exchange in the chronically infarcted rabbit heart.
AU   Litwin, S. E.
CS   Salt Lake City Veterans Affairs Med. Cent., Salt Lake City, UT, USA
SO   Journal of Investigative Medicine, (1996) Vol. 44, No. 1, pp. 147A.
      Meeting Info.: Meeting of the American Federation for Clinical Research, Western Region. Carmel, California, USA. February 14-17, 1996.
      ISSN: 1081-5589.
DT   Conference; (Meeting)
      Conference; Abstract; (Meeting Abstract)
LA   English
ED   Entered STN: 3 Apr 1996
      Last Updated on STN: 2 May 1996

L4   ANSWER 114 OF 473   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1996:13144 BIOSIS
DN   PREV199698585279
TI   Enhanced expression of the Na+-Ca-2+-exchanger alters the inotropic responsiveness in the failing   ***human***   heart.
AU   Flesch, Markus; Schwinger, Robert H. G.; Puetz, Frank; Suedkamp, Ferdinand; Mueller-Ehmsen, Jochen; Boehm, Michael
CS   Univ. Cologne, Cologne, Germany
SO   Circulation, (1995) Vol. 92, No. 8 SUPPL., pp. I588.
      Meeting Info.: 68th Scientific Session of the American Heart Association. Anaheim, California, USA. November 13-16, 1995.
      CODEN: CIRCAZ. ISSN: 0009-7322.
DT   Conference; (Meeting)

LA   English
ED   Entered STN: 4 Jan 1996
     Last Updated on STN: 28 Feb 1996

L4   ANSWER 115 OF 473   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1996:9799   BIOSIS
DN   PREV199698581934
TI   Enhanced expression of the Na+-Ca+2-2-exchanger and its functional
     relevance in the failing   ***human***   heart.
AU   Flesch, M.; Schwinger, R. H. G.; Mueller-Ehmsen, J.; Suedkarmp, F.; Puetz,
     F.; Boehm, M.
CS   Klinik III, Innere Med., Univ. Koeln, 50924 Koeln, Germany
SO   European Heart Journal, (1995) Vol. 16, No. ABSTR. SUPPL., pp. 458.
     Meeting Info.: XVIIth Congress of the European Society of Cardiology.
     Amsterdam, Netherlands. August 20-24, 1995.
     CODEN: EHJODF. ISSN: 0195-668X.
DT   Conference; (Meeting)
     Conference; Abstract; (Meeting Abstract)
LA   English
ED   Entered STN: 4 Jan 1996
     Last Updated on STN: 28 Feb 1996

L4   ANSWER 116 OF 473   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1995:544905   BIOSIS
DN   PREV199698559205
TI   Calcium transport proteins in the nonfailing and failing heart: Gene
     expression and function.
AU   Wankerl, M. [Reprint author]; Schwartz, K.
CS   INSERM Unite 153, Pavillon Rambuteau, Hopital Pitie-Salpetriere, 47
     Boulevard de l'Hopital, F-75651 Paris Cedex 13, France
SO   Journal of Molecular Medicine (Berlin), (1995) Vol. 73, No. 10, pp.
     487-496.
     ISSN: 0946-2716.
DT   Article
     General Review; (Literature Review)
LA   English
ED   Entered STN: 31 Dec 1995
     Last Updated on STN: 28 Feb 1996

L4   ANSWER 117 OF 473   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1995:463046   BIOSIS
DN   PREV199598477346
TI   Expression of a functionally active   ***human***   renal   ***sodium***
     -   ***calcium***   ***exchanger***   lacking a signal sequence.
AU   Loo, Tip W.; Ho, Cheryl; Clarke, David M. [Reprint author]
CS   Dep. Med., Univ. Toronto, Room 7342, Med. Sci. Build., 1 King's College
     Circle, Toronto, ON M5S 1A8, Canada
SO   Journal of Biological Chemistry, (1995) Vol. 270, No. 33, pp. 19345-19350.
     CODEN: JBCHA3. ISSN: 0021-9258.
DT   Article
LA   English
ED   Entered STN: 27 Oct 1995
     Last Updated on STN: 14 Dec 1995

L4   ANSWER 118 OF 473   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1995:326023   BIOSIS
DN   PREV199598340323
TI   Ca entry via Na/Ca exchange following intracellular store depletion in T
     lymphocytes.
AU   Gardner, Jeffey P. [Reprint author]; Balasubranianyam, M.;
     Rohowsky-Kochan, Christine; Reeves, John R.
CS   Dep. Pediatrics, UMD-New Jersey Med. Sch., Newark, NY 07103, USA
SO   Journal of Cellular Biochemistry Supplement, (1995) Vol. 0, No. 21A, pp.
     70.
     Meeting Info.: Keystone Symposium on Control and Manipulation of the
     Immune Response. Taos, New Mexico, USA. March 16-22, 1995.
     ISSN: 0733-1959.
DT   Conference; (Meeting)
     Conference; Abstract; (Meeting Abstract)
     Conference; (Meeting Poster)
LA   English
ED   Entered STN: 2 Aug 1995
     Last Updated on STN: 13 Sep 1995

L4   ANSWER 119 OF 473   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN

DN   PREV199598256620
TI   The organization of the   ***human***   gene of the   ***sodium***   -
      calcium   ***exchanger***   .
AU   Kraev, A.; Carafoli, E.
CS   Lab. Biochem. III, Swiss Federal Inst. Technol., CH-8092 Zurich,
      Switzerland
SO   Experientia (Basel), (1995) Vol. 51, No. ABSTR., pp. A55.
      Meeting Info.: 27th Annual Meeting of the Swiss Societies for Experimental
      Biology (USGEB/USSBE). Fribourg, Switzerland. March 30-31, 1995.
      CODEN: EXPEAM. ISSN: 0014-4754.
DT   Conference; (Meeting)
      Conference; Abstract; (Meeting Abstract)
LA   English
ED   Entered STN: 9 Jun 1995
      Last Updated on STN: 11 Jul 1995

L4   ANSWER 120 OF 473   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1995:205816   BIOSIS
DN   PREV199598220116
TI   An alternative splicing site modifies the carboxyl-terminal trans-membrane
      domains of the Na+/Ca-2+ exchanger.
AU   Gabellini, Nadia [Reprint author]; Iwata, Tomoko; Carafoli, Ernesto
CS   Dip. Chimica Biol., Univ. Studi Padova, Via Trieste 75, 35121 Padova,
      Italy
SO   Journal of Biological Chemistry, (1995) Vol. 270, No. 12, pp. 6917-6924.
      CODEN: JBCHA3. ISSN: 0021-9258.
DT   Article
LA   English
ED   Entered STN: 23 May 1995
      Last Updated on STN: 23 May 1995

L4   ANSWER 121 OF 473   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1995:203561   BIOSIS
DN   PREV199598217861
TI   Eosin, a Potent Inhibitor of the Plasma Membrane Ca Pump, Does Not Inhibit
      the Cardiac Na-Ca Exchanger.
AU   Gatto, Craig; Hale, Calvin C.; Xu, Wanyan; Milanick, Mark A. [Reprint
      author]
CS   MA415 Med. Sci. Building, Dep. Physiol., Univ. Missouri, Columbia, MO
      65212, USA
SO   Biochemistry, (1995) Vol. 34, No. 3, pp. 965-972.
      CODEN: BICHAW. ISSN: 0006-2960.
DT   Article
LA   English
ED   Entered STN: 23 May 1995
      Last Updated on STN: 9 Jun 1995

L4   ANSWER 122 OF 473   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1995:139802   BIOSIS
DN   PREV199598154102
TI   Alternative splicing modifies the C-terminal transmembrane domains of the
      Na+/Ca-2+ exchanger.
AU   Gabellini, N. [Reprint author]; Iwata, T.; Carafoll, E. [Reprint author]
CS   Dep. Biol. Chem., Univ. Padova, 35121 Padova, Italy
SO   Biophysical Journal, (1995) Vol. 68, No. 2 PART 2, pp. A412.
      Meeting Info.: 39th Annual Meeting of the Biophysical Society. San
      Francisco, California, USA. February 12-16, 1995.
      CODEN: BIOJAU. ISSN: 0006-3495.
DT   Conference; (Meeting)
      Conference; Abstract; (Meeting Abstract)
      Conference; (Meeting Poster)
LA   English
ED   Entered STN: 3 Apr 1995
      Last Updated on STN: 23 May 1995

L4   ANSWER 123 OF 473   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1995:139794   BIOSIS
DN   PREV199598154094
TI   The autoinhibitory regions of the Ca pump (C28) and the Na/Ca exchanger
      (XIP) bind to   ***human***   erythrocyte ankyrin and band 3.
AU   Xu, W.-Y.; Hale, C. C.; Milanick, M. A.
CS   Physiol., Univ. Mo., Columbia, MO 65212, USA
SO   Biophysical Journal, (1995) Vol. 68, No. 2 PART 2, pp. A411.
      Meeting Info.: 39th Annual Meeting of the Biophysical Society. San
      Francisco, California, USA. February 12-16, 1995.

L4   ANSWER 124 OF 473 BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1995:139788 BIOSIS
DN   PREV199598154088
TI   Characterization of the Na/Ca exchanger cDNA in Drosophila.
AU   Valdivia, C. [Reprint author]; Kofuji, P.; Lederer, W. J.; Schulze, D. H.
CS   Dep. Physiol., Univ. Maryland Sch. Med., Baltimore, MD 21201, USA
SO   Biophysical Journal, (1995) Vol. 68, No. 2 PART 2, pp. A410.
        Meeting Info.: 39th Annual Meeting of the Biophysical Society. San
        Francisco, California, USA. February 12-16, 1995.
        CODEN: BIOJAU. ISSN: 0006-3495.
DT   Conference; (Meeting)
        Conference; Abstract; (Meeting Abstract)
        Conference; (Meeting Poster)
LA   English
ED   Entered STN: 3 Apr 1995
        Last Updated on STN: 23 May 1995

L4   ANSWER 125 OF 473 BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1995:129869 BIOSIS
DN   PREV199598144169
TI   Ankyrin-G: A new ankyrin gene with neural-specific isoforms localized at
        the axonal initial segment and node of Ranvier.
AU   Kordeli, Ekaterini; Lambert, Stephen [Reprint author]; Bennett, Vann
CS   Dep. Cell Biol., Duke Univ. Med. Cent., Durham, NC 27710, USA
SO   Journal of Biological Chemistry, (1995) Vol. 270, No. 5, pp. 2352-2359.
        CODEN: JBCHA3. ISSN: 0021-9258.
DT   Article
LA   English
ED   Entered STN: 29 Mar 1995
        Last Updated on STN: 29 Mar 1995

L4   ANSWER 126 OF 473 BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1995:28650 BIOSIS
DN   PREV199598042950
TI   Copper toxicity in cultured   ***human***   skeletal muscle cells: The
        involvement of Na+/K+-ATPase and the Na+/Ca-2+-exchanger.
AU   Benders, Ad A. G. M.; Li, Jie; Lock, Robert A. C.; Bindels, Rene J. M.;
        Bonga, Sjoered E. Wendelaar; Veerkamp, Jacques H. [Reprint author]
CS   Dep. Biochem., Fac. Med., University Nijmegen, PO Box 9101, NL-6500 HB,
        Nijmegen, Netherlands
SO   Pfluegers Archiv European Journal of Physiology, (1994) Vol. 428, No. 5-6,
        pp. 461-467.
        CODEN: PFLABK. ISSN: 0031-6768.
DT   Article
LA   English
ED   Entered STN: 11 Jan 1995
        Last Updated on STN: 23 Feb 1995

L4   ANSWER 127 OF 473 BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1995:12793 BIOSIS
DN   PREV199598027093
TI   Enhanced gene expression and function of the cardiac Na+/Ca-2+-exchanger
        in end-stage   ***human***   heart failure.
AU   Reinecke, H. [Reprint author]; Studer, R. [Reprint author]; Vetter, R.;
        Holtz, J.; Drexler, H. [Reprint author]
CS   Medizinische Klinik III, Univ. Freiburg, Freiburg, Germany
SO   European Heart Journal, (1994) Vol. 15, No. ABSTR. SUPPL., pp. 199.
        Meeting Info.: Joint XIIth World Congress of Cardiology and the XVIth
        Congress of the European Society of Cardiology. Berlin, Germany. September
        10-14, 1994.
        CODEN: EHJODF. ISSN: 0195-668X.
DT   Conference; (Meeting)
        Conference; Abstract; (Meeting Abstract)
        Conference; (Meeting Poster)
LA   English
ED   Entered STN: 5 Jan 1995
        Last Updated on STN: 5 Jan 1995

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AN    1994:424586  BIOSIS
DN    PREV199497437586
TI    The    ***human***    cardiac    ***sodium***  -  ***calcium***
      ***exchanger***    expressed in Sf9 cells.
AU    Niggli, E. [Reprint author]; Lipp, P. [Reprint author]; Kofuji, P.;
      Schulze, D. H.; Lederer, W. J.
CS    Dep. Physiol., Univ. Bern, Bern, Switzerland
SO    Journal of Physiology (Cambridge), (1994) Vol. 477P, No. 0, pp. 17P.
      Meeting Info.: Scientific Meeting of the Physiological Society. Liverpool,
      England, UK. April 11-13, 1994.
      CODEN: JPHYA7. ISSN: 0022-3751.
DT    Conference; (Meeting)
      Conference; Abstract; (Meeting Abstract)
LA    English
ED    Entered STN: 3 Oct 1994
      Last Updated on STN: 10 Nov 1994

L4    ANSWER 129 OF 473  BIOSIS  COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN    1994:420849  BIOSIS
DN    PREV199497433849
TI    Further analysis of the brain Na+/Ca-2+ exchanger in Alzheimer's disease.
AU    Colvin, R. A.; Davis, N.; Wu, A.; Murphy, C. A.; Levengood, J.
CS    Dep. Biol. Sci., Ohio Univ. Coll. Osteopathic Med., Athens, OH 45701, USA
SO    Neurobiology of Aging, (1994) Vol. 15, No. SUPPL. 1, pp. S142-S143.
      Meeting Info.: Fourth International Conference on Alzheimer's Disease and
      Related Disorders. Minneapolis, Minnesota, USA. July 29-August 3, 1994.
      CODEN: NEAGDO. ISSN: 0197-4580.
DT    Conference; (Meeting)
      Conference; Abstract; (Meeting Abstract)
LA    English
ED    Entered STN: 3 Oct 1994
      Last Updated on STN: 4 Oct 1994

L4    ANSWER 130 OF 473  BIOSIS  COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN    1994:345720  BIOSIS
DN    PREV199497358720
TI    Cloning of the NCX2 isoform of the plasma membrane Na+-Ca-2+ exchanger.
AU    Li, Zhaoping; Matsuoka, Satoshi; Hryshko, Larry V.; Nicoll, Debora A.;
      Bersohn, Malcolm M.; Burke, Edmund P.; Lifton, Richard P.; Philipson,
      Kenneth D. [Reprint author]
CS    Cardiovascular Research Lab., MRL 3-645, UCLA Sch. Med., Los Angeles, CA
      90024-1760, USA
SO    Journal of Biological Chemistry, (1994) Vol. 269, No. 26, pp. 17434-17439.
      CODEN: JBCHA3. ISSN: 0021-9258.
DT    Article
LA    English
OS    EMBL-U08141; Genbank-U08141
ED    Entered STN: 8 Aug 1994
      Last Updated on STN: 1 Sep 1994

L4    ANSWER 131 OF 473  BIOSIS  COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN    1994:252520  BIOSIS
DN    PREV199497265520
TI    Cerebral vasospasm and free radicals.
AU    MacDonald, R. Loch [Reprint author]; Weir, Bryce K.
CS    Sect. Neurosurg., MC3026, Univ. Chicago Med. Cent., 5841 S. Maryland Ave.,
      Chicago, IL 60637, USA
SO    Free Radical Biology and Medicine, (1994) Vol. 16, No. 5, pp. 633-643.
      CODEN: FRBMEH. ISSN: 0891-5849.
DT    Article
      General Review; (Literature Review)
LA    English
ED    Entered STN: 8 Jun 1994
      Last Updated on STN: 9 Jun 1994

L4    ANSWER 132 OF 473  BIOSIS  COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN    1994:54008  BIOSIS
DN    PREV199497067008
TI    Changes in the Na+/Ca-2+ exchanger gene expression in aging rat brain and
      in  ***human***  brains with Alzheimer's pathology.
AU    Janapati, V.; Yu, L.; Colvin, R. A.
CS    Dep. Biol. Sci., Ohio Univ. Coll. Osteopathic Med., Athens, OH 45701, USA
SO    Society for Neuroscience Abstracts, (1993) Vol. 19, No. 1-3, pp. 1473.
      Meeting Info.: 23rd Annual Meeting of the Society for Neuroscience.
      Washington, D.C., USA. November 7-12, 1993.
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L4   ANSWER 133 OF 473 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1994:44022 BIOSIS
DN   PREV199497057022
TI   Functional consequences of altered expression of SR-Ca-2+-ATPase and Na
       +-Ca-2+-exchanger in failing   ***human***   myocardium.
AU   Hasenfuss, Gerd; Reinecke, Hans; Studer, Roland; Pieske, Burkert; Holtz,
       Juergen; Holubarsch, Christian; Just, Hanjoerg
CS   Univ. Freiburg, Med. Klinik III, Freiburg, Germany
SO   Circulation, (1993) Vol. 88, No. 4 PART 2, pp. I407.
       Meeting Info.: 66th Scientific Sessions of the American Heart Association.
       Atlanta, Georgia, USA. November 8-11, 1993.
       CODEN: CIRCAZ. ISSN: 0009-7322.
DT   Conference; (Meeting)
       Conference; Abstract; (Meeting Abstract)
LA   English
ED   Entered STN: 3 Feb 1994
       Last Updated on STN: 25 Mar 1994

L4   ANSWER 134 OF 473 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1994:43951 BIOSIS
DN   PREV199497056951
TI   Enhanced expression and function of the cardiac Na+/Ca-2+-exchanger in
       end-stage   ***human***   heart failure.
AU   Reinecke, Hans [Reprint author]; Studer, Roland [Reprint author]; Vetter,
       Roland; Just, Hanjorg [Reprint author]; Holtz, Juergen; Drexler, Helmut
CS   Div. Mol. Cardiol., Med. Clinic III, Univ. Freiburg, Freiburg, Germany
SO   Circulation, (1993) Vol. 88, No. 4 PART 2, pp. I408.
       Meeting Info.: 66th Scientific Sessions of the American Heart Association.
       Atlanta, Georgia, USA. November 8-11, 1993.
       CODEN: CIRCAZ. ISSN: 0009-7322.
DT   Conference; (Meeting)
       Conference; Abstract; (Meeting Abstract)
LA   English
ED   Entered STN: 3 Feb 1994
       Last Updated on STN: 25 Mar 1994

L4   ANSWER 135 OF 473 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1993:519165 BIOSIS
DN   PREV199396132572
TI   Is there a   ***sodium*** - ***calcium***   ***exchanger***   in
       macrophages and in lymphocytes.
AU   Donnadieu, Emmanuel; Trautmann, Alain [Reprint author]
CS   Lab. Neurobiologie, CNRS URA 295, Ecole Normale Superieure, 46 rue d'Ulm,
       F-75005 Paris, France
SO   Pfluegers Archiv European Journal of Physiology, (1993) Vol. 424, No. 5-6,
       pp. 448-455.
       CODEN: PFLABK. ISSN: 0031-6768.
DT   Article
LA   English
ED   Entered STN: 19 Nov 1993
       Last Updated on STN: 13 Jan 1994

L4   ANSWER 136 OF 473 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1993:503074 BIOSIS
DN   PREV199396127081
TI   Regional distribution in the rat central nervous system of a mRNA encoding
       a portion of the cardiac   ***sodium*** - ***calcium***
        exchanger   isolated from cerebellar granule neurons.
AU   Marlier, Lionel N. J.-L.; Zheng, Tian [Reprint author]; Tang, Jian;
       Grayson, Dennis R.
CS   Fidia-Georgetown Inst. Neurosci., Georgetown Univ., 3900 Reservoir Rd. NW,
       Washington, DC 20007, USA
SO   Molecular Brain Research, (1993) Vol. 20, No. 1-2, pp. 21-39.
       CODEN: MBREE4. ISSN: 0169-328X.
DT   Article
LA   English
ED   Entered STN: 5 Nov 1993
       Last Updated on STN: 13 Jan 1994

AN   1993:343079   BIOSIS
DN   PREV199396040079
TI   Mapping of the   ***human***   cardiac   ***sodium***   /   ***calcium***
        exchanger   gene (NCX1) by fluorescent in situ hybridization to
        chromosome region 2p22 fwdarw p23.
AU   McDaniel, L. D.; Lederer, W. J.; Kofuji, P.; Schulze, D. H.; Kieval, R.;
        Schultz, Roger A. [Reprint author]
CS   McDermott Cent., North Campus, Univ. Southwest Med. Cent., 6000 Harry
        Hines Blvd., Room 10.118, Dallas, TX 75235-8591, USA
SO   Cytogenetics and Cell Genetics, (1993) Vol. 63, No. 3, pp. 192-193.
        CODEN: CGCGBR. ISSN: 0301-0171.
DT   Article
LA   English
ED   Entered STN: 26 Jul 1993
        Last Updated on STN: 27 Jul 1993

AN   1993:331828   BIOSIS
DN   PREV199345026553
TI   Expression of the cardiac   ***sodium***   -   ***calcium***   -
        exchanger   by the vaccinia system.
AU   Iwata, T.; Guerini, D.; Carafoli, E.
CS   Lab. Biochem. III, ETH Zurich, Switzerland
SO   Experientia (Basel), (1993) Vol. 49, No. ABSTR., pp. A49.
        Meeting Info.: 25th Annual Meeting of the Swiss Society for Experimental
        Biology. Lausanne, Switzerland. March 25-26, 1993.
        CODEN: EXPEAM. ISSN: 0014-4754.
DT   Conference; (Meeting)
LA   English
ED   Entered STN: 16 Jul 1993
        Last Updated on STN: 31 Aug 1993

AN   1993:295664   BIOSIS
DN   PREV199396013889
TI   Stable expression of the cardiac   ***sodium***   -   ***calcium***
        exchanger   in CHO cells.
AU   Pijuan, Vivian [Reprint author]; Zhuang, Yingxin; Smith, Lucinda; Kroupis,
        Chris; Condrescu, Madalina; Aceto, Joseph F.; Reeves, John P.; Smith,
        Jeffrey Bingham
CS   Dep. Pharmacol., Sch. Med., Univ. Ala., Birmingham, AL 35294, USA
SO   American Journal of Physiology, (1993) Vol. 264, No. 4 PART 1, pp.
        C1066-C1074.
        CODEN: AJPHAP. ISSN: 0002-9513.
DT   Article
LA   English
ED   Entered STN: 23 Jun 1993
        Last Updated on STN: 8 Aug 1993

AN   1993:289456   BIOSIS
DN   PREV199345007581
TI   Myocardial gene expression of   ***sodium***   /   ***calcium***
        exchanger   and sarcoplasmic reticulum calcium-ATPase in
        human   heart failure.
AU   Reinecke, Hans [Reprint author]; Studer, Roland [Reprint author];
        Philipson, Kenneth D.; Bilger, Johannes [Reprint author]; Eschenhagen,
        Thomas; Boehm, Michael; Just, Hanjoerg [Reprint author]; Holtz, Juergen
        [Reprint author]; Drexler, Helmut [Reprint author]
CS   Arbeitsgruppe Mol.-Kardiol. Freiburg, Germany
SO   Circulation, (1992) Vol. 86, No. 4 SUPPL. 1, pp. I860.
        Meeting Info.: 65th Scientific Sessions of the American Heart Association.
        New Orleans, Louisiana, USA. November 16-19, 1992.
        CODEN: CIRCAZ. ISSN: 0009-7322.
DT   Conference; (Meeting)
LA   English
ED   Entered STN: 17 Jun 1993
        Last Updated on STN: 18 Jun 1993

AN   1993:267796   BIOSIS
DN   PREV199344129946
TI   Physiological role of the   ***sodium***   -   ***calcium***
        exchanger   in modulating platelet intracellular calcium and

AU   Li, Yun; Fyfe, Chris; Cragoe, Edward J.; Bose, Ratna
CS   Dep. Pharmacol., Univ. Manitoba, Winnipeg, Can. R3E 0W3, canada
SO   FASEB Journal, (1993) Vol. 7, No. 3-4, pp. A564.
      Meeting Info.: Meeting of the Federation of American Societies for
      Experimental Biology on Experimental Biology '93. New Orleans, Louisiana,
      USA. March 28-April 1, 1993.
      CODEN: FAJOEC. ISSN: 0892-6638.
DT   Conference; (Meeting)
LA   English
ED   Entered STN: 27 May 1993
      Last Updated on STN: 13 Jul 1993

L4   ANSWER 142 OF 473 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1993:251565 BIOSIS
DN   PREV199395130740
TI   Cloning of two isoforms of the rat brain   ***sodium*** - ***calcium***
         exchanger   gene and their functional expression in HeLa cells.
AU   Furman, Ian; Cook, Orna; Kasir, Judith; Rahamimoff, Hannah [Reprint
      author]
CS   Dep. Biochem., Hebrew Univ.-Hadassah Med. Sch., PO Box 1172, Jerusalem
      91010, Israel
SO   FEBS (Federation of European Biochemical Societies) Letters, (1993) Vol.
      319, No. 1-2, pp. 105-109.
      CODEN: FEBLAL. ISSN: 0014-5793.
DT   Article
LA   English
OS   Genbank-X68812; Genbank-X68813
ED   Entered STN: 21 May 1993
      Last Updated on STN: 13 Jul 1993

L4   ANSWER 143 OF 473 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1993:248378 BIOSIS
DN   PREV199395127553
TI   Delineation of the role of a   ***sodium*** ,   ***calcium***
         exchanger   in regulating intracellular calcium in T cells.
AU   Wacholtz, Mary C. [Reprint author]; Cragoe., Edward J., Jr.; Lipsky, Peter
      E.
CS   Harold C. Simmons Arthritis Res. Center, Dep. Internal Med., University
      Texas Southwestern Med. Center Dallas, Dallas, TX 75235, USA
SO   Cellular Immunology, (1993) Vol. 147, No. 1, pp. 95-109.
      CODEN: CLIMB8. ISSN: 0008-8749.
DT   Article
LA   English
ED   Entered STN: 21 May 1993
      Last Updated on STN: 22 May 1993

L4   ANSWER 144 OF 473 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1993:164433 BIOSIS
DN   PREV199395085483
TI   Cloning of the rat heart   ***sodium*** - ***calcium***
         exchanger   and its functional expression in HeLa cells.
AU   Low, Walter; Kasir, Judith; Rahamimoff, Hannah [Reprint author]
CS   Dep. Biochem., Hebrew University-Hadassah Med. Sch., P.O. Box 1172,
      Jerusalem, Israel
SO   FEBS (Federation of European Biochemical Societies) Letters, (1993) Vol.
      316, No. 1, pp. 63-67.
      CODEN: FEBLAL. ISSN: 0014-5793.
DT   Article
LA   English
OS   EMBL-X68191; Genbank-X68191
ED   Entered STN: 31 Mar 1993
      Last Updated on STN: 16 May 1993

L4   ANSWER 145 OF 473 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1993:151597 BIOSIS
DN   PREV199344070397
TI   Rhodopsin and phototransduction.
AU   Hargrave, Paul A.; McDowell, Hugh
CS   Dep. Ophthalmology, Sch. Med., Univ. Fla., Gainesville, Fla. 32610, USA
SO   Friedlander, M. [Editor]; Mueckler, M. [Editor]. Int. Rev. Cytol., (1992)
      pp. 49-97. International Review of Cytology; Molecular biology of
      receptors and transporters: Receptors.
      Publisher: Academic Press, Inc., 1250 Sixth Ave., San Diego, California
      92101, USA; Academic Press Ltd., 14 Belgrave Square, 24-28 Oval Road,
      London NW1 70X, England, UK. Series: International Review of Cytology.

L4   ANSWER 146 OF 473   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1993:137976   BIOSIS
DN   PREV199395070776
TI   Expression of the   ***sodium***   ,   ***calcium***   ***exchanger***
      in a diverse tissues: A study using the cloned   ***human***   cardiac
         sodium   ,   ***calcium***   ***exchanger***   .
AU   Kofuji, Paulo; Hadley, Robert W.; Kieval, Robert S.; Lederer, W. J.
      [Reprint author]; Schulze, Dan H.
CS   Dep. Physiology, Univ. Maryland Sch. Med., 660 W. Redwood Street,
      Baltimore, MD 21201, USA
SO   American Journal of Physiology, (1992) Vol. 263, No. 6 PART 1, pp.
      C1241-C1249.
      CODEN: AJPHAP. ISSN: 0002-9513.
DT   Article
LA   English
OS   Genbank-M96368
ED   Entered STN: 16 Mar 1993
      Last Updated on STN: 16 May 1993

L4   ANSWER 147 OF 473   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1993:24464   BIOSIS
DN   PREV199395012664
TI   Rapid calcium extrusion via the   ***sodium***   ,   ***calcium***
         exchanger   of the   ***human***   platelet.
AU   Valant, Peter A.; Adjei, Philip N.; Haynes, Duncan H.
CS   Dep. Mol. Cellular Pharmacol., University Miami Sch. Med., Miami, Fla.
      33101, USA
SO   Journal of Membrane Biology, (1992) Vol. 130, No. 1, pp. 63-82.
      CODEN: JMBBBO. ISSN: 0022-2631.
DT   Article
LA   English
ED   Entered STN: 23 Dec 1992
      Last Updated on STN: 24 Dec 1992

L4   ANSWER 148 OF 473   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1992:513874   BIOSIS
DN   PREV199243111324; BR43:111324
TI   CALCIUM EXTRUSION BY THE   ***SODIUM***   ***CALCIUM***
         EXCHANGER   OF THE   ***HUMAN***   PLATELET.
AU   HAYNES D H [Reprint author]; VALANT P A; ADJEI P N
CS   DEP MOLECULAR AND CELLULAR PHARMACOL, UNIV MIAMI SCH MED, MIAMI, FLA
      33101, USA
SO   (1991) pp. 592-603. BLAUSTEIN, M. P., R. DIPOLO AND J. P. REEVES (ED.).
      ANNALS OF THE NEW YORK ACADEMY OF SCIENCES, VOL. 639. SODIUM-CALCIUM
      EXCHANGE; SECOND INTERNATIONAL CONFERENCE, BALTIMORE, MARYLAND, USA, APRIL
      7-11, 1991. XIV+671P. NEW YORK ACADEMY OF SCIENCES: NEW YORK, NEW YORK,
      USA. ILLUS.
      Publisher: Series: Annals of the New York Academy of Sciences.
      ISSN: 007-8923. ISBN: 0-89766-694-1(PAPER), 0-89766-693-3(CLOTH).
DT   Book
      Conference; (Meeting)
FS   BR
LA   ENGLISH
ED   Entered STN: 11 Nov 1992
      Last Updated on STN: 24 Dec 1992

L4   ANSWER 149 OF 473   BIOSIS   COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1992:501661   BIOSIS
DN   PREV199294120186; BA94:120186
TI   GENETIC LINKAGE ANALYSIS IN FAMILIAL BENIGN HYPERCALCEMIA USING A
      CANDIDATE GENE STRATEGY I. STUDIES IN FOUR FAMILIES.
AU   HEATH H III [Reprint author]; LEPPERT M F; LIFTON R P; PENNISTON J T;
      EDENS M; JEROMINSKI L; LAAKSO K J; NELSON L; OTTERUD B; ET AL
CS   DIV ENDOCRINOL METABOLISM, UNIV UTAH MED CENT, 4C116 SOM, 50 NORTH MEDICAL
      DRIVE, SALT LAKE CITY, UTAH 84132, USA
SO   Journal of Clinical Endocrinology and Metabolism, (1992) Vol. 75, No. 3,
      pp. 846-851.
      CODEN: JCEMAZ. ISSN: 0021-972X.
DT   Article

AN 1992:494878 BIOSIS
DN PREV199243104078; BR43:104078
TI MOLECULAR FUNCTION OF THE   ***SODIUM***   ***CALCIUM***
    EXCHANGER   GUINEA-PIG RAT AND   ***HUMAN***   .
AU LEDERER W J [Reprint author]; KOFUJI P; SCHULZE D; HADLEY R; KIEVAL R;
    KIBRY M S; NIGGLI E
CS DEP PHYSIOLOGY, UNIV MD SCH MED, 660 W REDWOOD ST, BALTIMORE, MD 21201,
    USA
SO Journal of Molecular and Cellular Cardiology, (1992) Vol. 24, No. SUPPL.
    4, pp. S13.
    Meeting Info.: 2ND INTERNATIONAL SYMPOSIUM ON THE MAMMALIAN MYOCARDIUM:
    BIOCHEMICAL AND PHYSIOLOGICAL MECHANISMS UNDERLYING THE HEARTBEAT, LEEDS,
    ENGLAND, UK, JULY 26-29, 1992. J MOL CELL CARDIOL.
    CODEN: JMCDAY. ISSN: 0022-2828.
DT Conference; (Meeting)
FS BR
LA ENGLISH
ED Entered STN: 3 Nov 1992
    Last Updated on STN: 4 Nov 1992

AN 1992:339615 BIOSIS
DN PREV199243029165; BR43:29165
TI EVIDENCE FOR A BASOLATERAL   ***SODIUM***   ***CALCIUM***
    EXCHANGER   IN PERFUSED   ***HUMAN***   GASTRIC GLANDS USING
    CONFOCAL AND VIDEO IMAGING MICROSCOPY.
AU GEIBEL J [Reprint author]; MODLIN I
CS SURGICAL GASTROINTESTINAL PATHOBIOL RES GROUP, YALE UNIV SCH MED, NEW
    HAVEN, CONN, USA
SO Gastroenterology, (1992) Vol. 102, No. 4 PART 2, pp. A73.
    Meeting Info.: DIGESTIVE DISEASE WEEK AND THE 93RD ANNUAL MEETING OF THE
    AMERICAN GASTROENTEROLOGICAL ASSOCIATION, SAN FRANCISCO, CALIFORNIA, USA,
    MAY 9-15, 1992. GASTROENTEROLOGY.
    CODEN: GASTAB. ISSN: 0016-5085.
DT Conference; (Meeting)
FS BR
LA ENGLISH
ED Entered STN: 16 Jul 1992
    Last Updated on STN: 16 Jul 1992

AN 1992:323583 BIOSIS
DN PREV199294025424; BA94:25424
TI MOLECULAR CLONING AND CHARACTERIZATION OF THE   ***HUMAN***   CARDIAC
    SODIUM   ***CALCIUM***   ***EXCHANGER***   CDNA.
AU KOMURO I [Reprint author]; WENNINGER K E; PHILIPSON K D; IZUMO S
CS MOL MED UNIT, BETH ISRAEL HOSPITAL, BOSTON, MASS 02215, USA
SO Proceedings of the National Academy of Sciences of the United States of
    America, (1992) Vol. 89, No. 10, pp. 4769-4773.
    CODEN: PNASA6. ISSN: 0027-8424.
DT Article
FS BA
LA ENGLISH
ED Entered STN: 11 Jul 1992
    Last Updated on STN: 11 Jul 1992

AN 1992:277239 BIOSIS
DN PREV199294001889; BA94:1889
TI ACTIVATION OF A RELAXATION CASCADE IN ISOLATED CORONARY ARTERIES BY BRIEF
    ELECTRICAL PULSES.
AU KALSNER S [Reprint author]
CS DEP PHYSIOL, CITY UNIV NEW YORK MED SCH, CITY COLL NEW YORK, 138TH ST AND
    CONVENT AVE, NEW YORK, NY 10031, USA
SO Journal of Pharmacology and Experimental Therapeutics, (1992) Vol. 261,
    No. 1, pp. 209-224.
    CODEN: JPETAB. ISSN: 0022-3565.
DT Article
FS BA
LA ENGLISH

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L4    ANSWER 154 OF 473  BIOSIS  COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN    1992:224571  BIOSIS
DN    PREV199242106071; BR42:106071
TI    THE   ***HUMAN***   CARDIAC   ***SODIUM***       ***CALCIUM***
        ***EXCHANGER***   CLONING SEQUENCING AND EXPRESSION.
AU    KOFUJI P [Reprint author]; LEDERER W J; SCHULZE D H
CS    DEP PHARM AND EXP THER, UNIV MD, SCH MED, BALTIMORE, MD 21201, USA
SO    Biophysical Journal, (1992) Vol. 61, No. 2 PART 2, pp. A387.
      Meeting Info.: JOINT ANNUAL MEETING OF THE BIOPHYSICAL SOCIETY AND THE
      AMERICAN SOCIETY FOR BIOCHEMISTRY AND MOLECULAR BIOLOGY, HOUSTON, TEXAS,
      USA, FEBRUARY 9-13, 1992. BIOPHYS J.
      CODEN: BIOJAU. ISSN: 0006-3495.
DT    Conference; (Meeting)
FS    BR
LA    ENGLISH
ED    Entered STN: 5 May 1992
      Last Updated on STN: 6 May 1992


L4    ANSWER 155 OF 473  BIOSIS  COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN    1992:188721  BIOSIS
DN    PREV199293099671; BA93:99671
TI    MAPPING OF THE GENE FOR THE CARDIAC SARCOLEMMAL   ***SODIUM***
        ***CALCIUM***     ***EXCHANGER***   TO   ***HUMAN***   CHROMOSOME
      2P21-P23.
AU    SHIEH B-H [Reprint author]; XIA Y; SPARKES R S; KLISAK I; LUSIS A J;
      NICOLL D A; PHILIPSON K D
CS    DEP MEDICINE, MOLECULAR BIOLOGY INSTITUTE, UNIVERSITY CALIFORNIA, LOS
      ANGELES, CALIF 90024, USA
SO    Genomics, (1992) Vol. 12, No. 3, pp. 616-617.
      CODEN: GNMCEP. ISSN: 0888-7543.
DT    Article
FS    BA
LA    ENGLISH
ED    Entered STN: 13 Apr 1992
      Last Updated on STN: 14 Apr 1992


L4    ANSWER 156 OF 473  BIOSIS  COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN    1992:177148  BIOSIS
DN    PREV199242082148; BR42:82148
TI    THE   ***HUMAN***   CARDIAC   ***SODIUM***       ***CALCIUM***
        ***EXCHANGER***   CLONING SEQUENCING AND EXPRESSION.
AU    KOFUJI P [Reprint author]; LEDERER W J; SCHULZE D H
CS    DEP PHARM EXPER THER, UNIV MD SCH MED, BALTIMORE, MD 21201, USA
SO    FASEB Journal, (1992) Vol. 6, No. 1, pp. A387.
      Meeting Info.: JOINT MEETING OF THE AMERICAN SOCIETY FOR BIOCHEMISTRY AND
      MOLECULAR BIOLOGY/BIOPHYSICAL SOCIETY, HOUSTON, TEXAS, USA, FEBRUARY 9-13,
      1992. FASEB (FED AM SOC EXP BIOL) J.
      CODEN: FAJOEC. ISSN: 0892-6638.
DT    Conference; (Meeting)
FS    BR
LA    ENGLISH
ED    Entered STN: 2 Apr 1992
      Last Updated on STN: 3 Apr 1992


L4    ANSWER 157 OF 473  BIOSIS  COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN    1992:63467  BIOSIS
DN    PREV199242027367; BR42:27367
TI    MOLECULAR CHARACTERIZATION OF THE   ***HUMAN***   CARDIAC   ***SODIUM***
        ***CALCIUM***     ***EXCHANGER***   CDNA.
AU    KOMURO I [Reprint author]; WENNINGER K; PHILIPSON K D; IZUMO S
CS    BETH ISRAEL HOSP, HARVARD MED SCH, BOSTON, MASS, USA
SO    Circulation, (1991) Vol. 84, No. 4 SUPPL. 2, pp. II338.
      Meeting Info.: 64TH SCIENTIFIC SESSIONS OF THE AMERICAN HEART ASSOCIATION,
      ANAHEIM, CALIFORNIA, USA, NOVEMBER 11-14, 1991. CIRCULATION.
      CODEN: CIRCAZ. ISSN: 0009-7322.
DT    Conference; (Meeting)
FS    BR
LA    ENGLISH
ED    Entered STN: 21 Jan 1992
      Last Updated on STN: 21 Jan 1992


L4    ANSWER 158 OF 473  BIOSIS  COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN    1991:493686  BIOSIS
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TI   UNCHANGED EFFECTIVENESS OF THE SODIUM ION CHANNEL-ACTIVATOR BDF AND
      OUABAIN IN TERMINALLY FAILING COMPARED TO NONFAILING   ***HUMAN***
      MYOCARDIUM.
AU   SCHWINGER R H G [Reprint author]; BOEHM M; SCHMIDT U; SCHULZ C; ERDMANN E
CS   MED KLINIK I, KLINIKUM GROSSHADERN, MARCHIONINISTR 15, D-8000 MUENCHEN 70,
      W GER
SO   European Heart Journal, (1991) Vol. 12, No. ABSTR. SUPPL, pp. 54.
      Meeting Info.: ABSTRACTS SELECTED FOR PRESENTATION AT THE XIIITH CONGRESS
      OF THE EUROPEAN SOCIETY OF CARDIOLOGY, AMSTERDAM, NETHERLANDS, AUGUST
      18-22, 1991. EUR HEART J.
      CODEN: EHJODF. ISSN: 0195-668X.
DT   Conference; (Meeting)
FS   BR
LA   ENGLISH
ED   Entered STN: 3 Nov 1991
      Last Updated on STN: 4 Nov 1991

L4   ANSWER 159 OF 473 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1991:330254 BIOSIS
DN   PREV199141026804; BR41:26804
TI   EVIDENCE FOR THE ROLE OF A   ***SODIUM***   ***CALCIUM***
       EXCHANGER   IN GENERATING THE MITOGEN INDUCED CALCIUM SIGNAL IN T
      LYMPHOCYTES.
AU   WACHOLTZ M C [Reprint author]; CRAGOE E J; LIPSKY P E
CS   UNIV TEX SOUTHWESTERN MED CENT, DALLAS, TEX 75235, USA
SO   FASEB Journal, (1991) Vol. 5, No. 5, pp. A1455.
      Meeting Info.: 75TH ANNUAL MEETING OF THE FEDERATION OF AMERICAN SOCIETIES
      FOR EXPERIMENTAL BIOLOGY, ATLANTA, GEORGIA, USA, APRIL 21-25, 1991. FASEB
      (FED AM SOC EXP BIOL) J.
      CODEN: FAJOEC. ISSN: 0892-6638.
DT   Conference; (Meeting)
FS   BR
LA   ENGLISH
ED   Entered STN: 20 Jul 1991
      Last Updated on STN: 20 Jul 1991

L4   ANSWER 160 OF 473 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1991:218091 BIOSIS
DN   PREV199140103926; BR40:103926
TI   EFFECT OF CYCLIC AMP CYCLIC GMP AND PROTEIN KINASE ACTIVATION ON RESTING
      CYTOPLASMIC AND DENSE TUBULAR CALCIUM LEVELS IN THE   ***HUMAN***
      PLATELET.
AU   JOHANSSON J [Reprint author]; TAO J; JY W; HAYNES D H
CS   DEP MOL CELL PHARMACOL, UNIV MIAMI SCH MED, MIAMI, FLA 33101, USA
SO   Biophysical Journal, (1991) Vol. 59, No. 2 PART 2, pp. 336A.
      Meeting Info.: THIRTY-FIFTH ANNUAL MEETING OF THE BIOPHYSICAL SOCIETY, SAN
      FRANCISCO, CALIFORNIA, USA, FEBRUARY 24-28, 1991. BIOPHYS J.
      CODEN: BIOJAU. ISSN: 0006-3495.
DT   Conference; (Meeting)
FS   BR
LA   ENGLISH
ED   Entered STN: 5 May 1991
      Last Updated on STN: 14 Jun 1991

L4   ANSWER 161 OF 473 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1990:519135 BIOSIS
DN   PREV199090136411; BA90:136411
TI   A TETRODOTOXIN AND MANGANESE INSENSITIVE SODIUM CURRENT IN DUCHENNE
      MUSCULAR DYSTROPHY.
AU   BKAILY G [Reprint author]; JASMIN G; TAUTU C; PROCHEK L; YAMAMOTO T;
      SCULPTOREANU A; PEYROW M; JACQUES D
CS   DEP PHYSIOLOGY BIOPHYSICS, FAC MED, UNIVERSITY SHERBROOKE, SHERBROOKE,
      QUEBEC, CANADA J1H 5N4
SO   Muscle and Nerve, (1990) Vol. 13, No. 10, pp. 939-948.
      CODEN: MUNEDE. ISSN: 0148-639X.
DT   Article
FS   BA
LA   ENGLISH
ED   Entered STN: 19 Nov 1990
      Last Updated on STN: 20 Nov 1990

L4   ANSWER 162 OF 473 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1989:128315 BIOSIS
DN   PREV198987062968; BA87:62968
TI   AMILORIDE ANTIARRHYTHMIC AND ELECTROPHYSIOLOGICAL ACTIVITY IN THE DOG.

CS   DEP MED, UNIV CALGARY, HEALTH SCI CENTRE, 3330 HOSPITAL DRIVE NW, CALGARY,
      ALBERTA T2N 4N1, CANADA
SO   Circulation, (1988) Vol. 78, No. 6, pp. 1469-1477.
      CODEN: CIRCAZ. ISSN: 0009-7322.
DT   Article
FS   BA
LA   ENGLISH
ED   Entered STN: 28 Feb 1989
      Last Updated on STN: 28 Feb 1989

L4   ANSWER 163 OF 473 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1986:173060 BIOSIS
DN   PREV198681083476; BA81:83476
TI   INHIBITION OF   ***SODIUM***   -   ***CALCIUM***   ***EXCHANGER***
      ACTIVITY IN CARDIAC AND SKELETAL MUSCLE SARCOLEMMAL VESICLES BY MONOCLONAL
      ANTIBODY 44D-7.
AU   MICHALAK M [Reprint author]; QUACKENBUSH E J; LETARTE M
CS   DIV CARDIOLOGY, HOSPITAL SICK CHILDREN, UNIV TORONTO, TORONTO, ONTARIO,
      CANADA
SO   Journal of Biological Chemistry, (1986) Vol. 261, No. 1, pp. 92-95.
      CODEN: JBCHA3. ISSN: 0021-9258.
DT   Article
FS   BA
LA   ENGLISH
ED   Entered STN: 26 Apr 1986
      Last Updated on STN: 26 Apr 1986

L4   ANSWER 164 OF 473 BIOTECHNO COPYRIGHT 2004 Elsevier Science B.V. on STN
AN   2001:32924645   BIOTECHNO
TI   Identification and characterization of a   ***sodium***   /   ***calcium***
      exchanger , NCX-1, in osteoclasts and its role in bone resorptioɪ
AU   Moonga B.S.; Davidson R.; Sun L.; Adebanjo O.A.; Moser J.; Abedin M.;
      Zaidi N.; Huang C.L.-H.; Zaidi M.
CS   M. Zaidi, Mount Sinai Bone Program, Mount Sinai School of Medicine, One
      Gustave Levy Place, New York, NY 10029, United States.
      E-mail: mone.zaidi@mssm.edu
SO   Biochemical and Biophysical Research Communications, (***2001***),
      283/4 (770-775), 28 reference(s)
      CODEN: BBRCA0 ISSN: 0006-291X
DT   Journal; Article
CY   United States
LA   English
SL   English

L4   ANSWER 165 OF 473 BIOTECHNO COPYRIGHT 2004 Elsevier Science B.V. on STN
AN   2001:32695528   BIOTECHNO
TI   Cardiac   ***sodium*** - ***calcium***   ***exchanger*** : A
      double-edged sword
AU   Conway S.J.; Koushik S.V.
CS   S.J. Conway, Inst. of Molec. Med. and Genetics, Department of Cell
      Biology, Medical College of Georgia, 1120 15th Street, Augusta, GA
      30912-2640, United States.
      E-mail: sconway@mail.mcg.edu
SO   Cardiovascular Research, (***2001***), 51/2 (194-197), 44
      reference(s)
      CODEN: CVREAU ISSN: 0008-6363
PUI S000863630100356X
DT   Journal; Editorial
CY   Netherlands
LA   English

L4   ANSWER 166 OF 473 BIOTECHNO COPYRIGHT 2004 Elsevier Science B.V. on STN
AN   1998:28103285   BIOTECHNO
TI   Molecular cloning of a novel potassium-dependent   ***sodium*** -
      calcium   ***exchanger*** from rat brain
AU   Tsoi M.; Rhee K.-H.; Bungard D.; Li X.-F.; Lee S.-L.; Auer R.N.; Lytton
      J.
CS   J. Lytton, University of Calgary, Department of Medical Biochemistry,
      Health Sciences Centre, 3330 Hospital Dr. NW, Calgary, Alta. T2N 4N1,
      Canada.
      E-mail: jlytton@acs.ucalgary.ca
SO   Journal of Biological Chemistry,   ***(13 FEB 1998)*** , 273/7
      (4155-4162), 45 reference(s)
      CODEN: JBCHA3 ISSN: 0021-9258
DT   Journal; Article

LA   English
SL   English

AN   1996:26194636   BIOTECHNO
TI   Molecular biological studies of the cardiac   ***sodium***   -
        calcium   ***exchanger***
AU   Kraev A.; Chumakov I.; Carafoli E.
CS   Laboratory of Biochemistry III, Swiss Federal Institute Technology,
        Universitatsstrasse 16,CH-8092 Zurich, Switzerland.
SO   Annals of the New York Academy of Sciences, (***1996***   ), 779/-
        (103-109)
        CODEN: ANYAA0   ISSN: 0077-8923
DT   Journal; Conference Article
CY   United States
LA   English
SL   English

AN   1996:26125217   BIOTECHNO
TI   Colocalization of the dihydropyridine receptor, the plasma-membrane
        calcium ATPase isoform 31 and the   ***sodium***   /   ***calcium***
        exchanger   to the junctional-membrane domain of transverse tubule
        of rabbit skeletal muscle
AU   Sacchetto R.; Margreth A.; Pelosi M.; Carafoli E.
CS   Institute of Biochemistry, Swiss Federal Inst Technology (ETH),
        Universitatsstrasse,CH-8092 Zurich, Switzerland.
SO   European Journal of Biochemistry, (***1996***   ), 237/2 (483-488)
        CODEN: EJBCAI   ISSN: 0014-2956
DT   Journal; Article
CY   Germany, Federal Republic of
LA   English
SL   English

AN   1993:23337863   BIOTECHNO
TI   ***Sodium***   /   ***calcium***   ***exchanger***   in heart muscle:
        Molecular biology, cellular function, and its special role in
        excitation-contraction coupling
AU   Schulze D.; Kofuji P.; Hadley R.; Kirby M.S.; Kieval R.S.; Doering A.;
        Niggli E.; Lederer W.J.
CS   Department of Physiology, Univ. of Maryland School of Medicine, 660 W
        Redwood Street,Baltimore, MD 21201, United States.
SO   Cardiovascular Research, (***1993***   ), 27/10 (1726-1734)
        CODEN: CVREAU   ISSN: 0008-6363
DT   Journal; Conference Article
CY   United Kingdom
LA   English
SL   English

AN   1993:23118131   BIOTECHNO
TI   Stable expression of the cardiac   ***sodium***   -   ***calcium***
        exchanger   in CHO cells
AU   Pijuan V.; Zhuang Y.; Smith L.; Kroupis C.; Condrescu M.; Aceto J.F.;
        Reeves J.P.; Smith J.B.
CS   Dept. of Pharmacology, Schools of Medicine and Dentistry, Univ. of
        Alabama,Birmingham, AL 35294, United States.
SO   American Journal of Physiology - Cell Physiology, (***1993***   ), 264/4
        33-4 (C1066-C1074)
        CODEN: AJPCDD   ISSN: 0002-9513
DT   Journal; Article
CY   United States
LA   English
SL   English

AN   2002133747   CANCERLIT
DN   21602175   PubMed ID: 11735260
TI   Regulation of sodium-calcium exchange and mitochondrial energetics by
        Bcl-2 in the heart of transgenic mice.
CM   Comment in: J Mol Cell Cardiol. 2001 Dec;33(12):2079-82
AU   Zhu L; Yu Y; Chua B H; Ho Y S; Kuo T H
CS   Department of Pathology, Wayne State University School of Medicine,
        Detroit, Michigan 48201, USA.

L4   ANSWER 172 OF 473   CANCERLIT on STN
AN   2002110112   CANCERLIT
DN   21412509   PubMed ID: 11521739
TI   The effect of 5'-(N,N-dimethyl)-amiloride on cytotoxic activity of doxorubicin and vincristine in CEM cell lines.
AU   Radvakova I; Mirossay A; Mojzis J; Mirossay L
CS   Department of Pharmacology, Faculty of Medicine, Safarik University, Kosice, Slovak Republic.
SO   PHYSIOLOGICAL RESEARCH,   ***(2001)***   50 (3) 283-7.
      Journal code: 9112413. ISSN: 0862-8408.
CY   Czech Republic
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   MEDLINE; Priority Journals
OS   MEDLINE 2001478657
EM   200201
ED   Entered STN: 20020726
      Last Updated on STN: 20020726

L4   ANSWER 173 OF 473   CANCERLIT on STN
AN   2002039344   CANCERLIT
DN   21284070   PubMed ID: 11392069
TI   Gene therapy: a novel method for the treatment of myocardial ischemia and reperfusion injury--mini-review.
AU   Li F; Hayes J K; Wong K C
CS   Department of Anesthesiology, University of Utah School of Medicine, Salt Lake City, UT 84132, USA.
SO   ACTA ANAESTHESIOLOGICA SINICA,   ***(2000 Dec)***   38 (4) 207-15.   Ref: 73
      Journal code: 9432542. ISSN: 0529-5769.
CY   China (Republic: 1949-)
DT   Journal; Article; (JOURNAL ARTICLE)
      General Review; (REVIEW)
      (REVIEW, TUTORIAL)
LA   English
FS   MEDLINE; Priority Journals
OS   MEDLINE 2001317800
EM   200106
ED   Entered STN: 20020726
      Last Updated on STN: 20020726

L4   ANSWER 174 OF 473   CANCERLIT on STN
AN   2000445576   CANCERLIT
DN   20445576   PubMed ID: 10993480
TI   Inhibitors of Na+/Ca2+ exchanger prevent oxidant-induced intracellular Ca2+ increase and apoptosis in a   ***human***   hepatoma cell line.
AU   Kim J A; Kang Y S; Lee S H; Lee Y S
CS   College of Pharmacy, Yeungnam University, Kyongsan, Korea.
SO   FREE RADICAL RESEARCH,   ***(2000 Sep)***   33 (3) 267-77.
      Journal code: 9423872. ISSN: 1071-5762.
CY   Switzerland
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   MEDLINE; Priority Journals
OS   MEDLINE 2000443390
EM   200101
ED   Entered STN: 20010423
      Last Updated on STN: 20010423

L4   ANSWER 175 OF 473   CANCERLIT on STN
AN   2000380210   CANCERLIT
DN   20380210   PubMed ID: 10908415
TI   Na+/Ca2+ exchanger isoforms of rat odontoblasts and osteoblasts.

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DN    20170162    PubMed ID: 10707889
TI    N(omega)-nitro-L-arginine decreases resting cytosolic [Ca2+] and enhances
      heat stress-induced increase in cytosolic [Ca2+] in   ***human***   colon
      carcinoma T84 cells.
AU    Kiang J G; McClain D E
CS    Department of Cellular Injury, Walter Reed Army Institute of Research,
      Washington, DC 20307-5100, USA.. Dr. Juliann Kiang@WRSMTP-ccmail.army.mil
SO    CHINESE JOURNAL OF PHYSIOLOGY,   ***(1999 Sep 30)***   42 (3) 153-9.
      Journal code: 7804502. ISSN: 0304-4920.
CY    CHINA (REPUBLIC: 1949- )
DT    Journal; Article; (JOURNAL ARTICLE)
LA    English
FS    MEDLINE; Priority Journals
OS    MEDLINE 2000170162
EM    200003
ED    Entered STN: 20000515
      Last Updated on STN: 20000515

L4    ANSWER 180 OF 473   CANCERLIT on STN
AN    1999198954       CANCERLIT
DN    99198954    PubMed ID: 10100855
TI    Unique topology of the internal repeats in the cardiac Na+/Ca2+ exchanger.
AU    Iwamoto T; Nakamura T Y; Pan Y; Uehara A; Imanaga I; Shigekawa M
CS    Department of Molecular Physiology, National Cardiovascular Center
      Research Institute, Suita, Osaka, Japan.
SO    FEBS LETTERS,   ***(1999 Mar 12)***   446 (2-3) 264-8.
      Journal code: 0155157. ISSN: 0014-5793.
CY    Netherlands
DT    Journal; Article; (JOURNAL ARTICLE)
LA    English
FS    MEDLINE; Priority Journals
OS    MEDLINE 1999198954
EM    199904
ED    Entered STN: 19990519
      Last Updated on STN: 19990519

L4    ANSWER 181 OF 473   CANCERLIT on STN
AN    1998281762       CANCERLIT
DN    98281762    PubMed ID: 9620452
TI    TGF-beta1 up-regulates the mRNA for the Na+/Ca2+ exchanger in neonatal rat
      cardiac myocytes.
AU    Carrillo C; Cafferata E G; Genovese J; O'Reilly M; Roberts A B;
      Santa-Coloma T A
CS    Instituto de Investigaciones Bioquimicas Fundacion Campomar, Buenos Aires,
      Argentina.
SO    CELLULAR AND MOLECULAR BIOLOGY,   ***(1998 May)***   44 (3) 543-51.
      Journal code: 9216789. ISSN: 0145-5680.
CY    France
DT    Journal; Article; (JOURNAL ARTICLE)
LA    English
FS    MEDLINE; Priority Journals
OS    MEDLINE 1998281762
EM    199808
ED    Entered STN: 19980910
      Last Updated on STN: 19980910

L4    ANSWER 182 OF 473   CANCERLIT on STN
AN    1998233514       CANCERLIT
DN    98233514    PubMed ID: 9571987
TI    Overexpression of HSP-70 attenuates increases in [Ca2+]i and protects
        ***human***   epidermoid A-431 cells after chemical hypoxia.
AU    Kiang J G; Ding X Z; McClain D E
CS    Department of Clinical Physiology, Walter Reed Army Institute of Research,
      Washington, DC 20307-5100, USA.
SO    TOXICOLOGY AND APPLIED PHARMACOLOGY,   ***(1998 Apr)***   149 (2) 185-94.
      Journal code: 0416575. ISSN: 0041-008X.
CY    United States
DT    Journal; Article; (JOURNAL ARTICLE)
LA    English
FS    MEDLINE; Priority Journals
OS    MEDLINE 1998233514
EM    199805
ED    Entered STN: 19980610
      Last Updated on STN: 19980610
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AN    97182154      CANCERLIT
DN    97182154      PubMed ID: 9030200
TI    Modulation of cytokine production by   ***human***   mononuclear cells
      following impairment of Na, K-ATPase activity.
AU    Foey A D; Crawford A; Hall N D
CS    School of Pharmacy and Pharmacology, University of Bath. Bath Institute
      for Rheumatic Diseases, UK.
SO    BIOCHIMICA ET BIOPHYSICA ACTA,   ***(1997 Jan 10)***   1355 (1) 43-9.
      Journal code: 0217513. ISSN: 0006-3002.
CY    Netherlands
DT    Journal; Article; (JOURNAL ARTICLE)
LA    English
FS    MEDLINE; Priority Journals
OS    MEDLINE 97182154
EM    199703
ED    Entered STN: 19970409
      Last Updated on STN: 19970409


L4    ANSWER 184 OF 473   CANCERLIT on STN
AN    97175638      CANCERLIT
DN    97175638      PubMed ID: 9023293
TI    Nitrous oxide enhances Na+/Ca++ exchange in the neuroblastoma cell line
      SK-N-SH.
AU    Resendes M C; Kalogeros G C; Dixon S J; Philp R B
CS    Department of Pharmacology, The University of Western Ontario, London,
      Canada.
SO    JOURNAL OF PHARMACOLOGY AND EXPERIMENTAL THERAPEUTICS,   ***(1997 Feb)***
      280 (2) 795-801.
      Journal code: 0376362. ISSN: 0022-3565.
CY    United States
DT    Journal; Article; (JOURNAL ARTICLE)
LA    English
FS    MEDLINE; Priority Journals
OS    MEDLINE 97175638
EM    199703
ED    Entered STN: 19970409
      Last Updated on STN: 19970509


L4    ANSWER 185 OF 473   CANCERLIT on STN
AN    97073026      CANCERLIT
DN    97073026      PubMed ID: 8915774
TI    Na+/Ca2+ exchange in rat osteoblast-like UMR 106 cells.
AU    White K E; Gesek F A; Friedman P A
CS    Department of Pharmacology and Toxicology, Dartmouth Medical School,
      Hanover, New Hampshire, USA.
NC    R01 ES-05860 (NIEHS)
      R01 GM-34399 (NIGMS)
      T32 DK-07301 (NIDDK)
SO    JOURNAL OF BONE AND MINERAL RESEARCH,   ***(1996 Nov)***   11 (11)
      1666-75.
      Journal code: 8610640. ISSN: 0884-0431.
CY    United States
DT    Journal; Article; (JOURNAL ARTICLE)
LA    English
FS    MEDLINE; Priority Journals
OS    MEDLINE 97073026
EM    199703
ED    Entered STN: 19970409
      Last Updated on STN: 19970509


L4    ANSWER 186 OF 473   CANCERLIT on STN
AN    96250115      CANCERLIT
DN    96250115      PubMed ID: 8659866
TI    Na-Ca exchange in circulating blood cells.
AU    Gardner J P; Balasubramanyam M
CS    Department of Pediatrics, University of Medicine and Dentistry-New Jersey
      Medical School, Newark 07103, USA.
SO    ANNALS OF THE NEW YORK ACADEMY OF SCIENCES,   ***(1996 Apr 15)***   779
      502-14.  Ref: 27
      Journal code: 7506858. ISSN: 0077-8923.
CY    United States
DT    Journal; Article; (JOURNAL ARTICLE)
      General Review; (REVIEW)
      (REVIEW, TUTORIAL)
LA    English
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L4   ANSWER 187 OF 473   CANCERLIT on STN
AN   95370232   CANCERLIT
DN   95370232   PubMed ID: 7642578
TI   The putative amino-terminal signal peptide of the cloned rat brain
      Na(+)-Ca2+ exchanger gene (RBE-1) is not mandatory for functional
      expression.
AU   Furman I; Cook O; Kasir J; Low W; Rahamimoff H
CS   Department of Biochemistry, Hebrew University-Hadassah Medical School,
      Jerusalem, Israel.
SO   JOURNAL OF BIOLOGICAL CHEMISTRY,   ***(1995 Aug 11)***   270 (32) 19120-7.
      Journal code: 2985121R. ISSN: 0021-9258.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   MEDLINE; Priority Journals
OS   MEDLINE 95370232; GENBANK-X68812
EM   199509
ED   Entered STN: 19951012
      Last Updated on STN: 19970509

L4   ANSWER 188 OF 473   CANCERLIT on STN
AN   95030379   CANCERLIT
DN   95030379   PubMed ID: 7943783
TI   Procaine, lidocaine, and hypothermia inhibit calcium paradox in glial
      cells.
AU   Kim-Lee M H; Stokes B T; McDonald J S
CS   Department of Physiology, Ohio State University, Columbus 43210.
NC   NS10165 (NINDS)
SO   ANESTHESIA AND ANALGESIA,   ***(1994 Oct)***   79 (4) 728-33.
      Journal code: 1310650. ISSN: 0003-2999.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   MEDLINE; Abridged Index Medicus Journals; Priority Journals
OS   MEDLINE 95030379
EM   199411
ED   Entered STN: 19960517
      Last Updated on STN: 19970509

L4   ANSWER 189 OF 473   CANCERLIT on STN
AN   94323970   CANCERLIT
DN   94323970   PubMed ID: 7519371
TI   Sodium cyanide increases cytosolic free calcium: evidence for activation
      of the reversed mode of the Na+/Ca2+ exchanger and Ca2+ mobilization from
      inositol trisphosphate-insensitive pools.
AU   Kiang J G; Smallridge R C
CS   Department of Clinical Physiology, Walter Reed Army Institute of Research,
      Washington, DC 20307-5100.
SO   TOXICOLOGY AND APPLIED PHARMACOLOGY,   ***(1994 Aug)***   127 (2) 173-81.
      Journal code: 0416575. ISSN: 0041-008X.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   MEDLINE; Priority Journals
OS   MEDLINE 94323970
EM   199408
ED   Entered STN: 19941107
      Last Updated on STN: 19970509

L4   ANSWER 190 OF 473   CANCERLIT on STN
AN   92388658   CANCERLIT
DN   92388658   PubMed ID: 1387665
TI   A Na(+)-dependent Ca2+ exchanger generates the sustained increase in
      intracellular Ca2+ required for T cell activation.
AU   Wacholtz M C; Cragoe E J Jr; Lipsky P E
CS   Harold C. Simmons Arthritis Research Center, Department of Internal
      Medicine, University of Texas Southwestern Medical Center, Dallas 75235.
NC   AR09989 (NIAMS)
SO   JOURNAL OF IMMUNOLOGY,   ***(1992 Sep 15)***   149 (6) 1912-20.
      Journal code: 2985117R. ISSN: 0022-1767.

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DT    Journal; Article; (JOURNAL ARTICLE)
LA    English
FS    MEDLINE; Abridged Index Medicus Journals; Priority Journals
OS    MEDLINE 92388658
EM    199210
ED    Entered STN: 19990618
      Last Updated on STN: 19990618


L4    ANSWER 191 OF 473   CANCERLIT on STN
AN    92343724       CANCERLIT
DN    92343724    PubMed ID: 1636682
TI    Heat shock increases cytosolic free Ca2+ concentration via Na(+)-Ca2+
      exchange in    ***human***    epidermoid A 431 cells.
AU    Kiang J G; Koenig M L; Smallridge R C
CS    Department of Clinical Physiology, Walter Reed Army Institute of Research,
      Washington, DC 20307-5100.
SO    AMERICAN JOURNAL OF PHYSIOLOGY,    ***(1992 Jul)***   263 (1 Pt 1) C30-8.
      Journal code: 0370511. ISSN: 0002-9513.
CY    United States
DT    Journal; Article; (JOURNAL ARTICLE)
LA    English
FS    MEDLINE; Priority Journals
OS    MEDLINE 92343724
EM    199208
ED    Entered STN: 19941107
      Last Updated on STN: 19970509


L4    ANSWER 192 OF 473   CANCERLIT on STN
AN    92175913       CANCERLIT
DN    92175913    PubMed ID: 1531810
TI    Reperfusion paradox: a novel mode of glial cell injury.
AU    Kim-Lee M H; Stokes B T; Yates A J
CS    Department of Physiology, Ohio State University, Columbus 43210.
NC    NS10165 (NINDS)
SO    GLIA,    ***(1992)***   5 (1) 56-64.
      Journal code: 8806785. ISSN: 0894-1491.
CY    United States
DT    Journal; Article; (JOURNAL ARTICLE)
LA    English
FS    MEDLINE; Priority Journals
OS    MEDLINE 92175913
EM    199204
ED    Entered STN: 19941107
      Last Updated on STN: 19970509


L4    ANSWER 193 OF 473   CANCERLIT on STN
AN    87157179       CANCERLIT
DN    87157179    PubMed ID: 3828108
TI    Correlations between the 44D7 antigenic complex and the plasma membrane
      Na+-Ca2+ exchanger.
AU    Letarte M; Quackenbush E J; Baumal R; Michalak M
SO    BIOCHEMISTRY AND CELL BIOLOGY,    ***(1986 Nov)***   64 (11) 1160-9.
      Journal code: 8606068. ISSN: 0829-8211.
CY    Canada
DT    Journal; Article; (JOURNAL ARTICLE)
LA    English
FS    MEDLINE; Priority Journals
OS    MEDLINE 87157179
EM    198705
ED    Entered STN: 19941107
      Last Updated on STN: 19970509


L4    ANSWER 194 OF 473   CAPLUS   COPYRIGHT 2004 ACS on STN
AN    2001:816901  CAPLUS
DN    135:353862
TI    Protein and cDNA sequences of    ***human***    natrium-calcium exchanger
      protein sequence homolog, and uses thereof in therapy, diagnosis, and drug
      screening
IN    Wilm, Claudia
PA    Merck Patent G.m.b.H., Germany
SO    PCT Int. Appl., 41 pp.
      CODEN: PIXXD2
DT    Patent
LA    English
FAN.CNT 1
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PI   WO 2001083744      A2     20011108        WO 2001-EP4886    20010430 <--
     WO 2001083744      A3     20020418
        W:  CA, JP, US
        RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL,
           PT, SE, TR
     EP 1282706         A2     20030212        EP 2001-949305    20010430
        R:  AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
           IE, FI, CY, TR
     JP 2003531611      T2     20031028        JP 2001-580351    20010430
     US 2003096312      A1     20030522        US 2002-275116    20021101
PRAI EP 2000-109080     A      20000502
     WO 2001-EP4886     W      20010430


L4   ANSWER 195 OF 473   CAPLUS   COPYRIGHT 2004 ACS on STN
AN   2001:587549  CAPLUS
DN   135:301474
TI   Targeted inactivation of the    ***sodium***  -  ***calcium***
       ***exchanger***   (Ncx1) results in the lack of a heartbeat and abnormal
     myofibrillar organization
AU   Koushik, Srinagesh V.; Wang, Jian; Rogers, Rhonda; Moskophidis, Demetrius;
     Lambert, Nevin A.; Creazzo, Tony L.; Conway, Simon J.
CS   Institute of Molecular Medicine and Genetics, Medical College of Georgia,
     Augusta, GA, USA
SO   FASEB Journal ( ***2001*** ), 15(7), 1209-1211, 10.1096/fj.00-0696fje
     CODEN: FAJOEC; ISSN: 0892-6638
PB   Federation of American Societies for Experimental Biology
DT   Journal
LA   English
RE.CNT   34    THERE ARE 34 CITED REFERENCES AVAILABLE FOR THIS RECORD
               ALL CITATIONS AVAILABLE IN THE RE FORMAT


L4   ANSWER 196 OF 473   CAPLUS   COPYRIGHT 2004 ACS on STN
AN   2001:194433  CAPLUS
DN   135:135328
TI   Functional properties of failing   ***human***   ventricular myocytes
AU   Houser, Steven R.; Piacentino, Valentino, III; Mattiello, Julian; Weisser,
     Jutta; Gaughan, John P.
CS   Cardiovascular Research Group, Temple University School of Medicine,
     Philadelphia, PA, 19140, USA
SO   Trends in Cardiovascular Medicine ( ***2001*** ), Volume Date 2000,
     10(3), 101-107
     CODEN: TCMDEQ; ISSN: 1050-1738
PB   Elsevier Science Inc.
DT   Journal; General Review
LA   English
RE.CNT   28    THERE ARE 28 CITED REFERENCES AVAILABLE FOR THIS RECORD
               ALL CITATIONS AVAILABLE IN THE RE FORMAT


L4   ANSWER 197 OF 473   CAPLUS   COPYRIGHT 2004 ACS on STN
AN   2001:160000  CAPLUS
DN   135:253329
TI   A polymorphic GT repeat from the    ***human***   cardiac Na+Ca2+ exchanger
     intron 2 activates splicing
AU   Gabellini, Nadia
CS   Department of Biological Chemistry, University of Padova, Padua, 35121,
     Italy
SO   European Journal of Biochemistry ( ***2001*** ), 268(4), 1076-1083
     CODEN: EJBCAI; ISSN: 0014-2956
PB   Blackwell Science Ltd.
DT   Journal
LA   English
RE.CNT   38    THERE ARE 38 CITED REFERENCES AVAILABLE FOR THIS RECORD
               ALL CITATIONS AVAILABLE IN THE RE FORMAT


L4   ANSWER 198 OF 473   CAPLUS   COPYRIGHT 2004 ACS on STN
AN   2001:105893  CAPLUS
DN   135:148088
TI   Isolation and characterization of Na+/Ca2+ exchanger gene and splicing
     isoforms in mice
AU   Wakimoto, Koji; Kuro-o, Makoto; Yanaka, Noriyuki; Omori, Kenji; Komuro,
     Issei; Imai, Yuji; Nabeshima, Yo-Ichi
CS   Advanced Medical Research Department, Tanabe Seiyaku Co. Ltd., Osaka,
     532-8505, Japan
SO   DNA Sequence ( ***2000*** ), 11(1-2), 75-81
```

PB   Harwood Academic Publishers
DT   Journal
LA   English

L4   ANSWER 199 OF 473   CAPLUS   COPYRIGHT 2004 ACS on STN
AN   2000:744138   CAPLUS
DN   135:71985
TI   Transcriptional control of the Na+/Ca2+ exchanger
AU   Gabellini, Nadia; Zatti, Alessandra; Carafoli, Ernesto
CS   Department of Biological Chemistry, Padua, 5121, Italy
SO   International Congress Series (***2000***), 1208(Control and Diseases
     of Sodium Dependent Transport Proteins and Ion Channels), 69-72
     CODEN: EXMDA4; ISSN: 0531-5131
PB   Elsevier Science B.V.
DT   Journal
LA   English

L4   ANSWER 200 OF 473   CAPLUS   COPYRIGHT 2004 ACS on STN
AN   2000:744129   CAPLUS
DN   134:39966
TI   The mechanism of induction of THP-1 cell differentiation by bufalin, a
     potent Na+,K+-ATPase inhibitor
AU   Kurosawa, Masahiro; Tani, Yoshihiro; Numazawa, Satoshi; Yoshida, Takemi
CS   Department of Biochemical Toxicology, School of Pharmaceutical Sciences,
     Showa University, Tokyo, 142-8555, Japan
SO   International Congress Series (***2000***), 1208(Control and Diseases
     of Sodium Dependent Transport Proteins and Ion Channels), 35-37
     CODEN: EXMDA4; ISSN: 0531-5131
PB   Elsevier Science B.V.
DT   Journal
LA   English

L4   ANSWER 201 OF 473   CAPLUS   COPYRIGHT 2004 ACS on STN
AN   2000:727998   CAPLUS
DN   134:16007
TI   Impaired contractile performance of cultured rabbit ventricular myocytes
     after adenoviral gene transfer of Na+-Ca2+ exchanger
AU   Schillinger, Wolfgang; Janssen, Paul M. L.; Emami, Shahriyar; Henderson,
     Scott A.; Ross, Robert S.; Teucher, Nils; Zeitz, Oliver; Philipson,
     Kenneth D.; Prestle, Jurgen; Hasenfuss, Gerd
CS   Zentrum Innere Medizin, Abteilung Kardiologie und Pneumologie, Universitat
     Gottingen, Gottingen, 37075, Germany
SO   Circulation Research (***2000***), 87(7), 581-587
     CODEN: CIRUAL; ISSN: 0009-7330
PB   Lippincott Williams & Wilkins
DT   Journal
LA   English

L4   ANSWER 202 OF 473   CAPLUS   COPYRIGHT 2004 ACS on STN
AN   2000:555324   CAPLUS
DN   134:40417
TI   Is myocardial Na+/Ca2+ exchanger transcription a marker for different
     stages of myocardial dysfunction? Quantitative PCR of the messenger RNA in
     endomyocardial biopsies of patients with heart failure
AU   Piper, Cornelia; Bilger, Johannes; Henrichs, Eva-Maria; Schultheiss,
     Heinz-Peter; Horstkotte, Dieter; Doerner, Andrea
CS   Department of Cardiology, Heart Center North Rhine-Westphalia, University
     Hospital of the Ruhr University of Bochum, Bad Oeynhausen, Germany
SO   Journal of the American College of Cardiology (***2000***), 36(1),
     233-241
     CODEN: JACCDI; ISSN: 0735-1097
PB   Elsevier Science Inc.
DT   Journal
LA   English

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AN      2000:112627  CAPLUS
DN      132:291544
TI      Gene expression of Na+/Ca2+ exchanger during development in  ***human***
        heart
AU      Qu, Y.; Ghatpande, A.; El-Sherif, N.; Boutjdir, M.
CS      Department of Medicine, Cardiology Division, V.A. Medical Center and SUNY
        Health Science Center, Brooklyn, NY, USA
SO      Cardiovascular Research ( ***2000***  ), 45(4), 866-873
        CODEN: CVREAU; ISSN: 0008-6363
PB      Elsevier Science B.V.
DT      Journal
LA      English
RE.CNT  39      THERE ARE 39 CITED REFERENCES AVAILABLE FOR THIS RECORD
                ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4      ANSWER 204 OF 473  CAPLUS  COPYRIGHT 2004 ACS on STN
AN      1999:172048  CAPLUS
DN      130:279658
TI      Functional expression of the  ***human***  cardiac Na+/Ca2+ exchanger in
        Sf9 cells: rapid and specific Ni2+ transport
AU      Egger, M.; Ruknudin, A.; Lipp, P.; Kofuji, P.; Lederer, W. J.; Schulze, D.
        H.; Niggli, E.
CS      Department of Physiology, University of Bern, Bern, CH-3012, Switz.
SO      Cell Calcium ( ***1999***  ), 25(1), 9-17
        CODEN: CECADV; ISSN: 0143-4160
PB      Churchill Livingstone
DT      Journal
LA      English
RE.CNT  36      THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD
                ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4      ANSWER 205 OF 473  CAPLUS  COPYRIGHT 2004 ACS on STN
AN      1999:169628  CAPLUS
DN      130:309994
TI      The sarcoplasmic reticulum and the Na+/Ca2+ exchanger both contribute to
        the Ca2+ transient of failing  ***human***  ventricular myocytes
AU      Dipla, Konstantina; Mattiello, Julian A.; Margulies, Kenneth B.;
        Jeevanandam, Valluvan; Houser, Steven R.
CS      Temple University School of Medicine Department of Physiology,
        Philadelphia, PA, 19140, USA
SO      Circulation Research ( ***1999***  ), 84(4), 435-444
        CODEN: CIRUAL; ISSN: 0009-7330
PB      Lippincott Williams & Wilkins
DT      Journal
LA      English
RE.CNT  37      THERE ARE 37 CITED REFERENCES AVAILABLE FOR THIS RECORD
                ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4      ANSWER 206 OF 473  CAPLUS  COPYRIGHT 2004 ACS on STN
AN      1998:492909  CAPLUS
DN      129:200994
TI      Ionic mechanisms underlying  ***human***  atrial action potential
        properties: insights from a mathematical model
AU      Courtemanche, Marc; Ramirez, Rafael J.; Nattel, Stanley
CS      Research Center, Montreal Heart Institute, Montreal, QC, H1T 1C8, Can.
SO      American Journal of Physiology ( ***1998*** ), 275(1, Pt. 2), H301-H321
        CODEN: AJPHAP; ISSN: 0002-9513
PB      American Physiological Society
DT      Journal
LA      English
RE.CNT  64      THERE ARE 64 CITED REFERENCES AVAILABLE FOR THIS RECORD
                ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4      ANSWER 207 OF 473  CAPLUS  COPYRIGHT 2004 ACS on STN
AN      1997:704016  CAPLUS
DN      127:344428
TI      Molecular cloning of the  ***human***  brain Na+/Ca(2+) exchanger and
        study of its isoform expression in rat brain, normal  ***human***
        brain, and  ***human***  brain with Alzheimer's pathology (
        ***sodium***  /  ***calcium***   ***exchanger***  )
AU      Yu, Li
CS      Ohio Univ., Athens, OH, USA
SO      ( ***1997***  ) 154 pp.  Avail.: UMI, Order No. DA9736912
        From: Diss. Abstr. Int., B 1997, 58(6), 2894
DT      Dissertation
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L4   ANSWER 208 OF 473   CAPLUS   COPYRIGHT 2004 ACS on STN
AN   1997:567680 CAPLUS
DN   127:246561
TI   Alzheimer's amyloid-beta peptide inhibits sodium/calcium exchange measured
      in rat and   ***human***   brain plasma membrane vesicles
AU   Wu, A.; Derrico, C. A.; Hatem, L.; Colvin, R. A.
CS   Department of Biological Sciences, Program in Neurobiology, Ohio
      University College of Osteopathic Medicine, Athens, OH, 45701, USA
SO   Neuroscience (Oxford) (***1997***   ), 80(3), 675-684
      CODEN: NRSCDN; ISSN: 0306-4522
PB   Elsevier
DT   Journal
LA   English

L4   ANSWER 209 OF 473   CAPLUS   COPYRIGHT 2004 ACS on STN
AN   1996:432909 CAPLUS
DN   125:138943
TI   Role of the cardiac sarcolemmal Na+-Ca2+ exchanger in end-stage
       human   heart failure
AU   Reinecke, Hans; Studer, Roland; Vetter, Roland; Just, Hanjoerg; Holtz,
      Juergen; Drexler, Helmut
CS   Cardiology and Angiology Internal Medicine III, University of Freiburg,
      Freiburg, D-79106, Germany
SO   Annals of the New York Academy of Sciences (***1996***   ),
      779(Sodium-Calcium Exchange), 543-545
      CODEN: ANYAA9; ISSN: 0077-8923
PB   New York Academy of Sciences
DT   Journal
LA   English

L4   ANSWER 210 OF 473   CAPLUS   COPYRIGHT 2004 ACS on STN
AN   1996:432906 CAPLUS
DN   125:111719
TI   Functional relevance of an enhanced expression of the Na+-Ca2+ exchanger
      in the failing   ***human***   heart
AU   Flesch, M.; Puetz, F.; Schwinger, R. H. G.; Boehm, M.
CS   Clinic III for Internal Medicine, University of Cologne, Cologne, 50924,
      Germany
SO   Annals of the New York Academy of Sciences (***1996***   ),
      779(Sodium-Calcium Exchange), 539-542
      CODEN: ANYAA9; ISSN: 0077-8923
PB   New York Academy of Sciences
DT   Journal
LA   English

L4   ANSWER 211 OF 473   CAPLUS   COPYRIGHT 2004 ACS on STN
AN   1996:276654 CAPLUS
DN   124:339337
TI   Relationship between myocardial function and expression of calcium cycling
      proteins in nonfailing and failing   ***human***   myocardium
AU   Hasenfuss, Gerd; Reinecke, Hans; Studer, Roland; Pieske, Burkert; Meyer,
      Markus; Holtz, Juergen; Holubarsch, Christian; Drexler, Helmut; Just,
      Hanjoerg
CS   Medizinische Klinik III, Universitat Freiburg, Freiburg/Br., 79106,
      Germany
SO   Developments in Cardiovascular Medicine (***1995***   ), 169(Heart
      Hypertrophy and Failure), 103-116
      CODEN: DCMEDM; ISSN: 0166-9842
PB   Kluwer
DT   Journal; General Review
LA   English

L4   ANSWER 212 OF 473   CAPLUS   COPYRIGHT 2004 ACS on STN
AN   1996:209265 CAPLUS
DN   124:257323
TI   Cardiac Na+/Ca2+ exchange activity in patients with end-stage heart
      failure
AU   Reinecke, Hans; Studer, Roland; Vetter, Roland; Holtz, Juergen; Drexler,
      Helmut
CS   Innere Medizin III, Kardiologie und Angiologie, Universitatsklinik
      Freiburg, Freiburg, 79106, Germany
SO   Cardiovascular Research (***1996***   ), 31(1), 48-54
      CODEN: CVREAU; ISSN: 0008-6363
PB   Elsevier

LA   English

AN   1995:450999 CAPLUS
DN   122:210972
TI   The mode of action of exogenous gangliosides on cytosolic calcium of
        cultured   ***human***   hepatoma cells
AU   Cui, Wen; Liu, Yinkun; Zhang, Xiaying; Song, Jiaxi; Chen, Ruiqun
CS   Sch. Basic Med. SCi., Shanghai Med. Univ., Shanghai, 200032, Peop. Rep.
        China
SO   Shengwu Huaxue Yu Shengwu Wuli Xuebao (***1994***   ), 26(5), 499-503
        CODEN: SHWPAU; ISSN: 0582-9879
PB   Shanghai Kexue Jishu Chubanshe
DT   Journal
LA   Chinese

AN   1994:530939 CAPLUS
DN   121:130939
TI   Functional expression of   ***human***   renal Na+/Ca2+ exchanger in
        insect cells
AU   Loo, Tip W.; Clarke, David M.
CS   Department of Medicine, University of Toronto, Toronto, ON, M5S 1A8, Can.
SO   American Journal of Physiology (***1994***   ), 267(1, Pt. 2), F70-F74
        CODEN: AJPHAP; ISSN: 0002-9513
DT   Journal
LA   English

AN   1994:2857 CAPLUS
DN   120:2857
TI   Molecular and cellular biology of plasma membrane calcium ATPase
AU   Carafoli, Ernesto; Guerini, Danilo
CS   Inst. Biochem., Swiss Fed. Institute of Technology, Zurich, CH-8092,
        Switz.
SO   Trends in Cardiovascular Medicine (***1993***   ), 3(5), 177-84
        CODEN: TCMDEQ; ISSN: 1050-1738
DT   Journal; General Review
LA   English

AN   1993:210050 CAPLUS
DN   118:210050
TI   Potassium-dependent sodium/calcium exchange in   ***human***   platelets
AU   Kimura, Masayuki; Aviv, Abraham; Reeves, John P.
CS   New Jersey Med. Sch., Univ. Med. Dent. New Jersey, Newark, NJ, 07103, USA
SO   Journal of Biological Chemistry (***1993***   ), 268(10), 6874-7
        CODEN: JBCHA3; ISSN: 0021-9258
DT   Journal
LA   English

AN   1992:211743 CAPLUS
DN   116:211743
TI   Calcium extrusion by the   ***sodium*** - ***calcium***
        exchanger   of the   ***human***   platelet
AU   Haynes, Duncan H.; Valant, Peter A.; Adjei, Philip N.
CS   Sch. Med., Univ. Miami, Miami, FL, 33101, USA
SO   Annals of the New York Academy of Sciences (***1991***   ),
        639(Sodium-Calcium Exch.), 592-603
        CODEN: ANYAA9; ISSN: 0077-8923
DT   Journal
LA   English

AN   2001:56264 DISSABS   Order Number: AAI3004657
TI   Role of annexin V and VI in the   ***human***   heart
AU   Matteo D'Avenia, Rosalia Gerarda [Ph.D.]; Moravec, Christine S. [adviser]
CS   Cleveland State University (0466)
SO   Dissertation Abstracts International, (***2001***   ) Vol. 62, No. 2B, p.
        703. Order No.: AAI3004657. 114 pages.
        ISBN: 0-493-13605-3.
DT   Dissertation
FS   DAI

AN   97:71556 DISSABS   Order Number: AAR9736912
TI   MOLECULAR CLONING OF THE   ***HUMAN***   BRAIN NA+/CA(2+) EXCHANGER AND
      STUDY OF ITS ISOFORM EXPRESSION IN RAT BRAIN, NORMAL   ***HUMAN***
      BRAIN, AND   ***HUMAN***   BRAIN WITH ALZHEIMER'S PATHOLOGY (
      SODIUM / ***CALCIUM***   ***EXCHANGER***   )
AU   YU, LI [PH.D.]; COLVIN, ROBERT ALAN [advisor]
CS   OHIO UNIVERSITY (0167)
SO   Dissertation Abstracts International, (***1997***   ) Vol. 58, No. 6B, p.
      2894. Order No.: AAR9736912. 154 pages.
DT   Dissertation
FS   DAI
LA   English
ED   Entered STN: 19971104
      Last Updated on STN: 19971104

AN   94:9773 DISSABS   Order Number: AAR9406113
TI   MOLECULAR CHARACTERIZATION OF THE PLASMA MEMBRANE   ***SODIUM***   /
      CALCIUM   ***EXCHANGER***   (***SODIUM***   ***CALCIUM***
      EXCHANGER   )
AU   KOFUJI, PAULO [PH.D.]; LEDERER, W. J. [advisor]
CS   UNIVERSITY OF MARYLAND AT BALTIMORE (0373)
SO   Dissertation Abstracts International, (***1993***   ) Vol. 54, No. 9B, p.
      4548. Order No.: AAR9406113. 154 pages.
DT   Dissertation
FS   DAI
LA   English
ED   Entered STN: 19940218
      Last Updated on STN: 19940218

AN   2000-27947 DRUGU   P
TI   Inotropic effects of propofol on   ***human***   right atrial trabeculae.
AU   de Ruijter W; van Klarenbosch J; Stienen G J; de Lange J J
CS   Univ.Amsterdam-Free
LO   Amsterdam, Neth.
SO   Anesth.Analg. (90, No. 2, Suppl., S398, 2000)
      CODEN: AACRAT   ISSN: 0003-2999
AV   University Hospital Vrije Universiteit, Amsterdam, Netherlands.
LA   English
DT   Journal
FA   AB; LA; CT
FS   Literature

AN   1996-47681 DRUGU   T
TI   Increased sensitivity of   ***human***   heart to inotropic stimulation
      with Na channel activator or cardiac glycosides associated with decreased
      expression of sodium pump isoforms.
AU   McDonough A A; Wang J; Frank K; Muller Ehmsen J; Schwinger R H G
CS   Univ.Southern-California; Univ.Cologne
LO   Los Angeles, Cal., USA; Cologne, Ger.
SO   Circulation (94, No. 8, Suppl., I24, 1996)
      CODEN: CIRCAZ   ISSN: 0009-7322
AV   University of Southern California, Los Angeles, CA, U.S.A.
LA   English
DT   Journal
FA   AB; LA; CT
FS   Literature

AN   1995-14132 DRUGU   T P
TI   Clinical and in vivo antiarrhythmic potential of sodium-hydrogen exchange
      inhibitors.
AU   Duff H J
CS   Univ.Calgary
LO   Calgary, Alb., Can.
SO   Cardiovasc.Res. (29, No. 2, 189-93, 1995) 2 Tab. 46 Ref.
      CODEN: CVREAU   ISSN: 0008-6363
AV   Cardiovascular Research Group, University of Calgary, 3330 Hospital Drive
      NW, Calgary, Alberta, Canada T2N 4N1.

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DT      Journal
FA      AB; LA; CT
FS      Literature
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AN      2001046987   EMBASE
TI      Functional properties of failing   ***human***   ventricular myocytes.
AU      Houser S.R.; Piacentino III V.; Mattiello J.; Weisser J.; Gaughan J.P.
CS      Prof. S.R. Houser, Cardiovascular Research Group, Molecular/Cellular
        Cardiology Lab., Temple University School of Medicine, 3400 North Broad
        Street, Philadelphia, PA 19140, United States. srhouser@unix.temple.edu
SO      Trends in Cardiovascular Medicine, (2000) 10/3 (101-107).
        Refs: 29
        ISSN: 1050-1738   CODEN: TCMDEQ
PUI     S 1050-1738(00)00057-8
CY      United States
DT      Journal; General Review
FS      018       Cardiovascular Diseases and Cardiovascular Surgery
        021       Developmental Biology and Teratology
        022       Human Genetics
        029       Clinical Biochemistry
        037       Drug Literature Index
        005       General Pathology and Pathological Anatomy
LA      English
SL      English
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AN      2000226411   EMBASE
TI      Mechanisms of hydrogen peroxide-induced calcium dysregulation in PC12
        cells.
AU      Wang H.; Joseph J.A.
CS      Dr. H. Wang, Department of Neurology, Children's Hospital, Enders 3, 300
        Longwood Avenue, Boston, MA 02115, United States
SO      Free Radical Biology and Medicine, (15 Apr 2000) 28/8 (1222-1231).
        Refs: 50
        ISSN: 0891-5849   CODEN: FRBMEH
PUI     S 0891-5849(00)00241-0
CY      United States
DT      Journal; Article
FS      029       Clinical Biochemistry
        030       Pharmacology
        037       Drug Literature Index
        005       General Pathology and Pathological Anatomy
        008       Neurology and Neurosurgery
LA      English
SL      English
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AN      1998160329   EMBASE
TI      Calcium channels in cardiac hypertrophy and heart failure.
AU      Shorofsky S.R.; Balke C.W.; Gwathmey J.K.
CS      S.R. Shorofsky, Univ. of Maryland School of Medicine, Division of
        Cardiology, 22 South Greene Street, Baltimore, MD 21201, United States
SO      Heart Failure Reviews, (1998) 2/3 (163-171).
        Refs: 104
        ISSN: 1382-4147   CODEN: HFREFC
CY      Netherlands
DT      Journal; General Review
FS      018       Cardiovascular Diseases and Cardiovascular Surgery
LA      English
SL      English
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AN      94169689   EMBASE
DN      1994169689
TI      Sodium-calcium exchange in neonatal myocardium: Reversible inhibition by
        halothane.
AU      Baum V.C.; Wetzel G.T.
CS      Department of Anesthesiology, UCLA Medical Center,Los Angeles, CA
        90024-1778, United States
SO      Anesthesia and Analgesia, (1994) 78/6 (1105-1109).
```

AN   93034622   EMBASE
DN   1993034622
TI   [Biochemical alterations and disturbances of the excitation-contraction
      coupling in congestive heart failure].
      BIOCHEMISCHE VERANDERUNGEN UND STORUNGEN DER ELEKTROMECHANISCHEN KOPPLUNG
      BEI DER CHRONISCHEN HERZINSUFFIZIENZ.
AU   Holubarsch C.
CS   Medizinische Universitatsklinik, Hugstetter Strasse 55,W-7800 Freiburg,
      Germany
SO   Zeitschrift fur Kardiologie, (1992) 81/SUPPL. 4 (17-21).
      ISSN: 0300-5860   CODEN: ZKRDAX
CY   Germany
DT   Journal; Conference Article
FS   006   Internal Medicine
      018   Cardiovascular Diseases and Cardiovascular Surgery
      037   Drug Literature Index
LA   German
SL   English; German

AN   85205701   EMBASE
DN   1985205701
TI   Bartter's syndrome: A unifying hypothesis.
AU   Garrick R.; Ziyadeh F.N.; Jorkasky D.; Goldfarb S.
CS   Renal-Electrolyte Section, Department of Medicine, Hospital of the
      University of Pennsylvania, Philadelphia, PA 19104, United States
SO   American Journal of Nephrology, (1985) 5/5 (379-384).
      CODEN: AJNED
CY   United States
DT   Journal
FS   028   Urology and Nephrology
      003   Endocrinology
      005   General Pathology and Pathological Anatomy
LA   English

AN   84094778   EMBASE
DN   1984094778
TI   Regulation of calcium transport in cardiac cells.
AU   Shamoo A.E.; Ambudkar I.S.
CS   Membrane Biochemistry Research Laboratory, Department of Biological
      Chemistry, School of Medicine, University of Maryland, Baltimore, MD
      21201, United States
SO   Canadian Journal of Physiology and Pharmacology, (1984) 62/1 (9-22).
      CODEN: CJPPA3
CY   Canada
DT   Journal
FS   037   Drug Literature Index
      002   Physiology
      030   Pharmacology
      018   Cardiovascular Diseases and Cardiovascular Surgery
      029   Clinical Biochemistry
LA   English
SL   French

AN   1999203438   ESBIOBASE
TI   Sodium/calcium exchange contributes to contraction and relaxation in
      failed   ***human***   ventricular myocytes
AU   Gaughan J.P.; Furukawa S.; Jeevanandam V.; Hefner C.A.; Kubo H.;
      Margulies K.B.; McGowan B.S.; Mattiello J.A.; Dipla K.; Piacentino III
      V.; Li S.; Houser S.R.

3420 North Broad Street, Philadelphia, PA 19140, United States.
E-mail: jgaughan@debjohn@pond.com
SO   American Journal of Physiology - Heart and Circulatory Physiology, (
    1999), 277/2 46-2 (H714-H724), 30 reference(s)
DT   Journal; Article
CY   United States
LA   English
SL   English

AN   1998189833   ESBIOBASE
TI   Ionic mechanisms underlying ***human*** atrial action potential
      properties: Insights from a mathematical model
AU   Courtemanche M.; Ramirez R.J.; Nattel S.
CS   M. Courtemanche, Research Center, Montreal Heart Institute, 5000 E.
      Belanger St., Montreal, Que. H1T 1C8, Canada.
SO   American Journal of Physiology - Heart and Circulatory Physiology, (
    1998), 275/1 44-1 (H301-H321), 62 reference(s)
DT   Journal; Article
CY   United States
LA   English
SL   English

AN   1997180450   ESBIOBASE
TI   Na.sup.+/Ca.sup.2.sup.+ exchanger in Drosophila: Cloning, expression, and
      transport differences
AU   Ruknudin A.; Valdivia C.; Kofuji P.; Lederer W.J.; Schulze D.H.
CS   D.H. Schulze, Dept. of Microbiology and Immunology, 655 W. Baltimore St.,
      Baltimore, MD 21201, United States.
SO   American Journal of Physiology - Cell Physiology, (***1997***), 273/1
      42-1 (C257-C265), 34 reference(s)
DT   Journal; Article
CY   United States
LA   English
SL   English

LOCUS (LOC):   AL627278   GenBank (R)
GenBank ACC. NO. (GBN): AL627278 AL513382
GenBank VERSION (VER): AL627278.1 GI:16504263
CAS REGISTRY NO. (RN): 365924-97-6
SEQUENCE LENGTH (SQL): 258050
MOLECULE TYPE (CI):   DNA; linear
DIVISION CODE (CI):   Bacteria
DATE (DATE):   4 Jul 2003
DEFINITION (DEF):   Salmonella enterica serovar Typhi (Salmonella typhi)
                      strain CT18, complete chromosome; segment 14/20.
SOURCE: Salmonella enterica subsp. enterica serovar Typhi
ORGANISM (ORGN):   Salmonella enterica subsp. enterica serovar Typhi
                      Bacteria; Proteobacteria; Gammaproteobacteria;
                      Enterobacteriales; Enterobacteriaceae; Salmonella
NUCLEIC ACID COUNT (NA): 61275 a   71182 c   65531 g   60062 t
COMMENT:
      E-mail: parkhill@sanger.ac.uk
      Notes:
      Details of S. typhi sequencing at the Sanger Centre are available
      on the World Wide Web.
      (URL, http://www.sanger.ac.uk/Projects/S typhi/).
REFERENCE: 1 (bases 1 to 258050)
  AUTHOR (AU):   Parkhill,J.; Dougan,G.; James,K.D.; Thomson,N.R.;
                      Pickard,D.; Wain,J.; Churcher,C.; Mungall,K.L.;
                      Bentley,S.D.; Holden,M.T.G.; Sebaihia,M.; Baker,S.;
                      Basham,D.; Brooks,K.; Chillingworth,T.; Connerton,P.;
                      Cronin,A.; Davis,P.; Davies,R.M.; Dowd,L.; White,N.;
                      Farrar,J.; Feltwell,T.; Hamlin,N.; Haque,A.; Hien,T.T.;
                      Holroyd,S.; Jagels,K.; Krogh,A.; Larsen,T.S.;
                      Leather,S.; Moule,S.; O'Gaora,P.; Parry,C.; Quail,M.;
                      Rutherford,K.; Simmonds,M.; Skelton,J.; Stevens,K.;

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..258050	/organism="Salmonella enterica subsp. enterica serovar Typhi" /mol-type="genomic DNA" /strain="CT18" /db-xref="taxon:90370"
gene	69..1544	/gene="tolC" /note="synonym: STY3364"
CDS	69..1544	/gene="tolC" /note="Similar to Salmonella enteritidis outer membrane protein TolC precursor tolC SW:TOLC-SALEN (Q54001) (491 aa) fasta scores: E(): 0, 99.0% id in 491 aa, and to Escherichia coli outer membrane protein tolc precursor tolc or mtcb or muka or refI SW:TOLC-ECOLI (P02930) (495 aa) fasta scores: E(): 0, 89.7% id in 495 aa Orthologue of E. coli tolC (TOLC-ECOLI); Fasta hit to TOLC-ECOLI (495 aa), 90% identity in 495 aa overlap" /codon-start=1 /transl-table=11 /product="outer membrane protein TolC precursor" /protein-id="CAD07712.1" /db-xref="GI:16504264" /db-xref="GOA:Q8Z3N8" /db-xref="SPTREMBL:Q8Z3N8" /translation="MQMKKLLPILIGLSLSGFST LSQAENLMQVYQQARLSNPELRKS AADRDAAFEKINEARSPLLPQLGLGADYTYSNGY RDANGINSNETSASLQLTQTLFDM SKWRGLTLQEKAAGIQDVTYQTDQQTLILNTANA YFKVLNAIDVLSYTQAQKEAIYRQ LDQTTQRFNVGLVAITDVQNARAQYDTVLANEVT ARNNLDNAVEELRQVTGNYYPELA SLNVEHFKTDKPKAVNALLKEAENRNLSLLQARL SQDLAREQIRQAQDGHLPTLNLTA STGISDTSYSGSKTNSAQYDDSNMGQNKIGLNFS LPLYQGGMVNSQVKQAQYNFVGAS EQLESAHRSVVQTVRSSFNNINASISSINAYKQA VVSAQSSLDAMEAGYSVGTRTIVD VLDATTTLYDAKQQLANARYTYLINQLNIKYALG TLNEQDLLALNSTLGKPIPTSPES VAPETPEQDAAADGYNAHSAAPAVQPTAARANSN NGNPFRH"
gene	1757..2428	/gene="STY3365"
CDS	1757..2428	/gene="STY3365" /note="Orthologue of E. coli ygiB (YGIB-ECOLI); Fasta hit to YGIB-ECOLI (234 aa), 97% identity in 223 aa overlap. Contains a possible N-terminal signal sequence." /codon-start=1 /transl-table=11 /product="possible lipoprotein" /protein-id="CAD07713.1" /db-xref="GI:16504265"

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                                             /translation="MKRTKSIHHASFRKSWSARH
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                                             QAGMAPENQAQAQQSSGSFWMPLMAGYMMGRLMG
                                             GGAGFAQQPLFSSKNPASPAYGKY
                                             TDAAGKNYGAAQPGRTMTVPKTAMAPKPATTTTV
                                             TRGGFGESVAKQSTMQRSAAGTST RSMGG"
misc-feature     1835..1867                  /gene="STY3365"
                                             /note="PS00013 Prokaryotic
                                             membrane lipoprotein lipid
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gene             2434..3597                  /gene="STY3366"
CDS              2434..3597                  /gene="STY3366"
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                                             (387 aa), 50% identity in 392 aa
                                             overlap Orthologue of E. coli ygiC
                                             (YGIC-ECOLI); Fasta hit to
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                                             DQINAGNLPEGSDQFNSLQEKLIE
                                             RFAELREQYGFQLLHLTCCRDTVEDRGTIQYLQD
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gene             complement(3659..4489)      /gene="STY3367"
CDS              complement(3659..4489)      /gene="STY3367"
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                                             in 266 aa overlap"
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                                             /db-xref="SPTREMBL:Q8Z3N7"
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                                             AQRLVELLAPVPVALDKEAWGFDHGSWGVLIKMY
                                             PNADIPMVQLSVDSTKPAAWHFEM
                                             GRKLATLRDEGVMLVASGNVVHNLRTVRWHGDNI
                                             PYPWAASFNDFVKANLTWQGPVEQ
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gene             4588..5361                  /gene="STY3368"
CDS              4588..5361                  /gene="STY3368"
                                             /note="Orthologue of E. coli ygiE
                                             (YGIE-ECOLI); Fasta hit to
                                             YGIE-ECOLI (257 aa), 93% identity
                                             in 257 aa overlap. Contains
                                             multiple possible membrane
                                             spanning hydrophobic domains"
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                                        LGVLGQKPSNRVLAFSLGFAAGIM
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                                        GSIKRTAILLTLGISLHNFPEGIATFVTASSNLE
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gene          6004..7800              /gene="STY3370"
                                        /note="synonym: assT"
CDS           6004..7800              /gene="STY3370"
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                                        pneumoniae arylsulfate
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                                        KFANNVTVEYKENGKAMKDDYVVQTSAIVNHYMD
                                        NRSISDLQQTKVIKVAPGFEDRLY
                                        LVNTHTFTPQGAEFHWHGEKDKNAGILDAGPAGG
                                        ALPFDIAPYTFVVDTQGEYRWWLD
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                                        DQIIEVDKSGRVVDVWDLTKILDP
                                        MRDALLGALDAGAVCVNVDLAHAGQQAKLEPDTP
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                                        CKDTDFDFTYTQHTAWLSSKGTLTVFDNGDGRGL
                                        EQPALPTMKYSRFVEYKIDEKKGT
                                        VQQVWEYGKERGYDFYSPITSVVEYQKDRDTMFG
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gene          7820..8491              /gene="dsbA"
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misc-feature	7847..8488	/gene="dsbA" /note="Pfam match to entry PF01323 DSBA, DSBA oxidoreductase, score 12.90, E-value 1.9e-07"
gene	8506..9183	/gene="dsbB" /note="synonym: STY3372"
CDS	8506..9183	/gene="dsbB" /note="Similar to Enterobacter amnigenus disulfide isomerase dsbB TR:Q9XDP0 (EMBL:AF012826) (221 aa) fasta scores: E(): 0, 89.2% id in 158 aa. The Enterobacter amnigenus gene appears to contain a frameshift after codon 161; this gene is the same as the S. typhimurium gene" /codon-start=1 /transl-table=11 /product="disulfide isomerase" /protein-id="CAD07719.1" /db-xref="GI:16504271" /db-xref="GOA:Q8XEK0" /db-xref="SWISS-PROT:Q8XEK0" /translation="MDFIKGLWRDLRARPVDTLV RWQEQRFLWLLMAIAMGGLIILAH SFFQIYLYMAPCEQCVYIRYAMFVMVIGGVIAAI NPKNIVLKLIGCIAAFYGSIMGIK FSIKLNGIHHAVHNADPDSLFGVQGCSTDPTFPF NLPLAEWAPEWFKPTGDCGYDAPI VPDGVTLSSVQQWFVDLYQQSEGWYLLPPWHFMN MAQACMLAFGLCLILLLVMSGAWA LKLARGK"
gene	complement(9354..10007)	/gene="STY3373" /note="synonym: ribB"
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misc-feature	complement(9375..9923)	/gene="STY3373" /note="Pfam match to entry PF00926 DHBP-synthase, 3,4-dihydroxy-2-butanone 4-phosphate synthase, score 395.00, E-value 7.2e-115"
gene	10384..10740	/gene="STY3375"
CDS	10384..10740	/gene="STY3375" /note="Similar to Escherichia coli hypothetical 13.8 kDa protein in ribb-glgs intergenic region yqiC SW:YQIC-ECOLI (Q46868) (116 aa) fasta scores: E(): 1.3e-28, 80.7% id in 114 aa Orthologue of E. coli YQIC-ECOLI; Fasta hit to YQIC-ECOLI (116 aa), 81% identity in 114 aa overlap" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein"

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                                           EEVKPAPAIPPVDPQE"
gene            complement(10815..11018   /gene="STY3376"
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CDS             complement(10815..11018   /gene="STY3376"
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                                           /db-xref="GOA:P58615"
                                           /db-xref="SWISS-PROT:P58615"
                                           /translation="MNNNNVYSLNNFDFLARSFA
                                           RMQAEGRPVDIQAVTGNMDEEHRD
                                           WFCKRYALYCQQATQAKKLELEH"
gene            11282..11902               /gene="STY3377"
CDS             11282..11902               /gene="STY3377"
                                           /note="Orthologue of E. coli
                                           P76657; Fasta hit to P76657 (209
                                           aa), 72% identity in 201 aa
                                           overlap. Contains multiple
                                           possible membrane spanning
                                           hydrophobic domains and a possible
                                           N-terminal signal sequence."
                                           /codon-start=1
                                           /transl-table=11
                                           /product="putative membrane
                                           protein"
                                           /protein-id="CAD07723.1"
                                           /db-xref="GI:16504275"
                                           /db-xref="SPTREMBL:Q8Z3N3"
                                           /translation="MTLFAEYNSPYLFAIAFVFF
                                           IGVLEMISLIFGHFLSGALDAHLD
                                           HYDALSSGPAGQALHYLNIGRVPALVVLCLLAGY
                                           FGLFGILIQHGGIMLWQAPLSNLL
                                           LVPLSIVLSVFAVHYSEKILAPWLPRDESSALRE
                                           EEFIGGMAIITGHAAVAGTPCEGK
                                           FTDKFGQIHYLLLEPEKGKEFKKGDKVLIVCRLS
                                           ATRYLAERTFYV"
gene            11921..13600               /gene="STY3378"
CDS             11921..13600               /gene="STY3378"
                                           /note="Orthologue of E. coli
                                           YQIK-ECOLI; Fasta hit to
                                           YQIK-ECOLI (553 aa), 93% identity
                                           in 549 aa overlap. Contains a
                                           possible N-terminal signal
                                           sequence and a possible
                                           coiled-coil region between
                                           residues 345..446"
                                           /codon-start=1
                                           /transl-table=11
                                           /product="putative exported
                                           protein"
                                           /protein-id="CAD07724.1"
                                           /db-xref="GI:16504276"
                                           /db-xref="SPTREMBL:Q8Z3N2"
                                           /translation="MDDVFGILPSWMFTAIVAVI
                                           VLLIIGIIFARLYRRASAEQAFVR
                                           TGLGGQKVVMSGGAIVMPIFHEIIPINMNTLKLE
                                           VSRATVDSLITKDRMRVDVVVAFF
                                           VRVKPSVEGIATSAQTLGQRTLSPEDLRMLVEDK
                                           FVDALRATAAQMTMHELQDTRENF
                                           VQGVQNTVAEDLSKNGLELESVSLTNFNQTSKEH
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                                            ERNEVEQDVEVAVREKNRDALERKLEIEQQEAFM
                                            TLEQEQQVKTRTAEQNAKIAAFEA
                                            ERHREAEQTRILAERQIQETEIEREQAVRSRKVE
                                            AEREVRIKEIEQQQVTEIANQTKS
                                            IAIAAKSEQQSQAEARANDALADAVRAQQNVETT
                                            RQTAEADRAKQVALIAAAQDAETK
                                            AVELTVRAKAEKEAAELQAAAIIELAEAARKKGL
                                            AEAEAQRALNDAINVLSDEQTSLK
                                            FKLALLQSLPAVIEKSVEPMKSIDGIKIIQVDGL
                                            NRGATAGDVAAGGANGGNLAEQAL
                                            SAALTYRTQAPLIDSLLNEIGIAGGSLKALTTPL
                                            VSSATDEINREATIKEQ"
gene            complement(14060..15493    /gene="rfaE"
                )
                                            /note="synonym: STY3379"
CDS             complement(14060..15493    /gene="rfaE"
                )
                                            /EC-number="2.7.-.-"
                                            /note="Highly similar to
                                            Escherichia coli ADP-heptose
                                            synthase RfaE SW:RFAE-ECOLI
                                            (P76658) (477 aa) fasta scores:
                                            E(): 0, 93.5% id in 476 aa and to
                                            Salmonella enterica RfaE TR:Q9RFY8
                                            (EMBL:AF163661) (477 aa) fasta
                                            scores: E(): 0, 99.4% id in 477
                                            aa"
                                            /codon-start=1
                                            /transl-table=11
                                            /product="ADP-heptose synthase"
                                            /protein-id="CAD07725.1"
                                            /db-xref="GI:16504277"
                                            /db-xref="GOA:Q8XEW9"
                                            /db-xref="SPTREMBL:Q8XEW9"
                                            /translation="MKVNLPAFERAGVMVVGDVM
                                            LDRYWYGPTCRISPEAPVPVVKVN
                                            TVEERPGGAANVAMNIASLGANARLVGLTGIDDA
                                            ARALSKTLAEVNVKCDFVSVPTHP
                                            TITKLRVLSRNQQLIRLDFEEGFEGVDPQPLHER
                                            INQALGSIGALVLSDYAKGALTSV
                                            QTMISLARQAGVPVLIDPKGTDFERYRGATLLTP
                                            NLSEFEAVAGKCKSEDELVERGMK
                                            LIADYDLSALLVTRSEQGMTLLQPNKAPLHMPTQ
                                            AQEVYDVTGAGDTVIGVLAATLAA
                                            GNTLEEACYFANAAAGVVVGKLGTSTVSPIELEN
                                            AVRGRADTGFGVMTEEELRQAVAS
                                            ARKRGEKVVMTNGVFDILHAGHVSYLANARKLGD
                                            RLIVAVNSDASTKRLKGESRPVNP
                                            LEQRMIVLGALESVDWVVSFEEDTPQRLIAGILP
                                            DLLVKGGDYKPEEIAGSEEVWANG
                                            GEVMVLNFEDGCSTTNIIKKIQTESEK"
misc-feature    complement(14072..14464    /gene="rfaE"
                )
                                            /note="Pfam match to entry PF01467
                                            Cytidylyltransf,
                                            Cytidylyltransferase, score
                                            139.30, E-value 7e-38"
misc-feature    complement(15173..15343    /gene="rfaE"
                )
                                            /note="Pfam match to entry PF00294
                                            pfkB, pfkB family carbohydrate
                                            kinase, score 20.00, E-value
                                            2.3e-05"
misc-feature    complement(15272..15343    /gene="rfaE"
                )
                                            /note="PS00583 pfkB family of
                                            carbohydrate kinases signature 1"
gene            complement(15541..18384    /gene="STY3380"
                )
                                            /note="synonym: glnE"
CDS             complement(15541..18384    /gene="STY3380"
                )
                                            /note="Orthologue of E. coli glnE
                                            (GLNE-ECOLI); Fasta hit to
                                            GLNE-ECOLI (946 aa), 88% identity
```

```
                                        /codon-start=1
                                        /transl-table=11
                                        /product="adenyl-transferase"
                                        /protein-id="CAD07726.1"
                                        /db-xref="GI:16504278"
                                        /db-xref="GOA:Q8Z3N1"
                                        /db-xref="SPTREMBL:Q8Z3N1"
                                        /translation="MTPLSSPLSQYWQTVVERLP
                                        EGFTETSLSAQAKSVLTFSDFALD
                                        SVIAHPEWLAELESASPQADEWRHYAGWLQEALA
                                        GVCDDASLMRELRLFRRRIMVRIA
                                        WAQTLSLVDDETILQQLSHLAETLIVGARDWLYA
                                        ACCREWGTPCNPQGVPQPLLILGM
                                        GKLGGGELNFSSDIDLIFAWPEHGETRGGRRELD
                                        NAQFFTRLGQRLIKALDQPTMDGF
                                        VYRVDMRLRPFGDSGPLVLSFAALEDYYQEQGRD
                                        WERYAMVKARLMGDNDDAWSRELR
                                        AMLRPFVFRRYIDFSVIQSLRNMKGMIAREVRRR
                                        GLKDNIKLGAGGIREIEFIVQVFQ
                                        LIRGGREPSLQSRSLLPTLDAIAALHLLPENDVA
                                        QLRVAYLFLRRLENLLQSINDEQT
                                        QTLPADDLNRARLAWGMKAENWPQLVGELTDHMA
                                        NVRRVFNELIGDDEADTPQEEERS
                                        EPWREVWQDALQEDDSTPVLAHLADEDRRQVLTL
                                        IADFRKELDKRPIGPRGRQVLDQL
                                        MPHLLADVCSREDAAVTLSRITPLLAGIVTRTTY
                                        LELLSEFPGALKHLIMLCAASPMI
                                        ASQLARYPLLLDELLDPGTLYQPTATDAYRDELR
                                        QYLLRVPEEDEEQQLEALRQFKQA
                                        QLLRIAAADIAGTLPVMKVSDHLTWLAEAMIDAV
                                        VQQAWTQMVARYGQPAHLDERQGR
                                        GFAVVGYGKLGGWELGYSSDLDLIFLHDCPMDVM
                                        TNGEREIDGRQFYLRLAQRIMHLF
                                        STRTSSGILYEVDARLRPSGAAGMLVTSADAFAD
                                        YQQHEAWTWEHQALVRARVVYGDP
                                        QLTSQFDAVRRTIMTTARDGKTLQTEVREMREKM
                                        RAHLGNKHRDRFDIKADEGGITDI
                                        EFIAQYLVLRYAHEKPKLTRWSDNVRILELLAQN
                                        GIMDEHEAQALTVAYTTLRDELHH
                                        LALQELPGHVAQTCFSKERALVQASWRKWLVAV"
misc-feature      complement(16387..16416  /gene="STY3380"
                  )
                                        /note="PS00904 Protein
                                        prenyltransferases alpha subunit
                                        repeat signature"
gene              complement(18502..19803  /gene="STY3381"
                  )
CDS               complement(18502..19803  /gene="STY3381"
                  )
                                        /note="Orthologue of E. coli ygiF
                                        (YGIF-ECOLI); Fasta hit to
                                        YGIF-ECOLI (433 aa), 85% identity
                                        in 433 aa overlap"
                                        /codon-start=1
                                        /transl-table=11
                                        /product="conserved hypothetical
                                        protein"
                                        /protein-id="CAD07727.1"
                                        /db-xref="GI:16504279"
                                        /db-xref="SPTREMBL:Q8Z3N0"
                                        /translation="MAQEIELKFIVNHDAVDALR
                                        NHLHTLGGEHHAPSQLLNIYFETP
                                        DNWLRRHDMGLRIRGENGRYEMTMKIAGRVTGGL
                                        HQRPEYNVALSEPVLDLTQLPAEV
                                        WPDGNLPDGLASSVQPLFSTDFYREKWCLDVDGS
                                        RIEIALDLGDVKAGEFAEPICELE
                                        LELLRGDTRAVLKLAKQLLSQTGLRQGSLSKAAR
                                        GYHLAQGNAPRENTPTAILRTAAK
                                        ATVEQGLEASLDLALSQWQYHEELWLRGDESAKE
                                        HVLDAMGLVRHALMLFGGIVPRKA
                                        SAHLRDLLTQAEATMTSAVSAVTAVYSTQTAMAK
                                        LALTEWLVTKAWQPFLDAKAQAKM
                                        ADSFKRFADIHLSRHAAELKKVFGQPLGDKYRDQ
                                        LPRLTRDIDSVLLLAGYYDAMVAQ
                                        AWLENWQGLRHAIITGQRIEIEHFRNEAINQQPF
```

gene	20045..20659	/gene="STY3382"
CDS	20045..20659	/gene="STY3382"

/note="Orthologue of E. coli ygiM (YGIM-ECOLI); Fasta hit to YGIM-ECOLI (206 aa), 91% identity in 206 aa overlap. Contains a possible membrane spanning hydrophobic domain"
/codon-start=1
/transl-table=11
/product="putative membrane protein"
/protein-id="CAD07728.1"
/db-xref="GI:16504280"
/db-xref="SPTREMBL:Q8XFH7"
/translation="MPKLRLIGLTLLALSATAVS HAEETRYVSDELNTWVRSGPGDNY RLVGTVNAGEEVTLLQSDANYGQIKDSSGRTAWI PLKELNTTPSLRTRVPDLENQVKT LTDKLNNIDTTWNQRTADMQQKVAQSDSVINGLK EENQKLKNELIVAQKKVSAANLQL DDKQRTIIMQWFMYGGGVLGIGLLLGLVLPHMIP SRKRKDRWMN"

gene	20722..21963	/gene="STY3383"
		/note="synonym: cca"
CDS	20722..21963	/gene="STY3383"

/EC-number="2.7.7.25"
/note="Similar to Escherichia coli tRNA nucleotidyltransferase ccA SW:CCA-ECOLI (P06961) (412 aa) fasta scores: E(): 0, 89.5% id in 411 aa"
/codon-start=1
/transl-table=11
/product="tRNA nucleotidyltransferase"
/protein-id="CAD07729.1"
/db-xref="GI:16504281"
/db-xref="GOA:Q8Z3M9"
/db-xref="SPTREMBL:Q8Z3M9"
/translation="MKIYLVGGAVRDALLGLPVK DKDWVVVGATPQEMLDAGYQQVGR DFPVFLHPQTHEEYALARTERKSGSGYTGFTCYA APDVTLEADLQRRDLTINALARDD DGQIIDPYHGRRDLEARLLRHVSPAFGEDPLRVL RVARFAARYAHLSFRIADETLTLM REMTAAGELEHLTPERVWKETENALTTRNPQVYF QVLRDCGALRVLFPEIDALFGVPA PAKWHPEIDTGVHTLMTLSMAAMLSPQLDVRFAT LCHDVGKGLTPKNLWPRHHGHGPV GVKLVEQLCQRLRVPNDLRDLAKLVAAYHDLIHT FPILQPKTIVKLFDAIDAWRKPQR VEQIALTSEADVRGRTGFEASDYPQGRWLREAWQ VAQAVPTKEVVEAGFKGIEIREEL TKRRIAAVANWKEKRCPNPAS"

misc-feature	20893..21369	/gene="STY3383"

/note="Pfam match to entry PF01743 PolyA-pol, Poly A polymerase family, score 216.30, E-value 4.6e-61"

misc-feature	21403..21708	/gene="STY3383"

/note="Pfam match to entry PF01966 HD, HD domain, score 85.90, E-value 8.3e-22"

gene	complement(22068..22889)	/gene="STY3384"
		/note="synonym: bacA"
CDS	complement(22068..22889)	/gene="STY3384"

/note="Orthologue of E. coli bacA (BACA-ECOLI); Fasta hit to BACA-ECOLI (273 aa), 97% identity in 273 aa overlap"
/codon-start=1
/transl-table=11

```
                                        protein (putative undecaprenol
                                        kinase)"
                                        /protein-id="CAD07730.1"
                                        /db-xref="GI:16504282"
                                        /db-xref="GOA:Q8ZLY3"
                                        /db-xref="SWISS-PROT:Q8ZLY3"
                                        /translation="MSDMHSLLIAAILGVVEGLT
                                        EFLPVSSTGHMIIVGHLLGFEGDT
                                        AKTFEVVIQLGSILAVVVMFWRRLFGLIGIHFGR
                                        PLQREGESKGRLTLIHILLGMIPA
                                        VVLGLVFHDTIKSLFNPINVMYALVVGGLLLIAA
                                        ECLKPKEPRAPGLDDMTYRQAFMI
                                        GCFQCLALWPGFSRSGATISGGMLMGVSRYAASE
                                        FSFLLAVPMMMGATVLDLYKSWSF
                                        LTAADIPMFAVGFVTAFVVALIAIKTFLQLIKRI
                                        SFIPFAIYRFVVAAAVYVVFF"
gene            complement(22987..23349  /gene="folB"
                )
                                        /note="synonym: STY3385"
CDS             complement(22987..23349  /gene="folB"
                )
                                        /EC-number="4.1.2.25"
                                        /note="Similar to Escherichia coli
                                        dihydroneopterin aldolase folB
                                        SW:FOLB-ECOLI (P31055; P76659)
                                        (122 aa) fasta scores: E(): 0,
                                        93.3% id in 119 aa"
                                        /codon-start=1
                                        /transl-table=11
                                        /product="dihydroneopterin
                                        aldolase"
                                        /protein-id="CAD07731.1"
                                        /db-xref="GI:16504283"
                                        /db-xref="GOA:Q8Z3M7"
                                        /db-xref="SPTREMBL:Q8Z3M7"
                                        /translation="MMDIVFIEQLSVITTIGVYD
                                        WEQTIEQKLVFDIEMAWDNRKSAK
                                        SDDVADCLSYADIADTVINHVEGGRFALVERVAE
                                        EVADLLLSRFNSPWVRIKLSKPSA
                                        VARAANVGVIIERGNNLK"
misc-feature    complement(22999..23337  /gene="folB"
                )
                                        /note="Pfam match to entry PF02152
                                        FolB, Dihydroneopterin aldolase,
                                        score 176.60, E-value 5.7e-50"
gene            23453..24064             /gene="STY3386"
CDS             23453..24064             /gene="STY3386"
                                        /note="Orthologue of E. coli ygiH
                                        (YGIH-ECOLI); Fasta hit to
                                        YGIH-ECOLI (205 aa), 95% identity
                                        in 203 aa overlap. Contains
                                        multiple possible membrane
                                        spanning hydrophobic domains"
                                        /codon-start=1
                                        /transl-table=11
                                        /product="putative membrane
                                        protein"
                                        /protein-id="CAD07732.1"
                                        /db-xref="GI:16504284"
                                        /db-xref="GOA:Q8XGX7"
                                        /db-xref="SWISS-PROT:Q8XGX7"
                                        /translation="MSAIAPGMILFAYLCGSISS
                                        AILVCRIAGLPDPRESGSGNPGAT
                                        NVLRIGGKGAAVAVLIFDILKGMLPVWGAYALGV
                                        TPFWLGLIAIAACLGHIWPVFFGF
                                        KGGKGVATAFGAIAPIGWDLTGVMAGTWLLTVLL
                                        SGYSSLGAIVSALIAPFYVWWFKP
                                        QFTFPVSMLSCLILLRHHDNIQRLWRRQETKIWT
                                        KLKKKRQKD"
gene            complement(24314..25327  /gene="STY3387"
                )
CDS             complement(24314..25327  /gene="STY3387"
                )
                                        /note="Highly similar to
                                        Pasteurella haemolytica
```

gcP SW:GCP-PASHA (P36175) (325 aa)
fasta scores: E(): 0, 78.1% id in
319 aa and to Escherichia coli
probable O-sialoglycoprotein
endopeptidase SW:GCP-ECOLI () (337
aa) fasta scores: E(): 0, 95.0% id
in 337 aa"
/codon-start=1
/transl-table=11
/product="possible glycoprotease"
/protein-id="CAD07733.1"
/db-xref="GI:16504285"
/db-xref="GOA:Q8Z3M6"
/db-xref="SPTREMBL:Q8Z3M6"
/translation="MRVLGIETSCDETGIAIYDD
KKGLLANQLYSQVKLHADYGGVVP
ELASRDHVRKTVPLIQAALKEAALTASDIDAVAY
TAGPGLVGALLVGATVGRSLAFAW
NVPAIPVHHMEGHLLAPMLEDNPPDFPFVALLVS
GGHTQLISVTGIGQYELLGESIDD
AAGEAFDKTAKLLGLDYPGGPMLSKMASQGTAGR
FVFPRPMTDRPGLDFSFSGLKTFA
ANTIRSNGDDEQTRADIARAFEDAVVDTLMIKCK
RALESTGFKRLVMAGGVSANRTLR
AKLAEMMQKRRGEVFYARPEFCTDNGAMIAYAGM
VRFKAGVTADLGVTVRPRWPLAEL PAA"

misc-feature	complement(24386..25327)	/gene="STY3387"

/note="Pfam match to entry PF00814
Peptidase-M22, Glycoprotease
family, score 670.50, E-value
8.3e-198"

misc-feature	complement(24980..25042)	/gene="STY3387"

/note="PS01016 Glycoprotease
family signature"

gene	25555..25770	/gene="STY3388"
		/note="synonym: rpsU"
CDS	25555..25770	/gene="STY3388"

/note="Orthologue of E. coli rpsU
(RS21-ECOLI); Fasta hit to
RS21-ECOLI (70 aa), 100% identity
in 70 aa overlap"
/codon-start=1
/transl-table=11
/product="30S ribosomal subunit
protein S21"
/protein-id="CAD07734.1"
/db-xref="GI:16504286"
/db-xref="GOA:P02379"
/db-xref="SWISS-PROT:P02379"
/translation="MPVIKVRENEPFDVALRRFK
RSCEKAGVLAEVRRREFYEKPTTE
RKRAKASAVKRHAKKLARENARRTRLY"

misc-feature	25558..25719	/gene="STY3388"

/note="Pfam match to entry PF01165
Ribosomal-S21, Ribosomal protein
S21, score 127.90, E-value
1.9e-34"

misc-feature	25591..25629	/gene="STY3388"
		/note="PS01181 Ribosomal protein
		S21 signature"
gene	26006..27751	/gene="STY3389"
		/note="synonym: dnaG"
CDS	26006..27751	/gene="STY3389"

/note="Orthologue of E. coli dnaG
(PRIM-ECOLI); Fasta hit to
PRIM-ECOLI (581 aa), 86% identity
in 581 aa overlap"
/codon-start=1
/transl-table=11
/product="DNA primase"
/protein-id="CAD07735.1"
/db-xref="GI:16504287"
/db-xref="GOA:Q8Z3M5"

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                                    /translation="MAGRIPRVFINDLLARTDIV
                                    DLIDVRVKLKKQGKNYHACCPFHN
                                    EKTPSFTVNGEKQFYHCFGCGAHGNAIDFLMNYD
                                    KLEFVETVEELAAMHNLEIPYEAG
                                    TGLSQIERHQRQNLYQLMNGLNDFYQQSLTHPAA
                                    KPARDYLQKRGLSAEIIQRFAIGF
                                    APPGWDNALKRFGNNSDNKALLLDAGMLVNNEQG
                                    STYDRFRNRVMFPIRDKRGRVIGF
                                    GGRVLGNDTPKYLNSPETDIFHKGRQLYGLYEAQ
                                    QYSAEPQRLLVVEGYMDVVALAQY
                                    DINYAVASLGTSTTADHMHMLFRATNNVICCYDG
                                    DRAGRDAAWRALETAMPYMTDGRQ
                                    VRFMFLPDGEDPDTLVRKEGKAAFEARMEQAQPL
                                    STFLFNSLLPQVDLSSPDGSTQLA
                                    ALALPLINQVPGDTHRIQLRQTLGLKLGIFDDSQ
                                    LDRLVPKQAESGVSRPAPQLKRTT
                                    MRILIGLLVQNPDLAPLVPPLDALDQNKLPGLGL
                                    FKELVKTCLAQPGLTTGQLLELYR
                                    GTNDAATLEKLSMWDDIADKAIAEKTFTDSLNHM
                                    FDSLLQLRQEELIARDRTHGLSSE
                                    ERRELWTLNQELARK"
misc-feature    26111..26281        /gene="STY3389"
                                    /note="Pfam match to entry PF01807
                                    zf-CHC2, CHC2 zinc finger, score
                                    146.10, E-value 6.2e-40"
misc-feature    26780..27028        /gene="STY3389"
                                    /note="Pfam match to entry PF01751
                                    Toprim, Toprim domain, score
                                    91.80, E-value 1.4e-23"
gene            27766..29748        /gene="STY3390"
                                    /note="synonym: rpoD"
CDS             27766..29748        /gene="STY3390"
                                    /note="Orthologue of E. coli rpoD
                                    (RPSD-ECOLI); Fasta hit to
                                    RPSD-ECOLI (613 aa), 98% identity
                                    in 615 aa overlap"
                                    /codon-start=1
                                    /transl-table=11
                                    /product="RNA polymerase sigma-70
                                    factor"
                                    /protein-id="CAD07736.1"
                                    /db-xref="GI:16504288"
                                    /db-xref="GOA:Q8Z3M4"
                                    /db-xref="SPTREMBL:Q8Z3M4"
                                    /translation="MPHIVREAPDSRSERQRPKY
                                    KYALALNVDSYTVDTNQTNKCGYR
                                    LMEQNPQSQLKLLVTRGKEQGYLTYAEVNDHLPE
                                    DIVDSDQIEDIIQMINDMGIQVME
                                    EAPDADDLLLAENTTSTDEDAEEAAAQVLSSVES
                                    EIGRTTDPVRMYMREMGTVELLTR
                                    EGEIDIAKRIEDGINQVQCSVAEYPEAITYLLEQ
                                    YDRVEAEEARLSDLITGFVDPNAE
                                    EEMAPTATHVGSELSQEDLDDDEDEDEEDGDDDA
                                    ADDDNSIDPELAREKFAELRAQYV
                                    VTRDTIKAKGRSHAAAQEEILKLSEVFKQFRLVP
                                    KQFDYLVNSMRVMMDRVRTQERLI
                                    MKLCVEQCKMPKKNFITLFTGNETSETWFNAAIA
                                    MNKPWSEKLHDVAEEVQRCLQKLR
                                    QIEEETGLTIEQVKDINRRMSIGEAKARRAKKEM
                                    VEANLRLVISIAKKYTNRGLQFLD
                                    LIQEGNIGLMKAVDKFEYRRGYKFSTYATWWIRQ
                                    AITRSIADQARTIRIPVHMIETIN
                                    KLNRISRQMLQEMGREPTPEELAERMLMPEDKIR
                                    KVLKIAKEPISMETPIGDDEDSHL
                                    GDFIEDTTLELPLDSATTESLRAATHDVLAGLTA
                                    REAKVLRMRFGIDMNTDHTLEEVG
                                    KQFDVTRERIRQIEAKALRKLRHPSRSEVLRSFL
                                    DD"
misc-feature    29023..29706        /gene="STY3390"
                                    /note="Pfam match to entry PF00140
                                    sigma70, Sigma-70 factor, score
                                    462.50, E-value 3.5e-135"
misc-feature    29113..29154        /gene="STY3390"
                                    /note="PS00715 Sigma-70 factors
                                    family signature 1"
```

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gene            complement(29872..30378  /gene="mug"
                )
                                         /note="synonym: STY3391"
CDS             complement(29872..30378  /gene="mug"
                )
                                         /EC-number="3.2.2.-"
                                         /note="Similar to Escherichia coli
                                         G/U mismatch-specific DNA
                                         glycosylase Mug SW:MUG-ECOLI
                                         (P43342) (168 aa) fasta scores:
                                         E(): 0, 80.8% id in 167 aa
                                         Orthologue of E. coli MUG-ECOLI;
                                         Fasta hit to MUG-ECOLI (168 aa),
                                         81% identity in 167 aa overlap"
                                         /codon-start=1
                                         /transl-table=11
                                         /product="G/U mismatch-specific
                                         DNA glycosylase"
                                         /protein-id="CAD07737.1"
                                         /db-xref="GI:16504289"
                                         /db-xref="GOA:Q8XFG2"
                                         /db-xref="SPTREMBL:Q8XFG2"
                                         /translation="MVKDILAPGLRVVFCGINPG
                                         LSSANTGFPFAHPANRFWKVIHLA
                                         GFTDRQLKPEEAEKLLDFRCGVTKLVDRPTVQAT
                                         EVKLHELRSGGRNLIEKIEDYQPA
                                         ALAVLGKQAFEQGFSQRGIAWGKQKIAIGATMVW
                                         VLPNPSGLNRIKTEKLVEAYRELD QALIMRGL"
misc-feature    complement(29953..30369  /gene="mug"
                )
                                         /note="Pfam match to entry PF02299
                                         DNA-glycosylase, G:T/U
                                         mismatch-specific DNA glycosylase,
                                         score 285.30, E-value 7.6e-82"
tRNA            30504..30579             /product="tRNA-Met"
                                         /note="tRNA Met anticodon CAT,
                                         Cove score 93.86"
gene            complement(30659..31426  /gene="STY3392"
                )
CDS             complement(30659..31426  /gene="STY3392"
                )
                                         /note="Orthologue of E. coli
                                         YQJH-ECOLI; Fasta hit to
                                         YQJH-ECOLI (254 aa), 72% identity
                                         in 253 aa overlap"
                                         /codon-start=1
                                         /transl-table=11
                                         /product="conserved hypothetical
                                         protein"
                                         /protein-id="CAD07738.1"
                                         /db-xref="GI:16504290"
                                         /db-xref="SPTREMBL:Q8Z3M3"
                                         /translation="MTTSSARYPQRVRNELRFRE
                                         LTVLRVERISAGFQRIVLGGEALD
                                         GFTSLGFDDHTKVFFPEPGCRFTPPTVTEEGIIW
                                         GEGVRPVSRDYTPLYDEAHRELAL
                                         DFFIHDGGVASRWAMEAREGDTLTIGGPRGSLVV
                                         PEDYACQVYVCDESGMPALRRRLE
                                         SLSRLPARPAVTALVSIQDAAYRDYLAHLTDITV
                                         EYVVGGDEQAMQTRLSQLAIPESD
                                         YFIWITGEGKTVKRLSQCFEKGFDPHLVRAAAYW
                                         HRK"
gene            31661..32305             /gene="STY3393"
CDS             31661..32305             /gene="STY3393"
                                         /note="Orthologue of E. coli
                                         YQJI-ECOLI; Fasta hit to
                                         YQJI-ECOLI (207 aa), 69% identity
                                         in 215 aa overlap. Note
                                         hydrophylic N-terminus rich in the
                                         amino acid His."
                                         /codon-start=1
                                         /transl-table=11
                                         /product="conserved hypothetical
```

```
                                        /protein-id="CAD07739.1"
                                        /db-xref="GI:16504291"
                                        /db-xref="SPTREMBL:Q8Z3M2"
                                        /translation="MQNQHEGCCKNQDHKHDGCC
                                        KDREHQHEGCHSAHQHENASCGGE
                                        HRHGHGCGRHGQGGGRRQRFFGHGELRLVILDIL
                                        TRDASHGYELIKAIENLTGGGYTP
                                        SAGVIYPTLDFLQDQQFITISDEEGGRKKIAITA
                                        NGAQWLDENREHLTHIQARLKARC
                                        VGMELRKNPQMKRALDNFKAVLDLRINHSDINDA
                                        QIKRIIGVIDRAALEIAELD"
gene                 complement(32302..33870  /gene="cheM"
                     )
                                        /note="synonym: STY3394"
CDS                  complement(32302..33870  /gene="cheM"
                     )
                                        /note="Similar to many including:
                                        Escherichia coli methyl-accepting
                                        chemotaxis protein II Tar or CheM
                                        SW:MCP2-ECOLI (P07017; P76301)
                                        (553 aa) fasta scores: E(): 0,
                                        34.7% id in 519 aa Fasta hit to
                                        MCP3-ECOLI (546 aa), 35% identity
                                        in 524 aa overlap Fasta hit to
                                        MCP4-ECOLI (533 aa), 33% identity
                                        in 525 aa overlap Fasta hit to
                                        MCP1-ECOLI (551 aa), 37% identity
                                        in 531 aa overlap Paralogue of E.
                                        coli tar (MCP2-ECOLI); Fasta hit
                                        to MCP2-ECOLI (553 aa), 35%
                                        identity in 519 aa overlap"
                                        /codon-start=1
                                        /transl-table=11
                                        /product="methyl-accepting
                                        chemotaxis protein II"
                                        /protein-id="CAD07740.1"
                                        /db-xref="GI:16504292"
                                        /db-xref="GOA:Q8Z3M1"
                                        /db-xref="SPTREMBL:Q8Z3M1"
                                        /translation="MFLHNIKIRSKLFMAFGLFI
                                        VLMVVSSALSLFSLDRANTGMQDI
                                        ITNDYPTTVKANLLIDNFNDFIIAQQLMLLDEEG
                                        RWSQSSQKELSEISQRISALLDEL
                                        SRENSHDADSQKIINEIREARQQYLESRFRILKD
                                        IQSNNRQAAIQEMMTRTVQVQKVY
                                        KDKVQELIAVQDALMHEASVQVKEDFKNNRTLLI
                                        TLALISIAAGGVIGWYIVRSITRP
                                        LDDAVRFAEAIADGDLTRHITTDYKDETGVLLQA
                                        LMAMKTRLLDIVQEVQNGSESIST
                                        AAAQIVAGNQDLAARTEEQASSVEETAASMEQIT
                                        ATVKNTADHTSEATKLSAGAASVV
                                        KNNGEMMNQVTQKMRVINDTANRMSDIINIIDSI
                                        AFQTNILALNAAVEAARAGEHGRG
                                        FAVVAGEVRQLAQKSASSASEIRNLIEDSTSQTQ
                                        EGMHLVEKASALINGMVDNVEEMD
                                        VILREIGQASREQTDGISQINSAIGLIDAATQQN
                                        SCLVEESVAAAASLNEQALHLKEL
                                        VNVFRVREEDTQPA"
misc-feature         complement(32617..32799  /gene="cheM"
                     )
                                        /note="Pfam match to entry PF00015
                                        MCPsignal, Methyl-accepting
                                        chemotaxis protein (MCP) signaling
                                        domain, score 125.70, E-value
                                        1.7e-34"
misc-feature         complement(33085..33294  /gene="cheM"
                     )
                                        /note="Pfam match to entry PF00672
                                        DUF5, HAMP domain, score 59.90,
                                        E-value 5.4e-14"
gene                 complement(34258..35778  /gene="STY3395"
                     )
                                        /note="synonyms: aer, air"
CDS                  complement(34258..35778  /gene="STY3395"
                     )
```

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                                        (AER-ECOLI); Fasta hit to
                                        AER-ECOLI (506 aa), 84% identity
                                        in 506 aa overlap"
                                        /codon-start=1
                                        /transl-table=11
                                        /product="aerotaxis receptor
                                        protein"
                                        /protein-id="CAD07741.1"
                                        /db-xref="GI:16504293"
                                        /db-xref="GOA:Q8Z3M0"
                                        /db-xref="SPTREMBL:Q8Z3M0"
                                        /translation="MSSHPYVSQLNTPLDDDTTL
                                        MSTTDLESYITHANDTFVQVSGYQ
                                        LNELLARPHNLVRHPDMPKAAFADMWYTLKQGEP
                                        WSGIVKNRRKNGDHYWVRANAVPM
                                        IREGRVTGYMSIRTRATDDEIAAVEPLYQALNEG
                                        RCSKRIHKGLVVRQGLLGKLPAMP
                                        VRWRVRSIMGLMAVMLALALFGTDASWQALLLGA
                                        LAMLAGTALFEWQIVRPIENVATQ
                                        ALKVATGERNSVQHLNRSDELGLTLRAVGQLGLM
                                        CRWLINDVSSQVSSVRNGSERLAK
                                        GNNDLNEHTRQTVENVQETVTTMNQMAESVKLNS
                                        ETASAADKLSMAASSAATQGGEAM
                                        DTVIKTMDDIAHSTQRIGTITTLINDIAFQTNIL
                                        ALNAAVEAARAGEQGKGFAVVAGE
                                        VRHLASRSANAANDIRKLIDASATKVQSGSEQVH
                                        AAGRTMDDIVAQVQNVTLLIARIS
                                        QSTQEQTDGLSSLTRAVDELNRITQKNAALVEES
                                        AQVSAMVKHRASRLEDAVTVLH"
misc-feature     complement(34546..34728  /gene="STY3395"
                 )
                                        /note="Pfam match to entry PF00015
                                        MCPsignal, Methyl-accepting
                                        chemotaxis protein (MCP) signaling
                                        domain, score 123.40, E-value
                                        7.9e-34"
misc-feature     complement(35014..35223  /gene="STY3395"
                 )
                                        /note="Pfam match to entry PF00672
                                        DUF5, HAMP domain, score 28.80,
                                        E-value 0.00013"
misc-feature     complement(35416..35541  /gene="STY3395"
                 )
                                        /note="Pfam match to entry PF00785
                                        PAC, PAC motif, score 33.70,
                                        E-value 5.6e-08"
gene             36298..37587            /gene="STY3396"
CDS              36298..37587            /gene="STY3396"
                                        /note="Fasta hit to ARGM-ECOLI
                                        (406 aa), 35% identity in 373 aa
                                        overlap Fasta hit to ARGD-ECOLI
                                        (405 aa), 34% identity in 372 aa
                                        overlap Fasta hit to GOAG-ECOLI
                                        (421 aa), 35% identity in 405 aa
                                        overlap Fasta hit to GABT-ECOLI
                                        (426 aa), 34% identity in 379 aa
                                        overlap Orthologue of E. coli ygjG
                                        (OAT-ECOLI); Fasta hit to
                                        OAT-ECOLI (429 aa), 95% identity
                                        in 428 aa overlap"
                                        /codon-start=1
                                        /transl-table=11
                                        /product="probable
                                        aminotransferase"
                                        /protein-id="CAD07742.1"
                                        /db-xref="GI:16504294"
                                        /db-xref="GOA:Q8Z3L9"
                                        /db-xref="SPTREMBL:Q8Z3L9"
                                        /translation="MKALNREVIDYFKEHVNPGF
                                        LEYRKSVTAGGDYGAVEWQAGSLN
                                        TLVDTQGQEFIDCLGGFGIFNVGHRNPVVVSAVQ
                                        NQLAKQPLHSQELLDPLRAMLAKT
                                        LAALTPGKLKYSFFCNSGTESVEAALKLAKAYQS
                                        PRGKFTFIATSGAFHGKSLGALSA
                                        TAKSTFRRPFMPLLPGFRHVPFGNIDAMSMAFSE
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                                        PPQGYLTEVRKLCDEFGALMILDEVQTGMGRTGK
                                        MFACEHENVQPDILCLAKALGGGV
                                        MPIGATIATEEVFSVLFDNPFLHTTTFGGNPLAC
                                        AAALATINVLLEQNLPAQAEQKGD
                                        TLLDGFRQLAREYPNLVHEARGKGMLMAIEFVDN
                                        ETGYRFASEMFRQRVLVAGTLNNA
                                        KTIRIEPPLTLTIELCEQVLKSARNALAAMQVSV
                                        EEV"
misc-feature    36415..37500            /gene="STY3396"
                                        /note="Pfam match to entry PF00202
                                        aminotran-3, Aminotransferases
                                        class-III pyridoxal-phosphate,
                                        score 603.60, E-value 2.1e-209"
misc-feature    37009..37122            /gene="STY3396"
                                        /note="PS00600 Aminotransferases
                                        class-III pyridoxal-phosphate
                                        attachment site"
gene            37758..39775            /gene="STY3397"
                                        /pseudo
CDS             37758..39775            /gene="STY3397"
                                        /note="Highly similar to
                                        Escherichia coli 2,4-dienoyl-coa
                                        reductase [NADPH] fadH
                                        SW:FADH-ECOLI (P42593) (671 aa)
                                        fasta scores: E(): 0, 87.6% id in
                                        355 aa. Contains a framefhift
                                        mutation after codon 356 and a
                                        stop codon within the CDS. The
                                        sequence has been checked and is
                                        believed to be correct"
                                        /pseudo
                                        /codon-start=1
                                        /transl-table=11
                                        /product="probable oxidoreductase
                                        (pseudogene)."
misc-feature    37770..38750            /gene="STY3397"
                                        /note="Pfam match to entry PF00724
                                        oxidored-FMN, NADH:flavin
                                        oxidoreductase / NADH oxidase
                                        family, score 490.90, E-value
                                        9.8e-144"
                                        /pseudo
gene            complement(39856..40992 /gene="STY3400"
                )
                                        /note="synonym: ygjO"
CDS             complement(39856..40992 /gene="STY3400"
                )
                                        /note="Orthologue of E. coli ygjO
                                        (YGJO-ECOLI); Fasta hit to
                                        YGJO-ECOLI (388 aa), 91% identity
                                        in 378 aa overlap"
                                        /codon-start=1
                                        /transl-table=11
                                        /product="conserved hypothetical
                                        protein"
                                        /protein-id="CAD07744.1"
                                        /db-xref="GI:16504295"
                                        /db-xref="GOA:Q8Z3L8"
                                        /db-xref="SPTREMBL:Q8Z3L8"
                                        /translation="MSHVDDGFRSLTLKRFPQTD
                                        DVNPLLAWEAADEYLLQQLDETEI
                                        RGPVLILNDTFGALSCALAEHSPYSIGDSYLSEL
                                        GTRENLRHNGIAESSVTFLDSTAD
                                        YPQAPGVVLIKVPKTLALLEQQLRALRKVVTAQT
                                        RIIAGAKARDIHTSTLELFEKVLG
                                        PTTTTLAWKKARLINCTFSHPQLANAPQTLSWKL
                                        EDTGWTIHNHANVFSRTGLDIGAR
                                        FFMQHLPENLDGEIVDLGCGNGVIGLSLLAKNPQ
                                        ANVVFVDESPMAVDSSRLNVETNL
                                        PEAFERCEFMINNALSGVEPFRFNAVFCNPPFHQ
                                        KHALTDNIAWEMFHHARRCLKING
                                        ELYIVANRHLDYFHKLKKIFGNCATIATNNKFVI
                                        LKAVKQGRRR"
misc-feature    complement(40069..40089 /gene="STY3400"
                )
```

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gene            41078..41575    /gene="STY3401"
CDS             41078..41575    /gene="STY3401"
                                /note="Orthologue of E. coli ygjP
                                (YGJP-ECOLI); Fasta hit to
                                YGJP-ECOLI (179 aa), 88% identity
                                in 162 aa overlap"
                                /codon-start=1
                                /transl-table=11
                                /product="conserved hypothetical
                                protein"
                                /protein-id="CAD07745.1"
                                /db-xref="GI:16504296"
                                /db-xref="GOA:Q8XF71"
                                /db-xref="SPTREMBL:Q8XF71"
                                /translation="MTSLTYLQGYPEHLLAQVRA
                                LIAEQRLGAVLEKRYPGAHDYATD
                                KALYHYTQELKSQFLRNAPPINKVMYDSKIHVLK
                                NALGLHTAVSRVQGGKLKAKAEIR
                                VATVFRNAPEPFLRMIVVHELAHLKEKDHNKAFY
                                QLCCHMEPQYHQLEFDTRLWLTHQ ALSAQ"

gene            41727..42419    /gene="STY3402"
                                /note="synonym: ygjQ"
CDS             41727..42419    /gene="STY3402"
                                /note="Fasta hit to SANA-ECOLI
                                (239 aa), 39% identity in 219 aa
                                overlap Orthologue of E. coli ygjQ
                                (YGJQ-ECOLI); Fasta hit to
                                YGJQ-ECOLI (230 aa), 74% identity
                                in 230 aa overlap"
                                /codon-start=1
                                /transl-table=11
                                /product="conserved hypothetical
                                protein"
                                /protein-id="CAD07746.1"
                                /db-xref="GI:16504297"
                                /db-xref="SPTREMBL:Q8Z3L7"
                                /translation="MLSQCARFIRRLCFTRRALT
                                VACFLLVAAGVALFYSNWLIVNAS
                                QHLTWNDIQTVPARNVGLVLGAKPGNRYFTRRIN
                                TAAALYHAGKVKWLLVSGDNGKKE
                                YDEPSAMQQALIAKGVPEAAIFCDYAGFSTLDSV
                                VRARKVFGESRITIISQAFHNQRA
                                IWLAQQYGIDAIGVNAPDLNKRHGTYTRLREKLA
                                RVSAVLDAKILHRQPKYLGAGVTI
                                GADSAHGCPSRQ"

gene            42471..43505    /gene="STY3403"
CDS             42471..43505    /gene="STY3403"
                                /note="Similar to Escherichia coli
                                hypothetical protein YgjR
                                SW:YGJR-ECOLI (P42599; P42600;
                                P76661) (328 aa) fasta scores:
                                E(): 0, 83.1% id in 326 aa and to
                                Sus scrofa (Pig) dimeric
                                dihydrodiol dehydrogenase Sus2dD
                                TR:Q9TV69 (EMBL:AB021929) (335 aa)
                                fasta scores: E(): 2.9e-15, 25.4%
                                id in 346 aa"
                                /codon-start=1
                                /transl-table=11
                                /product="possible oxidoreductase"
                                /protein-id="CAD07747.1"
                                /db-xref="GI:16504298"
                                /db-xref="GOA:Q8Z3L6"
                                /db-xref="SPTREMBL:Q8Z3L6"
                                /translation="MTKIPFWSPLTFMIRFAVIG
                                TNWITRQFVDAAHETGKFRLAAVY
                                SRRLEQAQSFANDYPVEHLFTSLEAMAQSDAIEA
                                VYIASPNSLHFSQTQRFLQHKKHV
                                MCEKPLASNLAEVDAAIACARDNQRVLFEAFKTA
                                CLPNFLLLRESLPKIGRMHKALLN
                                YCQYSSRYQRYLNGENPNTFNPAFSNGSIMDIGY
                                YCLASAIALWGEPRSVQASANLLE
                                SGVDAHGVVVMDYGDFSVTLQHSKVSDSVLASEI
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                                        ALMQDLTQPQHINTMLYEAGAFAQLIENHAVEHP
                                        GLSLSRATAKWLTEIRRQTGVIFP
                                        ADDLTHPPTA"
misc-feature    42510..43151            /gene="STY3403"
                                        /note="Pfam match to entry PF01408
                                        GFO-IDH-MocA, Oxidoreductase
                                        family, score 177.50, E-value
                                        2.2e-49"
gene            43773..44741            /gene="STY3404"
CDS             43773..44741            /gene="STY3404"
                                        /note="Similar to Escherichia coli
                                        hypothetical protein YgjT
                                        SW:YGJT-ECOLI (P42601) (321 aa)
                                        fasta scores: E(): 0, 86.9% id in
                                        321 aa and to Alcaligenes sp
                                        tellurium resistance protein TerC
                                        SW:TERC-ALCSP (P18780) (346 aa)
                                        fasta scores: E(): 3.5e-12, 34.8%
                                        id in 325 aa. Contains multiple
                                        possible membrane spanning
                                        hydrophobic domains and a possible
                                        N-terminal signal sequence.
                                        Orthologue of E. coli ygjT
                                        (YGJT-ECOLI); Fasta hit to
                                        YGJT-ECOLI (321 aa), 87% identity
                                        in 321 aa overlap"
                                        /codon-start=1
                                        /transl-table=11
                                        /product="possible drug efflux
                                        protein"
                                        /protein-id="CAD07748.1"
                                        /db-xref="GI:16504299"
                                        /db-xref="GOA:Q8Z3L5"
                                        /db-xref="SPTREMBL:Q8Z3L5"
                                        /translation="MNTVGTPLLWGGFAVVVVIM
                                        LSIDLLLQGRRGAHAMSMKQAAGW
                                        SILWVTLSLLFNAAFWWYLAETQGREVADPQALA
                                        FLTGYLIEKSLAVDNVFVWLMLFS
                                        YFSVPPALQRRVLVYGVLGAIVLRTIMIFAGTWL
                                        ITQFEWLLYVFGAFLLFTGVKMAL
                                        AKEDESGIGEKPMVRWLRGHLRMTDTIENEHFFV
                                        RKNGLLYATPLLLVLIMVEFSDVI
                                        FAVDSIPAIFAVTTDPFIVLTSNLFAILGLRAMY
                                        FLLSGVAERFSMLKYGLAVILVFI
                                        GIKMLIVDFYHIPIAISLGVVFGILTITLVINTW
                                        VNHQRDKKLRAQ"
gene            44996..46240            /gene="STY3405"
CDS             44996..46240            /gene="STY3405"
                                        /note="Similar to Escherichia coli
                                        hypothetical protein SW:YGJU-ECOLI
                                        () (414 aa) fasta scores: E(): 0,
                                        93.2% id in 414 aa, and to
                                        Neisseria meningitidis MC58
                                        sodium/dicarboxylate symporter
                                        family protein TR:AAF42441
                                        (EMBL:AE002561) (409 aa) fasta
                                        scores: E(): 0, 68.5% id in 394
                                        aa. Contains possible membrane
                                        spanning hydrophobic domains.
                                        Orthologue of E. coli ygjU
                                        (YGJU-ECOLI); Fasta hit to
                                        YGJU-ECOLI (414 aa), 93% identity
                                        in 414 aa overlap"
                                        /codon-start=1
                                        /transl-table=11
                                        /product="probable membrane
                                        transport protein"
                                        /protein-id="CAD07749.1"
                                        /db-xref="GI:16504300"
                                        /db-xref="GOA:Q8Z3L4"
                                        /db-xref="SPTREMBL:Q8Z3L4"
                                        /translation="MATQRASGLLQRLAQGSLVK
                                        QILVGLVLGILLAWISKPVAEAVG
                                        LLGTLFVGALKAVAPVLVLMLVMASIANHQHGQK
                                        TNIRPILFLYLLGTFSAALAAVVF
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                                       VSNPIDALLNANYIGILVWAVGLG
                                       FALRHGNETTKNLVNDMSNAVTFMVKLVIRFAPV
                                       GIFGLVSSTLATTGFSTLWGYAHL
                                       LVVLIGCMLLVALVVNPLLVFWKIRRNPYPLVFA
                                       CLRESGVYAFFTRSSAANIPVNMA
                                       LCEKLNLDRDTYSVSIPLGATINMAGAAITITVL
                                       TLAAVHTLGVPVDLPTALLLSVVA
                                       SLCACGASGVAGGSLLLIPLACNMFGIPNDIAMQ
                                       VVAVGFIIGVLQDSCETALNSSTD
                                       VLFTAAACQAEDERLANNALRS"
misc-feature      45047..46189         /gene="STY3405"
                                       /note="Pfam match to entry PF00375
                                       SDF, Sodium:dicarboxylate
                                       symporter family, score 582.00,
                                       E-value 3.8e-171"
gene              46690..47352         /gene="STY3406"
CDS               46690..47352         /gene="STY3406"
                                       /note="Fasta hit to YGHB-ECOLI
                                       (219 aa), 63% identity in 216 aa
                                       overlap Fasta hit to DEDA-ECOLI
                                       (219 aa), 30% identity in 223 aa
                                       overlap Orthologue of E. coli
                                       YQJA-ECOLI; Fasta hit to
                                       YQJA-ECOLI (220 aa), 95% identity
                                       in 220 aa overlap. Contains
                                       multiple possible membrane
                                       spanning hydrophobic domains"
                                       /codon-start=1
                                       /transl-table=11
                                       /product="putative membrane
                                       protein"
                                       /protein-id="CAD07750.1"
                                       /db-xref="GI:16504301"
                                       /db-xref="GOA:Q8Z3L3"
                                       /db-xref="SPTREMBL:Q8Z3L3"
                                       /translation="MELLTQLLNALWAQDFETLA
                                       NPSMIGMLYFVLFMILFLENGLLP
                                       AAFLPGDSLLILVGVLIAKGAMGFPQTILLLTVA
                                       ASLGCWVSYIQGRWLGNTRTVQNW
                                       LSHLPAHYHQRAHHLFHKHGLSALLIGRFIAFVR
                                       TLLPTIAGISGLNNARFQFFNWMS
                                       GLLWVLILTSLGYLLGKTPVFMKYEDQLMSCLML
                                       LPVVLLFFGLAGSLVMLWKKKYGS RG"
misc-feature      46777..47259         /gene="STY3406"
                                       /note="Pfam match to entry PF00597
                                       DedA, DedA family, score 230.50,
                                       E-value 2.4e-65"
gene              47356..47739         /gene="STY3407"
CDS               47356..47739         /gene="STY3407"
                                       /note="Orthologue of E. coli yqjB
                                       (YQJB-ECOLI); Fasta hit to
                                       YQJB-ECOLI (127 aa), 68% identity
                                       in 127 aa overlap. Contains a
                                       possible N-terminal signal
                                       sequence."
                                       /codon-start=1
                                       /transl-table=11
                                       /product="putative exported
                                       protein"
                                       /protein-id="CAD07751.1"
                                       /db-xref="GI:16504302"
                                       /db-xref="SPTREMBL:Q8XF92"
                                       /translation="MLKPRITARQLIWISAFLLM
                                       LTILMMTWSTLRQQESTLAIRAVN
                                       QGASMPDGFSVLHHLDANGIHFKSITPKNDMLLI
                                       TFDSPAQSAAAKTVLDQTLPHGYV
                                       VAQQDDDNETVQWLSRLRESSHRFG"
gene              47884..48252         /gene="STY3408"
CDS               47884..48252         /gene="STY3408"
                                       /note="Orthologue of E. coli yqjC
                                       (YQJC-ECOLI); Fasta hit to
                                       YQJC-ECOLI (127 aa), 84% identity
                                       in 122 aa overlap. Contains a
                                       possible N-terminal signal
                                       sequence and possible coiled-coils
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```
                                              /codon-start=1
                                              /transl-table=11
                                              /product="putative exported
                                              protein"
                                              /protein-id="CAD07752.1"
                                              /db-xref="GI:16504303"
                                              /db-xref="SPTREMBL:Q8XF23"
                                              /translation="MKYRIALAITLFTLSAGSYA
                                              NSLCQEKEQDIQKEISYAEKHNNQ
                                              RRIEGLNKALSEVRANCTDSKLRAEHQKKIAEQK
                                              EEVAERQRDLAEAKAKGDADKIDK
                                              RERKLAEAQDELKKLEARDY"
gene            48294..48599                  /gene="STY3409"
CDS             48294..48599                  /gene="STY3409"
                                              /note="Fasta hit to YGAM-ECOLI
                                              (113 aa), 41% identity in 99 aa
                                              overlap Fasta hit to ELAB-ECOLI
                                              (101 aa), 44% identity in 101 aa
                                              overlap Fasta hit to HNS-ECOLI
                                              (136 aa), 31% identity in 110 aa
                                              overlap Orthologue of E. coli yqjD
                                              (YQJD-ECOLI); Fasta hit to
                                              YQJD-ECOLI (101 aa), 90% identity
                                              in 101 aa overlap"
                                              /codon-start=1
                                              /transl-table=11
                                              /product="conserved hypothetical
                                              protein"
                                              /protein-id="CAD07753.1"
                                              /db-xref="GI:16504304"
                                              /db-xref="SPTREMBL:Q8XEQ1"
                                              /translation="MSKDNTTEHLRAELKSLTDT
                                              LEEVLSSSGEKSKEELSKIRSKAE
                                              RALKESRYRLGETGDVIAKQTRVAAARADDYVRE
                                              NPWTGVGIGAAVGLVLGVLLTRR"
gene            48602..49000                  /gene="STY3410"
CDS             48602..49000                  /gene="STY3410"
                                              /note="Orthologue of E. coli yqjE
                                              (YQJE-ECOLI); Fasta hit to
                                              YQJE-ECOLI (134 aa), 89% identity
                                              in 130 aa overlap. Contains
                                              possible membrane spanning
                                              hydrophobic domains."
                                              /codon-start=1
                                              /transl-table=11
                                              /product="putative membrane
                                              protein"
                                              /protein-id="CAD07754.1"
                                              /db-xref="GI:16504305"
                                              /db-xref="SPTREMBL:Q8XFR8"
                                              /translation="MADSRQAQGPGKSVLGIGQR
                                              IVTIIVEMVETRLRLAVVELEEEK
                                              ANLFQLLLMVGLTMLFAAFGLMSLMVLVIWAIDP
                                              QYRLNAMIATTVVLLVLALIGGIW
                                              TLRKARQSTLLRHTRHELANDRQILEDDQS"
gene            48997..49296                  /gene="STY3411"
CDS             48997..49296                  /gene="STY3411"
                                              /note="Orthologue of E. coli
                                              YQJK-ECOLI; Fasta hit to
                                              YQJK-ECOLI (99 aa), 88% identity
                                              in 99 aa overlap"
                                              /codon-start=1
                                              /transl-table=11
                                              /product="conserved hypothetical
                                              protein"
                                              /protein-id="CAD07755.1"
                                              /db-xref="GI:16504306"
                                              /db-xref="SPTREMBL:Q8XGR1"
                                              /translation="MSSKGEREKRRKALLLSQIQQ
                                              QRLDLSASRRDWLETTGAYDRGWN
                                              TVLSLRSWALVGSSVMAIWTIRHPNMLVRWAKRG
                                              LGIWSAWRLVKTTLRQQQLRG"
gene            49451..49936                  /gene="STY3412"
CDS             49451..49936                  /gene="STY3412"
                                              /note="Fasta hit to YPHA-ECOLI
```

```
                                     overlap Orthologue of E. coli yqjF
                                     (YQJF-ECOLI); Fasta hit to
                                     YQJF-ECOLI (160 aa), 81% identity
                                     in 161 aa overlap. Contains
                                     possible membrane spanning
                                     hydrophobic domains."
                                     /codon-start=1
                                     /transl-table=11
                                     /product="putative membrane
                                     protein"
                                     /protein-id="CAD07756.1"
                                     /db-xref="GI:16504307"
                                     /db-xref="GOA:Q8Z3L2"
                                     /db-xref="SPTREMBL:Q8Z3L2"
                                     /translation="MILSSDNNDALNRAIAHENS
                                     SSRRIGLLENKMKKLEDIGVLIAR
                                     ILMPVLFITAGWGKISGYAGTQQYMEAMGVPGFL
                                     LPLTILLEFGGGLAILLGFLTRTT
                                     ALFTAGFTLLTALIFHSNFAEGVNSLMFMKNLTI
                                     AGGFLLLALTGPGAFSLDRLLNKK W"
gene            50004..50990         /gene="STY3413"
CDS             50004..50990         /gene="STY3413"
                                     /note="Orthologue of E. coli yqjG
                                     (YQJG-ECOLI); Fasta hit to
                                     YQJG-ECOLI (328 aa), 93% identity
                                     in 328 aa overlap"
                                     /codon-start=1
                                     /transl-table=11
                                     /product="conserved hypothetical
                                     protein"
                                     /protein-id="CAD07757.1"
                                     /db-xref="GI:16504308"
                                     /db-xref="SPTREMBL:Q8Z3L1"
                                     /translation="MGQLIDGVWHDTWYDTKSSG
                                     GKFQRSASAFRNWLTADGAPGPSG
                                     EGGFAAEKDRYHLYVSLACPWAHRTLIFRKLKGL
                                     EPFIPVSVVNPLMLENGWTFDDTF
                                     PAATGDTLYQHEFLYQLYLHADPHYSGRVTVPVL
                                     WDKKNHTIVSNESAEIIRMFNSAF
                                     DGLGAKAGDYYPPALQSKIDELNGWIYDNVNNGV
                                     YKAGFATSQQAYDEAVEKVFTALA
                                     RLEQILGQHRYLTGNQLTEADIRLWTTLVRFDPV
                                     YVTHFKCDKYRISDYLNLYGFLRD
                                     IYQIPGIAETVNMDHIRHHYFRSHKTINPTGIIS
                                     VGPWQDLLEPHGHDVRFG"
misc-feature    50610..50846         /gene="STY3413"
                                     /note="Pfam match to entry PF00043
                                     GST, Glutathione S-transferases.,
                                     score 20.40, E-value 3.5e-05"
gene            51114..51479         /gene="STY3414"
CDS             51114..51479         /gene="STY3414"
                                     /note="Fasta hit to YHAI-ECOLI
                                     (118 aa), 52% identity in 118 aa
                                     overlap Orthologue of E. coli yhaH
                                     (YHAH-ECOLI); Fasta hit to
                                     YHAH-ECOLI (121 aa), 90% identity
                                     in 118 aa overlap. Contains
                                     possible membrane spanning
                                     hydrophobic domains."
                                     /codon-start=1
                                     /transl-table=11
                                     /product="putative membrane
                                     protein"
                                     /protein-id="CAD07758.1"
                                     /db-xref="GI:16504309"
                                     /db-xref="SPTREMBL:Q8XG14"
                                     /translation="MDWYLKVLKNYLGFGGRARR
                                     KEYWMFILVNIIFTFVLGLLDAML
                                     GWQRAGGEGVLTTIYGVLIFLPWWAVQFRRLHDT
                                     DRSAWWLLLLLIPIIGWLIIIAFN
                                     CQNGTPGDNRFGPDPKRFS"
gene            complement(51518..52414  /gene="STY3415"
                )
CDS             complement(51518..52414  /gene="STY3415"
                )
```

```
                                          (316 aa), 37% identity in 286 aa
                                          overlap Orthologue of E. coli yhaJ
                                          (YHAJ-ECOLI); Fasta hit to
                                          YHAJ-ECOLI (298 aa), 97% identity
                                          in 298 aa overlap"
                                          /codon-start=1
                                          /transl-table=11
                                          /product="possible LysR-family
                                          transcriptional regulator"
                                          /protein-id="CAD07759.1"
                                          /db-xref="GI:16504310"
                                          /db-xref="GOA:Q8Z3L0"
                                          /db-xref="SPTREMBL:Q8Z3L0"
                                          /translation="MAKERALTLEALRVMDAIDR
                                          RGSFAAAADELGRVPSALSYTMQK
                                          LEEELDVVLFDRSGHRTKFTNVGRMLLERGRVLL
                                          EAADKLTTDAEALARGWETHLTLV
                                          TEALVPTPAFFPLIDRLAAKANTQLSLITEVLAG
                                          AWERLEQGRADIVIAPDMHFRSSS
                                          EINSRKLYTLMNVYVAAPDHSIHQEPEPLSEVTR
                                          VKYRGVAVADTARERPVLTVQLLD
                                          KQPRLTVSTIEDKRQALLAGLGVATMPYSMVEQD
                                          IAEGRLRVVSPESTSEIDIIMAWR
                                          RDSMGEAKAWCLREIPKLFAGK"
misc-feature      complement(51965..52390  /gene="STY3415"
                  )
                                          /note="Pfam match to entry PF00126
                                          HTH-1, Bacterial regulatory
                                          helix-turn-helix protein, lysR
                                          family, score 124.80, E-value
                                          1.6e-33"
misc-feature      complement(52256..52348  /gene="STY3415"
                  )
                                          /note="PS00044 Bacterial
                                          regulatory proteins, lysR family
                                          signature"
gene              52519..53220             /gene="STY3416"
CDS               52519..53220             /gene="STY3416"
                                          /note="Fasta hit to YHHW-ECOLI
                                          (231 aa), 35% identity in 237 aa
                                          overlap Orthologue of E. coli yhaK
                                          (YHAK-ECOLI); Fasta hit to
                                          YHAK-ECOLI (233 aa), 85% identity
                                          in 233 aa overlap"
                                          /codon-start=1
                                          /transl-table=11
                                          /product="conserved hypothetical
                                          protein"
                                          /protein-id="CAD07760.1"
                                          /db-xref="GI:16504311"
                                          /db-xref="SPTREMBL:Q8Z3K9"
                                          /translation="MITTRTAKQCGQADYGWLQA
                                          RYTFSFGHYFDPTLLGYASLRVLN
                                          QEVLAPGASFQPRTYPKVDILNLILDGEAEYRDS
                                          DGNHVQAKAGEALLLAAQPGISYS
                                          EHNLSKVKPLTRMQLWLDACPERENALVQKIPLS
                                          TAQQQLLASPDGEQNSLQLRQQVW
                                          VHHITLEKGESLNFQLHGPRAYLQSIHGTFHAMT
                                          HNEEREALTCGDGAFIRDEPNITL
                                          VADTPLRALLVDLPV"
gene              53244..53408             /gene="STY3417"
CDS               53244..53408             /gene="STY3417"
                                          /note="Orthologue of E. coli yhaL
                                          (YHAL-ECOLI); Fasta hit to
                                          YHAL-ECOLI (56 aa), 71% identity
                                          in 55 aa overlap"
                                          /codon-start=1
                                          /transl-table=11
                                          /product="conserved hypothetical
                                          protein"
                                          /protein-id="CAD07761.1"
                                          /db-xref="GI:16504312"
                                          /db-xref="SPTREMBL:Q8XFT9"
                                          /translation="MSKKSAKKRQPVVKPAVQEA
                                          MSAAVPLGYEEMLTELEAIVADAE
```

| gene | complement(53521..54831) | /gene="STY3418" |
| CDS | complement(53521..54831) | /gene="STY3418" |

/note="The N-terminus is highly similar to Escherichia coli hypothetical protein YhaN SW:YHAN-ECOLI (P42627) (187 aa) fasta scores: E(): 0, 77.7% id in 184 aa and the C-terminus of this proteins is highly similar to Escherichia coli hypothetical protein YhaM SW:YHAM-ECOLI () (188 aa) fasta scores: E(): 0, 92.0% id in 187 aa"
/codon-start=1
/transl-table=11
/product="conserved hypothetical protein"
/protein-id="CAD07762.1"
/db-xref="GI:16504313"
/db-xref="SPTREMBL:Q8Z3K8"
/translation="MFESKINPLWQSFILAVQEE
VKPALGCTEPISLALAAAAAAEL
DGTVERIDAWVSPNLMKNGMGVTVPGTGMVGLPI
AAALGALGGDAKAGLEVLKDASAK
AVADAKAMLAAGHVAVMLQEPCNDILFSRAKVYS
GDSWACVTIVGDHTNIVRIETDKG
VVFTQADNAQEEEKTSPLGVLSHTSLEEILAFVN
AVPFDAIRFILDAARLNGALSQEG
LRGSWGLHIGSTLAKQCDRGLLAKDLSTAILIRT
SAASDARMGGATLPAMSNSGSGNQ
GITATVPVMVVAEHVGADDECLARALMLSHLSAI
YIHHQLPRLSALCAATTAAMGAAA
GMAWLIDGRYDTIAMAISSMIGDVSGMICDGASN
SCAMKVSTSASAAWKAVLMALDDT
AVTGNEGIVAHNVEQSISNLCSLACRSMQQTDKQ
IIEIMASKAH"

| gene | complement(54857..56124) | /gene="STY3421" |

/pseudo

| CDS | complement(54857..56124) | /gene="STY3421" |

/note="Similar to Escherichia coli hypothetical protein YhaO SW:YHAO-ECOLI (P42628) (425 aa). Contains and in-frame stop at codon 38 and a frameshift after codon 237 The sequence has been checked and is believed to be correct"
/pseudo
/codon-start=1
/transl-table=11
/product="conserved hypothetical transport protein (pseudogene)"

| gene | complement(56502..57866) | /gene="tdcG" |

/note="synonym: STY3422"

| CDS | complement(56502..57866) | /gene="tdcG" |

/EC-number="4.2.1.13"
/note="Similar to Escherichia coli L-serine dehydratase TdcG SW:TDCG-ECOLI () (454 aa) fasta scores: E(): 0, 86.6% id in 454 aa"
/codon-start=1
/transl-table=11
/product="L-serine dehydratase"
/protein-id="CAD07764.1"
/db-xref="GI:16504314"
/db-xref="GOA:Q8Z3K7"
/db-xref="SPTREMBL:Q8Z3K7"
/translation="MISAFDIFKIGIGPSSSHTV

```
                                           ITVDLYGSLSLTGKGHATDTAIIMGLAGNTPQDV
                                           NIDSIPAFIQEVARSSRLSVAGGA
                                           HVVDFPVADSILFHAETLARHENGMRITAWHGQT
                                           PLLHKTYYSIGGGFIVEEERFGQS
                                           HDVEKSVPYDFHSASELLTLCERQGLSVSGLMMQ
                                           NELALRSKEQIDAGFARIWQVMAT
                                           GIERGMNTEGVLPGPLNVPRRAVALRRLLVSSDN
                                           LSRDPMNVIDWINMFALAVSEENA
                                           AGGRVVTALTNGACGIIPAVLAYYDKFRRPVNAN
                                           SIARYLLSAGAIGMLYKMNASISG
                                           AEVGCQGEVGVACSMAAAGLTELLGGSPAQVCIA
                                           AEIAMEHNLGLTCDPVAGQVQIPC
                                           IERNAINAVKAVNAARMALRRTSEPRVSLDKVIE
                                           TMYETGKDMNDKYRETSRGGLAIK VVCG"
```

gene	complement(57936..60230)	/gene="tdcE"

/note="synonym: STY3423"

CDS	complement(57936..60230)	/gene="tdcE"

/note="Fasta hit to PFLB-ECOLI
(759 aa), 79% identity in 752 aa
overlap Orthologue of E. coli yhaS
(TDCE-ECOLI); Fasta hit to
TDCE-ECOLI (746 aa), 93% identity
in 741 aa overlap"
/codon-start=1
/transl-table=11
/product="probable formate
acetyltransferase"
/protein-id="CAD07765.1"
/db-xref="GI:16504315"
/db-xref="GOA:Q8Z3K6"
/db-xref="SPTREMBL:Q8Z3K6"
/translation="MKVNIDTSDMLYAEAWRDFK
GTDWKEEINVCDFIQHNYTPYEGD
ESFLADATPATTALWEKVMAGIRIENATHAPVDF
DTNIATTITAHDAGYIEKELEKIV
GLQTDKPLKRALHPFGGVNMIKSSFHAYGREMDA
DFEYTFTDLRKTHNQGVFDVYSPD
MLRCRKSSVLTGLPDGYGRGRIIGDYRRVALYGI
RYLVRERELQFADLQSNLERGQNL
EATIRLREELAEHRRALLQMQEMAAKYGYDISRP
ARNAQEAVQWLYFAYLAAVKSQNG
GAMSLGRTASFLDIYIERDFNAGLLTEQQAQELI
DHFIMKIRMVRFLRTPEFDSLFSG
DPIWATEVIGGMGLDGRTLVTKNSFRYLHTLHTM
GPAPEPNLTILWSEALPVAFKKYA
AQVSIVTSSLQYENDDLMRTDFNSDDYAIACCVS
PMVIGKQMQFFGARANLAKTLLYA
INGGVDEKLKIQVGPKTAPLTDEVLDYDAVMESL
DHFMDWLAVQYISALNIIHYMHDK
YSYEASLMALHDRDVYRTMACGIAGLSVAADSLS
AIRYAQVKPIRDENGLAIDFAIEG
EYPQYGNNDERVDSIACDLVKRFMQKISVLPTYR
NAVPTQSILTITSNVVYGQKTGNT
PDGRRAGTPFAPGANPMHGRDRKGAVASLTSVAK
LPFTYAKDGISYTFSIVPAALGKE
DAVRKTNLVGLLDGYFHHEAQVEGGQHLNVNVMN
REMLLDAIEHPENYPNLTIRVSGY
AVRFNALTREQQQDVISRTFTQAM"

misc-feature	complement(57993..58331)	/gene="tdcE"

/note="Pfam match to entry PF01228
Gly-radical, Glycine radical,
score 233.10, E-value 4e-66"

misc-feature	complement(58005..58031)	/gene="tdcE"

/note="PS00850 Glycine radical
signature"

gene	complement(60264..61472)	/gene="tdcD"

/note="synonym: STY3424"

CDS	complement(60264..61472)	/gene="tdcD"

/EC-number="2.7.2.-"

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                              propionate kinase TdcD
                              SW:TDCD-ECOLI (P11868; P76666)
                              (402 aa) fasta scores: E(): 0,
                              82.1% id in 402 aa Fasta hit to
                              ACKA-ECOLI (400 aa), 41% identity
                              in 396 aa overlap"
                              /codon-start=1
                              /transl-table=11
                              /product="propionate kinase"
                              /protein-id="CAD07766.1"
                              /db-xref="GI:16504316"
                              /db-xref="GOA:Q8Z3K5"
                              /db-xref="SWISS-PROT:Q8Z3K5"
                              /translation="MNEFPVVLVINCGSSSIKFS
                              VLDVATCDVLMAGIADGMNTENAF
                              LSINGDKPINLSHSNYEDALKAIAFELEKRDLTD
                              SVALIGHRIAHDGELFTQSVIITD
                              EIIDNIRRVSPLAPLHNYANLSGIDAARRLFPAV
                              RQVAVFDTSFHQTLAPEAYLYGLP
                              WEYFSSLGVRRYGFHGTSHRYVSRRAYELLDLDE
                              KNSGLIVAHLGNGASICAVRNGQS
                              VDTSMGMTPLEGLMMGTRSGDVDFGAMAWIAKET
                              GQTLSDLERVVNKESGLLGISGLS
                              SDLRVLEKAWHEGHERARLAIKTFVHRIARHIAG
                              HAASLHRLDGIIFTGGIGENSVLI
                              RQLVIEHLGVLGLTLDVEMNKQPNSHGERIISVN
                              PSQVICAVIPTNEEKMIALDAIHL
                              GNVKAPVEFA"
misc-feature    complement(60312..61457 /gene="tdcD"
                )
                              /note="Pfam match to entry PF00871
                              Acetate-kinase, Acetokinase
                              family, score 732.00, E-value
                              2.6e-216"
misc-feature    complement(60825..60878 /gene="tdcD"
                )
                              /note="PS01076 Acetate and
                              butyrate kinases family signature
                              2"
misc-feature    complement(61419..61454 /gene="tdcD"
                )
                              /note="PS01075 Acetate and
                              butyrate kinases family signature
                              1"
gene            complement(61539..62869 /gene="tdcC"
                )
                              /note="synonym: STY3426"
                              /pseudo
CDS             complement(61539..62869 /gene="tdcC"
                )
                              /note="Similar to Escherichia coli
                              threonine/serine transporter TdcC
                              SW:TDCC-ECOLI (P11867) (443 aa)
                              fasta scores: E(): 0, 95.0% id in
                              259 aa. Contains a frameshift
                              after codon 260. The sequence has
                              been checked and is believed to be
                              correct"
                              /pseudo
                              /codon-start=1
                              /transl-table=11
                              /product="threonine/serine
                              transporter (pseudogene)"
gene            complement(62890..63879 /gene="STY3427"
                )
                              /note="synonym: tdcB"
CDS             complement(62890..63879 /gene="STY3427"
                )
                              /note="Orthologue of E. coli tdcB
                              (THD2-ECOLI); Fasta hit to
                              THD2-ECOLI (329 aa), 95% identity
                              in 329 aa overlap"
                              /codon-start=1
                              /transl-table=11
                              /product="catabolic threonine
```

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                                           FISWFPMLLLIGVWIFFMRQMQGGGGKGAMSFGK
                                           SKARMLTEDQIKTTFADVAGCDEA
                                           KEEVAELVEYLREPSRFQKLGGKIPKGVLMVGPP
                                           GTGKTLLAKAIAGEAKVPFFTISG
                                           SDFVEMFVGVGASRVRDMFEQAKKAAPCIIFIDE
                                           IDAVGRQRGAGLGGGHDEREQTLN
                                           QMLVEMDGFEGNEGIIVIAATNRPDVLDPALLRP
                                           GRFDRQVVVGLPDVRGREQILKVH
                                           MRRVPLATDIDAAIIARGTPGFSGADLANLVNEA
                                           ALFAARGNKRVVSMVEFEKAKDKI
                                           MMGAERRSMVMTEAQKESTAYHEAGHAIIGRLVP
                                           EHDPVHKVTIIPRGRALGVTFFLP
                                           EGDAISASRQKLESQISTLYGGRLAEEIIYGVEH
                                           VSTGASNDIKVATNLARNMVTQWG
                                           FSEKLGPLLYAEEEGEVFLGRSVAKAKHMSDETA
                                           RIIDQEVKALIERNYNRARQILTD
                                           NMDILHAMKDALMKYETIDAPQIDDLMARREVRP
                                           PAGWEDPNGTNNSDSNGTPQAPRP
                                           VDEPRTPNPGNTMSEQLGDK"
misc-feature         complement(113372..1140   /gene="STY3474"
                     10)
                                           /note="Pfam match to entry PF01434
                                           Peptidase-M41, Peptidase family
                                           M41, score 443.90, E-value
                                           1.4e-129"
misc-feature         complement(114026..1145   /gene="STY3474"
                     89)
                                           /note="Pfam match to entry PF00004
                                           AAA, ATPases associated with
                                           various cellular activities (AAA),
                                           score 352.20, E-value 5.4e-102"
misc-feature         complement(114221..1142   /gene="STY3474"
                     77)
                                           /note="PS00674 AAA-protein family
                                           signature"
misc-feature         complement(114551..1145   /gene="STY3474"
                     74)
                                           /note="PS00017 ATP/GTP-binding
                                           site motif A (P-loop)"
misc-feature         complement(114737..1147   /gene="STY3474"
                     60)
                                           /note="PS00017 ATP/GTP-binding
                                           site motif A (P-loop)"
gene                 complement(115251..1158   /gene="STY3475"
                     77)
                                           /note="synonym: ftsJ"
CDS                  complement(115251..1158   /gene="STY3475"
                     77)
                                           /note="Orthologue of E. coli ftsJ
                                           (FTSJ-ECOLI); Fasta hit to
                                           FTSJ-ECOLI (209 aa), 100% identity
                                           in 208 aa overlap"
                                           /codon-start=1
                                           /transl-table=11
                                           /product="cell division protein"
                                           /protein-id="CAD07814.1"
                                           /db-xref="GI:16504362"
                                           /db-xref="GOA:Q8Z3H3"
                                           /db-xref="SPTREMBL:Q8Z3H3"
                                           /translation="MTGKKRSASSSRWLQEHFSD
                                           KYVQQAQKKGLRSRAWFKLDEIQQ
                                           SDKLFKPGMTVVDLGAAPGGWSQYVVTQIGGKGR
                                           IIACDLLPMDPIVGVDFLQGDFRD
                                           ELVMKALLERVGDSKVQVVMSDMAPNMSGTPAVD
                                           IPRAMYLVELALDMCRDVLAPGGS
                                           FVVKVFQGEGFDEYLREIRSLFTKVKVRKPDSSR
                                           ARSREVYIVATGRK"
misc-feature         complement(115254..1158   /gene="STY3475"
                     35)
                                           /note="Pfam match to entry PF01728
                                           FtsJ, FtsJ cell division protein,
                                           score 367.20, E-value 1.7e-106"
gene                 115965..116297            /gene="STY3476"
CDS                  115965..116297            /gene="STY3476"
                                           /note="Orthologue of E. coli yhbY
```

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                                          YHBY-ECOLI (97 aa), 96% identity
                                          in 97 aa overlap. Note codon 14
                                          offers an alternative
                                          translational start site."
                                          /codon-start=1
                                          /transl-table=11
                                          /product="conserved hypothetical
                                          protein"
                                          /protein-id="CAD07815.1"
                                          /db-xref="GI:16504363"
                                          /db-xref="GOA:Q8XG58"
                                          /db-xref="SPTREMBL:Q8XG58"
                                          /translation="MTRFQSQRKQKYTMNLSTKQ
                                          KQHLKGLAHPLKPVVMLGNNGLTE
                                          GVLAEIEQALEHHELIKVKIASEDRETKTLIVDA
                                          IVRETGACNVQVIGKTLVLYRPTK ERKISLPR"
misc-feature      116010..116087          /gene="STY3476"
                                          /note="PS01301 Uncharacterized
                                          protein family UPF0044 signature"
misc-feature      116049..116261          /gene="STY3476"
                                          /note="Pfam match to entry PF01985
                                          UPF0044, Uncharacterised protein
                                          family UPF0044, score 27.60,
                                          E-value 0.00026"
gene              complement(116453..1169  /gene="STY3477"
                  29)
                                          /note="synonym: greA"
CDS               complement(116453..1169  /gene="STY3477"
                  29)
                                          /note="Fasta hit to GREB-ECOLI
                                          (158 aa), 35% identity in 155 aa
                                          overlap Orthologue of E. coli greA
                                          (GREA-ECOLI); Fasta hit to
                                          GREA-ECOLI (158 aa), 97% identity
                                          in 158 aa overlap"
                                          /codon-start=1
                                          /transl-table=11
                                          /product="transcription elongation
                                          factor"
                                          /protein-id="CAD07816.1"
                                          /db-xref="GI:16504364"
                                          /db-xref="GOA:Q8XGQ9"
                                          /db-xref="SWISS-PROT:Q8XGQ9"
                                          /translation="MQAIPMTLRGAEKLREELDF
                                          LKSVRRPEIIAAIAEAREHGDLKE
                                          NAEYHAAREQQGFCEGRIKDIEAKLSNAQVIDVT
                                          KMPNNGRVIFGATVTVLNLDTDEE
                                          QTYRIVGDDEADFKQNLISVNSPIARGLIGKEQD
                                          DVVVIKTPGGDVEYEVLKVEYL"
misc-feature      complement(116456..1169  /gene="STY3477"
                  29)
                                          /note="Pfam match to entry PF01272
                                          GreA-GreB, Prokaryotic
                                          transcription elongation factor,
                                          GreA/GreB, score 365.40, E-value
                                          5.8e-106"
misc-feature      complement(116519..1165  /gene="STY3477"
                  69)
                                          /note="PS00830 Prokaryotic
                                          transcription elongation factors
                                          signature 2"
misc-feature      complement(116786..1169  /gene="STY3477"
                  11)
                                          /note="PS00829 Prokaryotic
                                          transcription elongation factors
                                          signature 1"
gene              117177..118610           /gene="STY3479"
CDS               117177..118610           /gene="STY3479"
                                          /note="Orthologue of E. coli dacB
                                          (PBP4-ECOLI); Fasta hit to
                                          PBP4-ECOLI (477 aa), 94% identity
                                          in 477 aa overlap"
                                          /codon-start=1
                                          /transl-table=11
                                          /product="Penicillin-binding
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                                         carboxypeptidase)"
                                         /protein-id="CAD07817.1"
                                         /db-xref="GI:16504365"
                                         /db-xref="GOA:Q8Z3H2"
                                         /db-xref="SPTREMBL:Q8Z3H2"
                                         /translation="MRFSRFIIGLTTSIAFSVQA
                                         ANIDEYIKQLPAGANLALMVQKIG
                                         APAPAIDYHSQQMALPASTQKVITALAALIQLGP
                                         DFRFTTTLETKGNVDNGILKGDLI
                                         ARFGGDPTLRRQDIRNMVATLKKSGVTQIDGNVL
                                         IDTSIFASHDKAPGWPWNDLTQCF
                                         SAPPAAAIVDRNCFSVSLYSAQKPNDLAFIRVAS
                                         YYPVTMFSQVRTLPRGSADAQYCE
                                         LDVVPGDLNRYTLTGCLPQRADPLPLAFAIQDGA
                                         SYAGAILKQELKEAGITYRGTLLR
                                         QTQVNEPGTIVASKQSAPLHDLLKIMLKKSDNMI
                                         ADTVFRMIGHVRFNVPGTWRAGSD
                                         AVRQILRQQAGIDIGNTIIADGSGLSRHNLIAPA
                                         TMMQVLQYIAQHDNELNFISMLPL
                                         AGYDGSLQYRAGLHQAGVDGKVSAKTGSLQGVYN
                                         LAGFITTASGQRMAFVQYLSGYAV
                                         PPADQRNRRIPLVRFESRLYKDIYQNN"
misc-feature        117354..118514       /gene="STY3479"
                                         /note="Pfam match to entry PF02113
                                         Peptidase-S13, D-Ala-D-Ala
                                         carboxypeptidase 3 (S13) family,
                                         score 713.90, E-value 7.3e-211"
gene                complement(118741..1199  /gene="STY3480"
                    13)
CDS                 complement(118741..1199  /gene="STY3480"
                    13)
                                         /note="Orthologue of E. coli yhbZ
                                         (YHBZ-ECOLI); Fasta hit to
                                         YHBZ-ECOLI (390 aa), 96% identity
                                         in 390 aa overlap"
                                         /codon-start=1
                                         /transl-table=11
                                         /product="probable GTP-binding
                                         protein"
                                         /protein-id="CAD07818.1"
                                         /db-xref="GI:16504366"
                                         /db-xref="SPTREMBL:Q8Z3H1"
                                         /translation="MKFVDEASILVVAGDGGNGC
                                         VSFRREKYIPKGGPDGGDGGDGGD
                                         VWMEADENLNTLIDYRFEKSFRAERGQNGASRDC
                                         TGKRGKDVTIKVPVGTRVIDQGTG
                                         ETMGDMTKHGQRLLVAKGGWHGLGNTRFKSSVNR
                                         TPRQKTNGTPGDKRDLLLELMLLA
                                         DVGMLGMPNAGKSTFIRAVSAAKPKVADYPFTTL
                                         VPSLGVVRMDSEKSFVVADIPGLI
                                         EGAAEGAGLGIRFLKHLERCRVLLHLIDIDPIDG
                                         SDPVENARIIIGELEKYSQDLAAK
                                         PRWLVFNKIDLMDKSEAEEKAKAIAEALGWEGKY
                                         YLISAASQLGVKDLCWDVMTFIIE
                                         NPIAQAEEAKQPEKVEFMWDDYHRQQLAEVEEDA
                                         DDDWDDDWDEDDEEGVEFIYKR"
misc-feature        complement(118759..1198  /gene="STY3480"
                    68)
                                         /note="Pfam match to entry PF01018
                                         GTP1-OBG, GTP1/OBG family, score
                                         603.10, E-value 1.7e-177"
misc-feature        complement(119236..1192  /gene="STY3480"
                    77)
                                         /note="PS00905 GTP1/OBG family
                                         signature"
misc-feature        complement(119395..1194  /gene="STY3480"
                    18)
                                         /note="PS00017 ATP/GTP-binding
                                         site motif A (P-loop)"
gene                complement(119929..1208  /gene="STY3481"
                    94)
CDS                 complement(119929..1208  /gene="STY3481"
                    94)
                                         /note="Orthologue of E. coli yhbE
                                         (YHBE-ECOLI); Fasta hit to
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                                     in 321 aa overlap. Contains
                                     multiple possible membrane
                                     spanning hydrophobic domains."
                                     /codon-start=1
                                     /transl-table=11
                                     /product="putative membrane
                                     protein"
                                     /protein-id="CAD07819.1"
                                     /db-xref="GI:16504367"
                                     /db-xref="GOA:Q8Z3H0"
                                     /db-xref="SPTREMBL:Q8Z3H0"
                                     /translation="MKQQAGIGILLALTTAMCWG
                                     ALPIAMKQVLEVMEPSTIVFYRFL
                                     MASIGLGAILAVKRKLPPLRIFRKPRWLVLLAIA
                                     TCGLFGNFILFSSSLQYLSPTASQ
                                     VIGQLSPVGMMVASVFILKEKMRGTQVIGALMLL
                                     SGLVMFFNTSLIEIFTRLTDYTWG
                                     VIFGVGAAMVWVSYGVAQKVLLRRLASQQILFLL
                                     YTLCTIALLPLAKPMVIAQLSDWQ
                                     LACLIFCGLNTLVGYGALAEAMARWQAAQVSAII
                                     TLTPLFTLLFSDLLSMAWPDFFAR
                                     PMLNLLGYLGAFVVVAGAMYSAIGHRIWGGLRKH
                                     ETVVSQPRSGE"
misc-feature    complement(120019..1203  /gene="STY3481"
                90)
                                         /note="Pfam match to entry PF00892
                                         DUF6, Integral membrane protein
                                         DUF6, score 55.10, E-value
                                         1.5e-12"
misc-feature    complement(120463..1208  /gene="STY3481"
                46)
                                         /note="Pfam match to entry PF00892
                                         DUF6, Integral membrane protein
                                         DUF6, score 98.80, E-value
                                         1.1e-25"
gene            complement(121024..1212  /gene="STY3482"
                81)
                                         /note="synonym: rpmA"
CDS             complement(121024..1212  /gene="STY3482"
                81)
                                         /note="Orthologue of E. coli rpmA
                                         (RL27-ECOLI); Fasta hit to
                                         RL27-ECOLI (84 aa), 95% identity
                                         in 84 aa overlap"
                                         /codon-start=1
                                         /transl-table=11
                                         /product="50S ribosomal subunit
                                         protein L27"
                                         /protein-id="CAD07820.1"
                                         /db-xref="GI:16504368"
                                         /db-xref="GOA:Q8XGK4"
                                         /db-xref="SWISS-PROT:Q8XGK4"
                                         /translation="MAHKKAGGSTRNGRDSEAKR
                                         LGVKRFGGEAVLAGSIIVRQRGTK
                                         FHAGTNVGCGRDHTLFAKADGKVKFEVKGPKNRK
                                         YISIVAE"
misc-feature    complement(121033..1212  /gene="STY3482"
                78)
                                         /note="Pfam match to entry PF01016
                                         Ribosomal-L27, Ribosomal L27
                                         protein, score 201.00, E-value
                                         1.8e-56"
misc-feature    complement(121138..1211  /gene="STY3482"
                82)
                                         /note="PS00831 Ribosomal protein
                                         L27 signature"
gene            complement(121301..1216  /gene="STY3483"
                12)
                                         /note="synonym: rplU"
CDS             complement(121301..1216  /gene="STY3483"
                12)
                                         /note="Orthologue of E. coli rplU
                                         (RL21-ECOLI); Fasta hit to
                                         RL21-ECOLI (103 aa), 99% identity
                                         in 103 aa overlap"
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                                         /transl-table=11
                                         /product="50S ribosomal subunit
                                         protein L21"
                                         /protein-id="CAD07821.1"
                                         /db-xref="GI:16504369"
                                         /db-xref="GOA:Q8XGA0"
                                         /db-xref="SPTREMBL:Q8XGA0"
                                         /translation="MYAVFQSGGKQHRVSEGQTV
                                         RLEKLDIATGETIEFAEVLMIANG
                                         EEVKIGVPFVDGGVIKAEVVAHGRGEKVKIVKFR
                                         RRKHYRKQQGHRQWFTDVKITGIS A"
misc-feature    complement(121325..1216  /gene="STY3483"
                12)
                                         /note="Pfam match to entry PF00829
                                         Ribosomal-L21p, Ribosomal
                                         prokaryotic L21 protein, score
                                         202.30, E-value 7.6e-57"
misc-feature    complement(121331..1213  /gene="STY3483"
                99)
                                         /note="PS01169 Ribosomal protein
                                         L21 signature"
gene            121871..122842           /gene="STY3484"
                                         /note="synonym: ispB"
CDS             121871..122842           /gene="STY3484"
                                         /note="Orthologue of E. coli ispB
                                         (ISPB-ECOLI); Fasta hit to
                                         ISPB-ECOLI (323 aa), 96% identity
                                         in 323 aa overlap"
                                         /codon-start=1
                                         /transl-table=11
                                         /product="octaprenyl-diphosphate
                                         synthase"
                                         /protein-id="CAD07822.1"
                                         /db-xref="GI:16504370"
                                         /db-xref="GOA:Q8XFR7"
                                         /db-xref="SPTREMBL:Q8XFR7"
                                         /translation="MNLEKINELTAQDMAGVNAT
                                         ILEQLNSDVQLINQLGYYIISGGG
                                         KRIRPMIAVLAARAVGYQGNAHVTIAALIEFIHT
                                         ATLLHDDVVDESDMRRGKATANAA
                                         FGNAASVLVGDFIYTRAFQMMTSLGSLKVLEVMS
                                         EAVNVIAEGEVLQLMNVNDPDITE
                                         ENYMRVIYSKTARLFEAAAQCSGILAGCTPEQEK
                                         GLQDYGRYLGTAFQLIDDLLDYSA
                                         DGEHLGKNVGDDLNEGKPTLPLLHAMRHGTPEQS
                                         AMIRTAIEQGNGRHLLEPVLEAMT
                                         TCGSLEWTRQRAEEEADKAISALQILPDTPWREA
                                         LIGLAHIAVQRDR"
misc-feature    121961..122725           /gene="STY3484"
                                         /note="Pfam match to entry PF00348
                                         polyprenyl-synt, Polyprenyl
                                         synthetases, score 433.30, E-value
                                         2.2e-126"
misc-feature    122111..122155           /gene="STY3484"
                                         /note="PS00723 Polyprenyl
                                         synthetases signature 1"
misc-feature    122477..122515           /gene="STY3484"
                                         /note="PS00444 Polyprenyl
                                         synthetases signature 2"
gene            123075..123362           /gene="STY3485"
                                         /note="synonym: nlp"
CDS             123075..123362           /gene="STY3485"
                                         /note="Orthologue of E. coli
                                         Ner-like protein (Nlp) involved in
                                         the regulation of sugar metabolism
                                         (NLP-ECOLI); Fasta hit to
                                         NLP-ECOLI (92 aa), 87% identity in
                                         92 aa overlap"
                                         /codon-start=1
                                         /transl-table=11
                                         /product="Ner-like regulatory
                                         protein"
                                         /protein-id="CAD07823.1"
                                         /db-xref="GI:16504371"
                                         /db-xref="SPTREMBL:Q8Z3G9"
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                                   SDDVEMMLEANRIGGRHGLGMSDQIENRIIEAKS
                                   RGIYEAPGMALLHIAYERLLTGIH
                                   NEDTIEQYHSHGRQLGKLLYQGRWFDSQALMLRD
                                   GLQRWVASQITGEVTLELRRGNDY
                                   SILNTVSDNLTYKAERLTMEKGESVFSPDDRIGQ
                                   LTMRNLDITDTREKLFGYAKAGLL
                                   TASSATGLPQVENLENKAK"
     misc-feature    108776..109987    /gene="STY3470"
                                   /note="Pfam match to entry PF00764
                                   Arginosuc-synth, Arginosuccinate
                                   synthase, score 755.20, E-value
                                   3.5e-237"
     misc-feature    108782..108808    /gene="STY3470"
                                   /note="PS00564 Argininosuccinate
                                   synthase signature 1"
     misc-feature    109118..109153    /gene="STY3470"
                                   /note="PS00565 Argininosuccinate
                                   synthase signature 2"
     tRNA            complement(110275..1103    /product="tRNA-Leu"
                     61)
                                   /note="tRNA Leu anticodon GAG,
                                   Cove score 67.81"
     gene            complement(110375..1107    /gene="secG"
                     07)
                                   /note="synonym: STY3471"
     CDS             complement(110375..1107    /gene="secG"
                     07)
                                   /note="Similar to Escherichia coli
                                   protein-export membrane protein
                                   SecG secG SW:SECG-ECOLI (P33582)
                                   (110 aa) fasta scores: E(): 0,
                                   98.2% id in 109 aa"
                                   /codon-start=1
                                   /transl-table=11
                                   /product="protein-export membrane
                                   protein"
                                   /protein-id="CAD07810.1"
                                   /db-xref="GI:16504358"
                                   /db-xref="GOA:Q8XGE4"
                                   /db-xref="SPTREMBL:Q8XGE4"
                                   /translation="MYEALLVVFLIVAIGLVGLI
                                   MLQQGKGADMGASFGAGASATLFG
                                   SSGSGNFMTRMTAVLATLFFIISLVLGNINSNKT
                                   NKGSEWENLSAPAKTEQTQPAAPA QPTSDIPR"
     gene            complement(110930..1122    /gene="STY3472"
                     67)
     CDS             complement(110930..1122    /gene="STY3472"
                     67)
                                   /note="Similar to Escherichia coli
                                   MrsA protein a phosphoglucomutase
                                   (PGM) /phosphomannomutase(PMM)
                                   -family protein SW:MRSA-ECOLI
                                   (P31120) (445 aa) fasta scores:
                                   E(): 0, 96.0% id in 445 aa"
                                   /codon-start=1
                                   /transl-table=11
                                   /product="PGM/PMM-family protein"
                                   /protein-id="CAD07811.1"
                                   /db-xref="GI:16504359"
                                   /db-xref="GOA:Q8XF81"
                                   /db-xref="SPTREMBL:Q8XF81"
                                   /translation="MSNRKYFGTDGIRGRVGNAP
                                   ITPDFVLKLGWAAGKVLARHGSRK
                                   IIIGKDTRISGYMLESALEAGLAAAGLSASFTGP
                                   MPTPAVAYLTRTFRAEAGIVISAS
                                   HNPFYDNGIKFFSIDGTKLPDDVEEAIEAEMEKE
                                   ITCVDSAELGKASRIVDAAGRYIE
                                   FCKGTFPNELSLNGLKVVVDCANGATYHIAPNVL
                                   RELGATVIAIGCEPNGVNINEEVG
                                   ATDVRALQARVLAEKADLGIALDGDGDRVIMVDH
                                   EGNKVDGDQIMYIIAREGLRQGQL
                                   RGGAVGTLMSNMGLELALKQLGIPFARAKVGDRY
                                   VLEKLQEKGWRIGAENSGHVILLD
                                   KTTTGDGIVAGLQVLAAMVRNHMSLHDLCSGMKM
                                   FPQILVNVRYTAGSGDPLENEAVK
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                                            DEAQVTAFAHRIADAVKAV"
misc-feature     complement(110972..1122    /gene="STY3472"
                 61)

                                            /note="Pfam match to entry PF00408
                                            PGM-PMM,
                                            Phosphoglucomutase/phosphomannomut
                                            ase, score 653.70, E-value
                                            9.4e-193"
misc-feature     complement(111938..1119    /gene="STY3472"
                 82)

                                            /note="PS00710 Phosphoglucomutase
                                            and phosphomannomutase
                                            phosphoserine signature"
gene             complement(112260..1131    /gene="STY3473"
                 08)

                                            /note="synonym: folP"
CDS              complement(112260..1131    /gene="STY3473"
                 08)

                                            /note="Orthologue of E. coli folP
                                            (DHPS-ECOLI); Fasta hit to
                                            DHPS-ECOLI (282 aa), 92% identity
                                            in 282 aa overlap"
                                            /codon-start=1
                                            /transl-table=11
                                            /product="dihydropteroate
                                            synthase"
                                            /protein-id="CAD07812.1"
                                            /db-xref="GI:16504360"
                                            /db-xref="GOA:Q8Z3H4"
                                            /db-xref="SPTREMBL:Q8Z3H4"
                                            /translation="MKLFAQGATLDLTHPHVMGI
                                            LNVTPDSFSDGGAHNTLIEAVKHA
                                            NLMVNTGATIIDVGGESTRPGAAEVSVEEELDRV
                                            IPVLEAIAQRFEVWISVDTSKPEV
                                            IREAARAGAHIINDVRSLSEPGALEAAAETGLPV
                                            SLMHMQGNPKTMQEAPKYDDVFAE
                                            VNRYFIEQIARCEKAGIAKEKLLLDPGFGFGKNL
                                            SHNYTLLARLGEFHHFNLPLLVGM
                                            SRKTMVGQLLNVGPSDRLNGSLACAVIAAMQGAQ
                                            IIRVHDVKETVEAMRVVEATLSAK GNKRYE"
misc-feature     complement(112296..1130    /gene="STY3473"
                 57)

                                            /note="Pfam match to entry PF00809
                                            DHPS, Dihydropteroate synthase,
                                            score 525.00, E-value 5.5e-154"
misc-feature     complement(112917..1129    /gene="STY3473"
                 58)

                                            /note="PS00793 Dihydropteroate
                                            synthase signature 2"
misc-feature     complement(113013..1130    /gene="STY3473"
                 60)

                                            /note="PS00792 Dihydropteroate
                                            synthase signature 1"
gene             complement(113213..1151    /gene="STY3474"
                 47)

                                            /note="synonym: ftsH"
CDS              complement(113213..1151    /gene="STY3474"
                 47)

                                            /note="Orthologue of E. coli
                                            (FTSH-ECOLI); Fasta hit to
                                            FTSH-ECOLI (644 aa), 98% identity
                                            in 644 aa overlap. Contains a
                                            possible membrane spanning
                                            hydrophobic domain and a possible
                                            N-terminal signal sequence."
                                            /codon-start=1
                                            /transl-table=11
                                            /product="cell division protein"
                                            /protein-id="CAD07813.1"
                                            /db-xref="GI:16504361"
                                            /db-xref="GOA:Q8XGY2"
                                            /db-xref="SWISS-PROT:Q8XGY2"
                                            /translation="MAKNLILWLVIAVVLMSVFQ
                                            SFGPSESNGRKVDYSTFLQEVNQD
                                            QVREARINGREINVTKKDSNRYTTYIPINDPKLL
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                                    /protein-id="CAD07768.1"
                                    /db-xref="GI:16504317"
                                    /db-xref="GOA:Q8Z3K4"
                                    /db-xref="SPTREMBL:Q8Z3K4"
                                    /translation="MHITYDLPVAIEDILEAKKR
                                    LAGKIYKTGMPRSNYFSERCKGEI
                                    FLKFENMQRTGSFKIRGAFNKLSSLTEAEKRKGV
                                    VACSTGNHAQGVSLSCAMLGIDGK
                                    VVMPKGAPKSKVAATCDYSAEVVLHGDNFNDTIA
                                    KVSEIVETEGRIFIPPYDDPKVIA
                                    GQGTIGLEIMEDLYDVDNVIVPIGGGGLIAGIAI
                                    AIKSINPTIKVIGVQAENVHGMAA
                                    SYYAGEITAHRTTGTLADGCDVSRPGNLTYEIVR
                                    ELVDDIVLVSEDEIRNSMIALIQR
                                    NKVITEGAGALACAALLSGKLDSHIQNRKTVSII
                                    SGGNIDLSRVSQITGLVDA"
misc-feature        complement(62941..63819   /gene="STY3427"
                    )

                                    /note="Pfam match to entry PF00291
                                    PALP, Pyridoxal-phosphate
                                    dependent enzyme, score 314.00,
                                    E-value 1.8e-90"
misc-feature        complement(63694..63735   /gene="STY3427"
                    )

                                    /note="PS00165 Serine/threonine
                                    dehydratases pyridoxal-phosphate
                                    attachment site"
gene                complement(63977..64915   /gene="STY3428"
                    )

                                    /note="synonym: tdcA"
CDS                 complement(63977..64915   /gene="STY3428"
                    )

                                    /note="Orthologue of E. coli tdcA
                                    (TDCA-ECOLI); Fasta hit to
                                    TDCA-ECOLI (312 aa), 89% identity
                                    in 311 aa overlap"
                                    /codon-start=1
                                    /transl-table=11
                                    /product="TDC operon
                                    transcriptional activator"
                                    /protein-id="CAD07769.1"
                                    /db-xref="GI:16504318"
                                    /db-xref="GOA:Q8Z3K3"
                                    /db-xref="SPTREMBL:Q8Z3K3"
                                    /translation="MNTLVLPKTQHLVVFQEVIR
                                    SGSIGSAAKSLGLTQPAVSKIISD
                                    VEAYFGVELIVRKNTGVTLTEAGQVLLSWSESIT
                                    REMKNMINEMNSMTCNTVVDVSFG
                                    FPSLIGFTFMSDMIHKFKEVFPKAQVSMYEAQLS
                                    SFLPALRDGRLDFAIGTLSNEMQL
                                    QDLHVEPLFESEFVLVASKSRTCTGTITLESLKD
                                    EQWALPQTNMGYYSELLTTLQRNG
                                    ISIENIVKTDSVVTIYNLVLNADFLTVIPCDMTT
                                    PFGSNQFITIPIKDTLPVARYAAV
                                    WSKNYRIKKAASVLVELAKQYSSYNGCRRRQLIE
                                    IE"
misc-feature        complement(64463..64891   /gene="STY3428"
                    )

                                    /note="Pfam match to entry PF00126
                                    HTH-1, Bacterial regulatory
                                    helix-turn-helix protein, lysR
                                    family, score 128.50, E-value
                                    1.2e-34"
misc-feature        complement(64757..64849   /gene="STY3428"
                    )

                                    /note="PS00044 Bacterial
                                    regulatory proteins, lysR family
                                    signature"
gene                complement(65959..66334   /gene="rnpB"
                    )
misc-RNA            complement(65959..66334   /gene="rnpB"
                    )

                                    /note="hit to rnpB M1 RNA
                                    component of ribonuclease P 1..377
                                    score: 1818 percent id: 98.67"
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CDS              complement(66367..67512  /gene="STY3429"
                 )
                                          /note="Fasta hit to YBBZ-ECOLI
                                          (381 aa), 56% identity in 376 aa
                                          overlap Orthologue of E. coli yhaD
                                          (YHAD-ECOLI); Fasta hit to
                                          YHAD-ECOLI (381 aa), 86% identity
                                          in 381 aa overlap"
                                          /codon-start=1
                                          /transl-table=11
                                          /product="conserved hypothetical
                                          protein"
                                          /protein-id="CAD07770.1"
                                          /db-xref="GI:16504319"
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                                          /db-xref="SPTREMBL:Q8Z3K2"
                                          /translation="MKIVIAPDSYKESLSAAEVA
                                          QAIEKGFREIFPDAQYVSVPVADG
                                          GEGTVEAMIAATQGVERAAWVTGPLGEKVKACWG
                                          MSGDGKTAFIEMAAASGLALVPPE
                                          KRNPLITTSRGTGELILQALESGASNIIIGIGGS
                                          ATNDGGAGMMQALGAKLRDANGAD
                                          IGYGGGSLHCLSNIDISELDPRLKLCAIRVACDV
                                          SNPLIGDNGASRIFGPQKGATEEN
                                          IVELDRNLAHYADIIKKSLNVDVKAAPGAGAAGG
                                          MGAALMAFLGAELRSGIEIVTAAL
                                          NLEEHIHDCTLVVTGEGRIDSQSIRGKVPIGVAN
                                          VAKKYHKPVIGIAGSLTHDVGIVH
                                          HYGIDAVFSVLTRIVTLEEAFRGAFDNIYRASRN
                                          VAAALAIGMRSAG"
misc-feature     complement(67258..67281  /gene="STY3429"
                 )
                                          /note="PS00017 ATP/GTP-binding
                                          site motif A (P-loop)"
gene             complement(67610..68494  /gene="garR"
                 )
                                          /note="synonym: STY3430"
CDS              complement(67610..68494  /gene="garR"
                 )
                                          /EC-number="1.1.1.60"
                                          /note="Similar to Escherichia coli
                                          2-hydroxy-3-oxopropionate
                                          reductase GarR or B3125
                                          SW:GARR-ECOLI (P23523) (294 aa)
                                          fasta scores: E(): 0, 96.9% id in
                                          294 aa Fasta hit to YIHU-ECOLI
                                          (298 aa), 37% identity in 280 aa
                                          overlap Fasta hit to YGBJ-ECOLI
                                          (302 aa), 35% identity in 280 aa
                                          overlap Fasta hit to YBBQ-ECOLI
                                          (292 aa), 44% identity in 289 aa
                                          overlap Orthologue of E. coli yhaE
                                          (YHAE-ECOLI); Fasta hit to
                                          YHAE-ECOLI (294 aa), 97% identity
                                          in 294 aa overlap"
                                          /codon-start=1
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                                          e reductase"
                                          /protein-id="CAD07771.1"
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                                          /db-xref="GOA:Q8Z3K1"
                                          /db-xref="SPTREMBL:Q8Z3K1"
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                                          KAGYSLVVSDRNPEAIADVIAAGA
                                          ETASTAKAIAEQCDAIITMLPNSPHVKEVALGEN
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                                          EISDALKAKGVEMLDAPVSGGEPKAIDGTLSVMV
                                          GGDKAIFDKYYDLMKAMAGSVVHT
                                          GDIGAGNVTKLANQVIVALNIAAMSEALTLATKA
                                          GVNPDLVYQAIRGGLAGSTVLDAK
                                          APMVMDRNFKPGFRIDLHIKDLANALDTSHGVGA
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                        )                        /note="PS00895
                                                 3-hydroxyisobutyrate dehydrogenase
                                                 signature"
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                                                 /note="synonym: STY3431"
     CDS                complement(68526..69296  /gene="garL"
                        )
                                                 /EC-number="4.1.2.-"
                                                 /note="Similar to Escherichia coli
                                                 5-keto-4-deoxy-D-glucarate
                                                 aldolase GarL SW:GARL-ECOLI
                                                 (P23522) (256 aa) fasta scores:
                                                 E(): 0, 90.6% id in 256 aa Fasta
                                                 hit to P76469 (267 aa), 45%
                                                 identity in 256 aa overlap"
                                                 /codon-start=1
                                                 /transl-table=11
                                                 /product="5-keto-4-deoxy-D-glucara
                                                 te aldolase"
                                                 /protein-id="CAD07772.1"
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                                                 /db-xref="SPTREMBL:Q8XGF9"
                                                 /translation="MNNAIFPNKFKAALAAQQVQ
                                                 IGCWSALASPITTEVLGLAGFDWL
                                                 VLDGEHAPNDVTTLIPQLMALKGSASAPVVRVPT
                                                 NEPVIIKRMLDIGFYNFLIPFVET
                                                 QEEAARAVASTRYPPEGIRGVSVSHRANMFGTVP
                                                 DYFAQSNKNITIIVQIESQLGVDN
                                                 VDAIAATEGVDGIFVGPSDLAAALGHLGNASHPD
                                                 VQQTIQHIFARAKAHGKPCGILAP
                                                 VEADARRYLEWGATFVAVGSDLGAFRASTQKLAD
                                                 TFKK"
     gene               69827..71398             /gene="garD"
                                                 /note="synonym: STY3432"
     CDS                69827..71398             /gene="garD"
                                                 /EC-number="4.2.1.42"
                                                 /note="Similar to Escherichia coli
                                                 D-galactarate dehydratase gard or
                                                 b3128 SW:GARD-ECOLI (P39829) (523
                                                 aa) fasta scores: E(): 0, 93.5% id
                                                 in 523 aa Fasta hit to UXAA-ECOLI
                                                 (495 aa), 33% identity in 511 aa
                                                 overlap"
                                                 /codon-start=1
                                                 /transl-table=11
                                                 /product="D-galactarate
                                                 dehydratase"
                                                 /protein-id="CAD07773.1"
                                                 /db-xref="GI:16504322"
                                                 /db-xref="GOA:Q8Z3K0"
                                                 /db-xref="SPTREMBL:Q8Z3K0"
                                                 /translation="MANIEIRQESPSAFYIKVHE
                                                 TDNVAIIVNDHGLKAGTRFPDGLE
                                                 LTEHIPQGHKVALTDIPAHGEIIRYGEVIGYAVR
                                                 DIPRGSWIDESLVELPKAPPLNTL
                                                 PLATKVPEPLPPLEGYTFEGYRNADGSVGTKNLL
                                                 GITTSVHCVAGVVDYVVKVIERDL
                                                 LPKYPNVDGVVGLNHLYGCGVAINAPAAVVPIRT
                                                 IHNIALNPNFGGEVMVIGLGCEKL
                                                 QPERLLEGTEDVPAIAVENASIVRLQDEQHVGFK
                                                 SMVDDILRVAERHLTKLNQRQRET
                                                 CPASELVVGMQCGGSDAFSGVTANPAVGYASDLL
                                                 VRCGATVMFSEVTEVRDAIHLLTP
                                                 RAINEAVGKRLLDEMAWYDNYLDMGKTDRSANPS
                                                 PGNKKGGLANVVEKALGSIAKSGK
                                                 SAIVEVLSPGQRPTKRGLIYAATPASDFVCGTQQ
                                                 VASGITVQVFTTGRGTPYGLMAVP
                                                 VIKMATRTELANRWYDLMDINAGTIATGEETIED
                                                 VGWKLFHFILDVASGRKKTFSDQW
                                                 GLHNQLAVFNPAPVT"
     gene               complement(71638..72585  /gene="STY3433"
                        )
```

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                        )
                                            /note="Similar to several
                                            Eukaryotic carbohydrate kinases
                                            e.g. Lycopersicon esculentum
                                            fructokinase fk or frk2 TR:Q42896
                                            (EMBL:U62329) (328 aa) fasta
                                            scores: E(): 2.2e-22, 29.0% id in
                                            317 aa"
                                            /codon-start=1
                                            /transl-table=11
                                            /product="possible carbohydrate
                                            kinase"
                                            /protein-id="CAD07774.1"
                                            /db-xref="GI:16504323"
                                            /db-xref="GOA:Q8Z3J9"
                                            /db-xref="SPTREMBL:Q8Z3J9"
                                            /translation="MNITIATLSELLVEFLAKKE
                                            NQGFSSPGEFWGPYPSGAPAIFAD
                                            QVAKLGFRSLLFSCVGNDAFGVMNITRLSRDGVN
                                            VQGISVLPNATTGSAFVSYRSQAQ
                                            RDFIFNMPDSACGLLSADHLDETLLRQYRHFHIM
                                            GSSLFSFRLIDAVRKAISIVKENG
                                            GTISFDPNIRKEMLKIREMSQAFEYILDYTDFFL
                                            PSDGELDYFGLSKSRDEEKIVARL
                                            HKRGIAHVIIKRGARGASYYSKDEQHHVAGYPVK
                                            VVDPTGAGDCFGATFVSLFLAGYS
                                            VPDALAHANAAGSLAISARGPMEGTSTLAQIKEL
                                            MRQQN"
     misc-feature    complement(71788..71991 /gene="STY3433"
                        )
                                            /note="Pfam match to entry PF00294
                                            pfkB, pfkB family carbohydrate
                                            kinase, score 67.30, E-value
                                            3.5e-20"
     misc-feature    complement(72076..72480 /gene="STY3433"
                        )
                                            /note="Pfam match to entry PF00294
                                            pfkB, pfkB family carbohydrate
                                            kinase, score 27.00, E-value
                                            1.5e-07"
     misc-feature    complement(73103..73399 /note="Pfam match to entry PF00455
                        )                    deoR, Bacterial regulatory
                                            proteins, deoR family, score
                                            61.40, E-value 2.6e-16"
     misc-feature    complement(73295..73399 /note="PS00894 Bacterial
                        )                    regulatory proteins, deoR family
                                            signature"
     gene            73763..74617            /gene="STY3435"
                                            /note="synonym: gatY"
     CDS             73763..74617            /gene="STY3435"
                                            /note="Fasta hit to AGAY-ECOLI
                                            (286 aa), 64% identity in 284 aa
                                            overlap Fasta hit to P77704 (278
                                            aa), 40% identity in 277 aa
                                            overlap Orthologue of E. coli gatY
                                            (GATY-ECOLI); Fasta hit to
                                            GATY-ECOLI (286 aa), 65% identity
                                            in 283 aa overlap"
                                            /codon-start=1
                                            /transl-table=11
                                            /product="tagatose-bisphosphate
                                            aldolase"
                                            /protein-id="CAD07775.1"
                                            /db-xref="GI:16504324"
                                            /db-xref="GOA:Q8XGZ9"
                                            /db-xref="SPTREMBL:Q8XGZ9"
                                            /translation="MFIISSKNMLQKAQHAGYAV
                                            PAFNIHNLETLQVVVETAAEMRSP
                                            LIVAGTPGTFSYAGMGNIVAIAGDLAREYNLPLA
                                            IHLDHHESLADIESKVMAGIRSVM
                                            IDGSHFPFEENVALVKSVVDFCHRYDTSVEAELG
                                            RLGGIEDDLVVDSKDALYTNPQQA
                                            REFVARTGIDSLAVAIGTAHGMYAAEPKLDFERL
                                            AEIRALVDIPLVLHGASGLPESDI
                                            RQAISLGVCKVNVATELKIAFSDALKEYFLQNPK
```

misc-feature	73766..74614	/gene="STY3435" /note="Pfam match to entry PF01116 F-bP-aldolase, Fructose-bisphosphate aldolase class-II, score 494.60, E-value 7.4e-145"
misc-feature	73979..74014	/gene="STY3435" /note="PS00602 Fructose-bisphosphate aldolase class-II signature 1"
misc-feature	74153..74188	/gene="STY3435" /note="PS00806 Fructose-bisphosphate aldolase class-II signature 2"
gene CDS	74628..75542 74628..75542	/gene="STY3436" /gene="STY3436" /note="Similar to Bacillus subtilis 1-phosphofructokinase fruk or fruB SW:K1PF-BACSU (O31714) (303 aa) fasta scores: E(): 9.9e-28, 31.8% id in 305 aa" /codon-start=1 /transl-table=11 /product="possible carbohydrate kinase" /protein-id="CAD07776.1" /db-xref="GI:16504325" /db-xref="GOA:Q8Z3J8" /db-xref="SPTREMBL:Q8Z3J8" /translation="MIYTLTLNSAIDMNIFSDPL QPNIVNRTHHTEFCPNGKGVNVAL VLDHFQIPAHILGIFGGFTGHYIVESLRTRKMPV TPAWVEEPTRINIFIHDGKQEYKL VNPGSYIPDECKKQIITIISQLPDAEYLVISGSL PQGIESRFYAEIMHICQQKNIGVI LDISHPSLRQLLEFKPLLIKPNDEEVKAIFGLTV SDDNDAKNTLTTLHALGAQNVLLT LGAKGMYFSNGIDYWFCSAPTVDLVSSACAGDAA LAAFLSQWLSTGEVEYALSLASAT GADVASSAGLGQLAAIETLLSQIHVRKL"
misc-feature	75006..75392	/gene="STY3436" /note="Pfam match to entry PF00294 pfkB, pfkB family carbohydrate kinase, score 67.00, E-value 4.2e-20"
gene CDS	75569..76996 75569..76996	/gene="STY3437" /gene="STY3437" /note="Similar to Escherichia coli PTS system, fructose-like-1 IIBC component FrvB SW:PTVB-ECOLI (P32154) (485 aa) fasta scores: E(): 0, 32.4% id in 475 aa. Note, like the example given, the predicted product of this CDS contains only one hydrophilic IIB domain. Contains possible membrane spanning hydrophobic domains. Fasta hit to PTVB-ECOLI (485 aa), 32% identity in 474 aa overlap Paralogue of E. coli fruA (PTFB-ECOLI); Fasta hit to PTFB-ECOLI (563 aa), 42% identity in 471 aa overlap" /codon-start=1 /transl-table=11 /product="PTS system, sugar phosphotransferase enzyme IIBC component" /protein-id="CAD07777.1" /db-xref="GI:16504326" /db-xref="GOA:Q8Z3J7" /db-xref="SPTREMBL:Q8Z3J7" /translation="MKKIIAVTGCPTGIAHTFMA EEALKNAAKKLSVEIKVETNGASG VENAIQPADLVDIAGVIIAADKDVLPDRFNGLPV

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                                      PIRKGESTTSTEIIEKESLGRQIYKHLMSGVSNM
                                      LPFVVAGGILIAVSLLWGIYSADP
                                      NSAEYNATAAMLMKIGQQAFSIMVPVFTAYIAFS
                                      ISGRPGMVAGFVGGLLANTTGAGF
                                      LGGIIAGFAAGYLMLWVKNRLEGLPRQYEGLKSI
                                      FIMPLIGVLVIGVLMSLLGQPVAA
                                      INNSMMNWLASLQEANPILLGIVVGAMCSFDFGG
                                      PVNKAAYVTGTLLLGQGNFYFMAG
                                      VSAACITPPLVIALATTFFPKGFSEEERAAGMVN
                                      YILGCTHITEGAIPFAAKDPLRVI
                                      PMMMIASSISAVLSYSLRIQVPAPHGGFLILPLV
                                      SQPLAWVLCILAGSACGAMMLGLW
                                      RLWAVRKNSVNTTPVAKAGGQNAAL"
gene         76983..77789             /gene="STY3438"
CDS          76983..77789             /gene="STY3438"
                                      /note="This CDS is similar to the
                                      phosphotransferase enzyme IIA and
                                      HPr (phosphoryl carrier protein)
                                      domains of PTF family sugar
                                      transport proteins , e.g. the
                                      N-terminus of Xanthomonas
                                      campestris multiphosphoryl
                                      transfer protein FruB
                                      SW:PTF1-XANCP (P45597) (837 aa)
                                      fasta scores: E(): 2.9e-22, 36.0%
                                      id in 225 aa Paralogue of E. coli
                                      fruB (PTFA-ECOLI); Fasta hit to
                                      PTFA-ECOLI (376 aa), 36% identity
                                      in 372 aa overlap"
                                      /codon-start=1
                                      /transl-table=11
                                      /product="PTS-transport family
                                      phosphoryl transfer protein"
                                      /protein-id="CAD07778.1"
                                      /db-xref="GI:16504327"
                                      /db-xref="GOA:Q8Z3J6"
                                      /db-xref="SPTREMBL:Q8Z3J6"
                                      /translation="MQLCEHDIFISDERLDKVTA
                                      LHRVVEKLSAAGNTTPDYLRGMLD
                                      REAQISTYLGNGIAIPHGTPESRDAVLQTGVKVI
                                      VFRHGVDWGDGNTAYLVTGIAARS
                                      NEHLEILRQLTRVLSDDAILQALAKAESPSQVLA
                                      LLTGSTTNTPAAMELHEGEQATFV
                                      IHNPHGLHARPSAVLVKFIKQFQSHITVENLDNA
                                      SGPVDGKNLMRVVSLGAKKGHRLL
                                      FRAQGEDAQQALREIGELIASGAGEMITVPVTPP
                                      PEVMQPKRSWLSRLFN"
misc-feature 77040..77216             /gene="STY3438"
                                      /note="Pfam match to entry PF00359
                                      PTS-EIIA-2,
                                      phosphoenolpyruvate-dependent
                                      sugar phosphotransferase system,
                                      EIIA 2, score 79.50, E-value
                                      6.1e-21"
misc-feature 77118..77168             /gene="STY3438"
                                      /note="PS00372 PTS EIIA domains
                                      phosphorylation site signature 2"
misc-feature 77445..77681             /gene="STY3438"
                                      /note="Pfam match to entry PF00381
                                      PTS-HPr, PTS HPr component
                                      phosphorylation sites, score
                                      115.00, E-value 1.5e-30"
misc-feature 77478..77501             /gene="STY3438"
                                      /note="PS00369 PTS HPR component
                                      histidine phosphorylation site
                                      signature"
gene         77987..79258             /gene="STY3439"
                                      /pseudo
CDS          77987..79258             /gene="STY3439"
                                      /note="Similar to Escherichia coli
                                      putative tagatose 6-phosphate
                                      kinase gatz SW:GATZ-ECOLI () (420
                                      aa) fasta scores: E(): 0, 76.1% id
                                      in 331 aa. Note contains a stop
                                      codon after codon 331. The
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/pseudo
/codon-start=1
/transl-table=11
/product="putative sugar kinase
(pseudogene)"

gene   79273..79737   /gene="STY3441"
                                /note="synonym: gatA"
CDS   79273..79737   /gene="STY3441"
                                /note="Orthologue of E. coli gatA
                                (PTKA-ECOLI); Fasta hit to
                                PTKA-ECOLI (150 aa), 63% identity
                                in 150 aa overlap"
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                                /transl-table=11
                                /product="PTS system,
                                galactitol-specific IIA component"
                                /protein-id="CAD07780.1"
                                /db-xref="GI:16504328"
                                /db-xref="GOA:Q8Z3J5"
                                /db-xref="SPTREMBL:Q8Z3J5"
                                /translation="MSQLFVRTGITFDSSQQALA
                                HIGKEMLAKGVVHDSYPQALVERE
                                ASFPTGIALERHAVAIPHCEAVHAKSPAIYLIRP
                                DKPVMFQQADDDEEIAVSLIIALI
                                VENPAAQLKLLRRLFGALQIPDTIEALLSAPDAE
                                LASCFEHKVLTAEQCVQV"

gene   79768..80052   /gene="STY3442"
                                /note="synonym: gatB"
CDS   79768..80052   /gene="STY3442"
                                /note="Orthologue of E. coli gatB
                                (PTKB-ECOLI); Fasta hit to
                                PTKB-ECOLI (94 aa), 79% identity
                                in 94 aa overlap"
                                /codon-start=1
                                /transl-table=11
                                /product="PTS system,
                                galactitol-specific IIB component"
                                /protein-id="CAD07781.1"
                                /db-xref="GI:16504329"
                                /db-xref="GOA:Q8Z3J4"
                                /db-xref="SPTREMBL:Q8Z3J4"
                                /translation="MKRKVIVACGGAVATSTMAA
                                EEIKELCDANHIELDLVQCRVTEI
                                ETYMDGADLICTTARVDRAFGDIPVVHGMPFVSG
                                VGIEALQQKILSILMG"

gene   80056..81429   /gene="STY3443"
                                /note="synonym: gatC"
CDS   80056..81429   /gene="STY3443"
                                /note="Fasta hit to SGCC-ECOLI
                                (437 aa), 43% identity in 432 aa
                                overlap Orthologue of E. coli gatC
                                (PTKC-ECOLI); Fasta hit to
                                PTKC-ECOLI (451 aa), 85% identity
                                in 446 aa overlap. Contains
                                possible membrane spanning
                                hydrophobic domains."
                                /codon-start=1
                                /transl-table=11
                                /product="PTS system,
                                galactitol-specific IIC component"
                                /protein-id="CAD07782.1"
                                /db-xref="GI:16504330"
                                /db-xref="GOA:Q8Z3J3"
                                /db-xref="SPTREMBL:Q8Z3J3"
                                /translation="MFSEIMRYILDLGPTVMLPL
                                VIIVFSKLLGMKLGDCFKSGLHIG
                                IGFVGIGLVIGLMLDSIGPAAKAMAEHFQINLHV
                                IDVGWPGSSPMTWASQIALVAIPV
                                AIGVNVLMLVTRMTRVVNVDIWNIWHMTFTGAML
                                HLATGSYWLGILGVVVHAAFVYKL
                                GDWFAKDTRDYFGLEGIAIPHGSSAYLSPVAVLV
                                DTIIEKIPGLNRIHFSADDVQKRF
                                GPFGEPVTVGFVMGLVIGVLAGYDTKAVLQLAVK
                                TAAVMLLMPRVIKPIMDGLTPIAK

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                                          LIFIPLTILIAVLVPGNQVLPFGD
                                          LATIGFFIAMAVAVHQGNLFRTLISGVIIMGITL
                                          WIATQTIGLHTQLAANAGALKAGA
                                          QVASLDQGGSPITWLLIQLFTWQNIVGFAVIAII
                                          YLAGVLLTWRRARQFVAAEKATAL QQSQIAS"
     gene            81473..82516         /gene="STY3444"
                                          /note="synonym: gatD"
     CDS             81473..82516         /gene="STY3444"
                                          /note="Fasta hit to YDJJ-ECOLI
                                          (347 aa), 32% identity in 338 aa
                                          overlap Orthologue of E. coli gatD
                                          (GATD-ECOLI); Fasta hit to
                                          GATD-ECOLI (346 aa), 68% identity
                                          in 344 aa overlap"
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                                          /transl-table=11
                                          /product="galactitol-1-phosphate
                                          dehydrogenase"
                                          /protein-id="CAD07783.1"
                                          /db-xref="GI:16504331"
                                          /db-xref="GOA:Q8Z3J2"
                                          /db-xref="SPTREMBL:Q8Z3J2"
                                          /translation="MKSVVIHAEGDVRVEERPLP
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                                          IFAQGAHYYPITLGHEFSGYVESYGTGVTDMQPG
                                          DAVACVPLLPCFHCPQCERGYFSL
                                          CKQYQFVGSRSEGGNAEYVVVKRANLFRLPSDMP
                                          IEDGAFIEPITVGLHAFHLAQGCE
                                          GKNVIIVGAGTIGLLALQCARELGARSVTAIDIN
                                          PQKLELAKALGATHTCNSREMTAD
                                          DIQTALSDIQFDQLVLETAGTPQTVSLAIDITGP
                                          RAQLALVGTLHHDLTLTTRTFGLI
                                          LRKELTLLGSWMNYSAPWPGEEWETAARLLAEKR
                                          LQLTPLIAHRGDAESFAEAVKALN
                                          GAPMQGKILLQLS"
     misc-feature    81503..82510         /gene="STY3444"
                                          /note="Pfam match to entry PF00107
                                          adh-zinc, Zinc-binding
                                          dehydrogenases, score 285.90,
                                          E-value 5.2e-82"
     misc-feature    81644..81688         /gene="STY3444"
                                          /note="PS00059 Zinc-containing
                                          alcohol dehydrogenases signature"
     gene            82627..83400         /gene="STY3445"
                                          /note="synonym: gatR"
     CDS             82627..83400         /gene="STY3445"
                                          /note="Fasta hit to SRLR-ECOLI
                                          (257 aa), 37% identity in 257 aa
                                          overlap Fasta hit to YGBI-ECOLI
                                          (265 aa), 32% identity in 253 aa
                                          overlap Fasta hit to YCIT-ECOLI
                                          (249 aa), 31% identity in 261 aa
                                          overlap Fasta hit to AGAR-ECOLI
                                          (269 aa), 36% identity in 254 aa
                                          overlap Fasta hit to FUCR-ECOLI
                                          (243 aa), 31% identity in 236 aa
                                          overlap Fasta hit to GLPR-ECOLI
                                          (252 aa), 32% identity in 241 aa
                                          overlap Orthologue of E. coli
                                          gatR-2 (GATR-ECOLI); Fasta hit to
                                          GATR-ECOLI (259 aa), 73% identity
                                          in 257 aa overlap"
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                                          /transl-table=11
                                          /product="galactitol utilization
                                          operon repressor"
                                          /protein-id="CAD07784.1"
                                          /db-xref="GI:16504332"
                                          /db-xref="GOA:Q8Z3J1"
                                          /db-xref="SPTREMBL:Q8Z3J1"
                                          /translation="MNSFERRNKIVDLINTQGSV
                                          LVMDLSNTFGISEVTIRADLRLLE
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                                          ELMIV"
misc-feature      82642..83334            /gene="STY3445"
                                          /note="Pfam match to entry PF00455
                                          deoR, Bacterial regulatory
                                          proteins, deoR family, score
                                          255.80, E-value 5.8e-73"
misc-feature      82642..82746            /gene="STY3445"
                                          /note="PS00894 Bacterial
                                          regulatory proteins, deoR family
                                          signature"
gene              complement(83558..84421 /gene="STY3446"
                  )
CDS               complement(83558..84421 /gene="STY3446"
                  )
                                          /note="Orthologue of E. coli yraL
                                          (YRAL-ECOLI); Fasta hit to
                                          YRAL-ECOLI (286 aa), 97% identity
                                          in 285 aa overlap"
                                          /codon-start=1
                                          /transl-table=11
                                          /product="conserved hypothetical
                                          protein"
                                          /protein-id="CAD07785.1"
                                          /db-xref="GI:16504333"
                                          /db-xref="GOA:Q8Z3J0"
                                          /db-xref="SPTREMBL:Q8Z3J0"
                                          /translation="MKQNESADNSQGQLFIVPTP
                                          IGNLADITQRALEVLQAVDLIAAE
                                          DTRHTGLLLQHFGINARLFALHDHNEQQKAETLV
                                          AKLKEGQNIALVSDAGTPLINDPG
                                          YHLVRTCREAGIRVVPLPGPCAAITALSAAGLPS
                                          DRFCYEGFLPAKSKGRRDALKAIE
                                          AEPRTLIFYESTHRLLDSLEDMVAVWGESRYVVL
                                          ARELTKTWETIHGAPVGELLAWVK
                                          EDENRRKGEMVLIVEGHKAQEDDLPADALRTLAL
                                          LQAELPLKKAAALAAEIHGVKKNA
                                          LYKYALAQQEE"
misc-feature      complement(83780..84385 /gene="STY3446"
                  )
                                          /note="Pfam match to entry PF00590
                                          TP-methylase, Tetrapyrrole
                                          (Corrin/Porphyrin) Methylases.,
                                          score 239.80, E-value 3.8e-68"
misc-feature      complement(84116..84151 /gene="STY3446"
                  )
                                          /note="PS01296 Uncharacterized
                                          protein family UPF0011 signature"
gene              84485..86536            /gene="STY3447"
CDS               84485..86536            /gene="STY3447"
                                          /note="Orthologue of E. coli yraM
                                          (YRAM-ECOLI); Fasta hit to
                                          YRAM-ECOLI (678 aa), 79% identity
                                          in 684 aa overlap. Contains a
                                          possible N-terminal signal
                                          sequence."
                                          /codon-start=1
                                          /transl-table=11
                                          /product="possible exported
                                          protein"
                                          /protein-id="CAD07786.1"
                                          /db-xref="GI:16504334"
                                          /db-xref="SPTREMBL:Q8Z3I9"
                                          /translation="MVPSTFSRLNAARALPVVLA
                                          ALLFAGCGTQAPDQSAAYMQGSAQ
                                          ADSAFYLHQMQQSADDSKTNWQLLAIHALLKEGK
                                          SQQAVELFNQPPQNLNDTQRREQS
                                          LLAVEIKLAQKDVAGAQALLDKLKPADFAPHQQA
                                          RYWQAQIVASQGRPSLTLLRALIA
                                          QEPLLAAKEKQKNIDATWQALSAMTPDQARTLVI
                                          NADENVLQGWLDLQRVWFDNRNDP
                                          DMLKAGIADWQKRYPQNPGAKMLPTQLVNVQRFK
                                          PASTSKIALLLPLNGQAAVFGRTI
```

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                                         QPQMTNGVASPSQASVRDLTDDAP
                                         SQSATPVSAPQTPPAQPATASAPADPSAELKIYD
                                         TSSQPLDQVLAQVQQDGASIVVGP
                                         LLKNNVEALMKSNTPLNVLALNQPETVRSFPNIC
                                         YFALSPEDEARDAAHHIYEQGKQS
                                         PLLLIPRSALGDRVANAFTQEWQKLGGGIVLQQK
                                         FGSVAELKMGVNGGAGIALTGSPV
                                         AASVPAQPGVTIGGLTIPAPPTDAQITGGGRVDA
                                         VYILATPEEIGFIKPMIAMRNGTQ
                                         SGATLYASSRSAQGTSGPDFRLEMEGLQYSEIPM
                                         LAGGNTPLMQQALSAVHNDYSLAR
                                         MYAMGVDAWTLANHFSQMRQVQGFEINGNTGALT
                                         ASPDCVINRKLSWLKYQQGEIVPA S"
misc-feature    84698..84721             /gene="STY3447"
                                         /note="PS00017 ATP/GTP-binding
                                         site motif A (P-loop)"
gene            86494..86889             /gene="yraN"
                                         /note="synonym: STY3448"
CDS             86494..86889             /gene="yraN"
                                         /note="Similar to Escherichia coli
                                         hypothetical 14.8 kDa protein in
                                         agai-mtr intergenic region yraN
                                         SW:YRAN-ECOLI (P45465) (131 aa)
                                         fasta scores: E(): 0, 82.4% id in
                                         131 aa, and to Haemophilus
                                         influenzae hypothetical protein
                                         Hi1656 hi1656 SW:YRAN-HAEIN
                                         (P45300) (119 aa) fasta scores:
                                         E(): 4e-19, 53.2% id in 109 aa,
                                         and to Xylella fastidiosa
                                         hypothetical protein Xf0554 xf0554
                                         TR:Q9PFV3 (EMBL:AE003902) (121 aa)
                                         fasta scores: E(): 3.9e-17, 49.1%
                                         id in 116 aa Similar to the
                                         C-terminal of E. coli
                                         SW:YRAN-ECOLI"
                                         /codon-start=1
                                         /transl-table=11
                                         /product="conserved hypothetical
                                         protein"
                                         /protein-id="CAD07787.1"
                                         /db-xref="GI:16504335"
                                         /db-xref="SWISS-PROT:Q8Z3I8"
                                         /translation="MAQIPARGDCSRQLTRKQAG
                                         DAWEAAARLWLESKGLRFIAANVR
                                         ERGGEIDLIMRDGKTTVFVEVRYRRSGLYGGAAA
                                         SVTRSKQHKLLHTARLWLARQNGS
                                         FDTVDCRFDVLAFTGNEIEWFRDAFNDHS"
misc-feature    86557..86841             /gene="yraN"
                                         /note="Pfam match to entry PF02021
                                         UPF0102, Uncharacterised protein
                                         family UPF0102, score 192.20,
                                         E-value 8.1e-54"
gene            86911..87501             /gene="STY3449"
CDS             86911..87501             /gene="STY3449"
                                         /note="Similar to Methanococcus
                                         jannaschii probable phosphoheptose
                                         isomerase lpca or gmha or mj1335
                                         SW:LPCA-METJA (Q58731) (187 aa)
                                         fasta scores: E(): 3.3e-27, 42.5%
                                         id in 186 aa Fasta hit to
                                         LPCA-ECOLI (192 aa), 42% identity
                                         in 166 aa overlap Orthologue of E.
                                         coli yraO (YRAO-ECOLI); Fasta hit
                                         to YRAO-ECOLI (196 aa), 98%
                                         identity in 194 aa overlap"
                                         /codon-start=1
                                         /transl-table=11
                                         /product="probable phosphoheptose
                                         isomerase"
                                         /protein-id="CAD07788.1"
                                         /db-xref="GI:16504336"
                                         /db-xref="GOA:Q8Z3I7"
                                         /db-xref="SPTREMBL:Q8Z3I7"
                                         /translation="MLERIKVCFTESIQTQIAAA
```

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                                        LCCGNGTSAANAQHFAASMINRFETERPSLPAIA
                                        LNTDNVVLTAIANDRLHDEVYAKQ
                                        VRALGHAGDVLLAISTRGNSRDIVKAVEAAVTRD
                                        MTIVALTGYDGGELAGLLGPQDVE
                                        IRIPSHHSARIQEMHMLTVNCLCGLIDNTLFPHQ
                                        DD"
misc-feature      87013..87489          /gene="STY3449"
                                        /note="Pfam match to entry PF01380
                                        SIS, SIS domain, score 157.10,
                                        E-value 3.1e-43"
gene              87511..88086          /gene="STY3450"
CDS               87511..88086          /gene="STY3450"
                                        /note="Fasta hit to OSMY-ECOLI
                                        (201 aa), 32% identity in 183 aa
                                        overlap Orthologue of E. coli yraP
                                        (YRAP-ECOLI); Fasta hit to
                                        YRAP-ECOLI (191 aa), 93% identity
                                        in 191 aa overlap. Contains a
                                        possible N-terminal signal
                                        sequence."
                                        /codon-start=1
                                        /transl-table=11
                                        /product="possible lipoprotein"
                                        /protein-id="CAD07789.1"
                                        /db-xref="GI:16504337"
                                        /db-xref="SPTREMBL:Q8XG47"
                                        /translation="MKAFSPLAVLISALLLQGCV
                                        AAAVVGTAAVGTKAATDPRSVGTQ
                                        VDDGTLELRVSSALSKDEQIKKETRINVTAYQGK
                                        VLLVGQSPNSELSARAKQIAMGVE
                                        GTTEVYNEIRQGQPIGLGTASNDTWITTKVRSQL
                                        LTSDQVKSSNVKVTTENGEVFLLG
                                        LVTEREGKAAADIASRVSGVKRVTTAFTYIK"
misc-feature      87535..87567          /gene="STY3450"
                                        /note="PS00013 Prokaryotic
                                        membrane lipoprotein lipid
                                        attachment site"
gene              complement(88153..88788 /gene="STY3451"
                  )
CDS               complement(88153..88788 /gene="STY3451"
                  )
                                        /note="Orthologue of E. coli yraR
                                        (YRAR-ECOLI); Fasta hit to
                                        YRAR-ECOLI (226 aa), 88% identity
                                        in 210 aa overlap. Note lacks the
                                        N-terminal 15 amino acids of the
                                        E. coli orthologue."
                                        /codon-start=1
                                        /transl-table=11
                                        /product="conserved hypothetical
                                        protein"
                                        /protein-id="CAD07790.1"
                                        /db-xref="GI:16504338"
                                        /db-xref="SPTREMBL:Q8Z3I6"
                                        /translation="MSQVLITGATGLVGGHLLRM
                                        LINTPQVSAIAAPTRRPLTDIVGV
                                        YNPHDPQLTDALAQVTDPVDIVFCCLGTTRREAG
                                        SKAAFIHADYTLVVDTALTGRRLG
                                        AQHMLVVSAMGANAHSPFFYNRVKGEMEEALIAQ
                                        NWPRLTIARPSMLLGDRTTRRVNE
                                        TLFAPLFRLLPGNWKSIDARDVARAMLAEALEPA
                                        QEGVTILTSSQLREKAG"
gene              88919..89437          /gene="STY3452"
CDS               88919..89437          /gene="STY3452"
                                        /note="Similar to several
                                        including: Bacillus subtilis
                                        general stress protein 18 yfkM
                                        SW:GS18-BACSU (P80876) (171 aa)
                                        fasta scores: E(): 0, 64.9% id in
                                        168 aa, and to Pyrococcus furiosus
                                        protease I pfpI SW:PFPI-PYRFU
                                        (Q51732) (166 aa) fasta scores:
                                        E(): 6.5e-24, 47.9% id in 167 aa
                                        Orthologue of E. coli yhbO
                                        (YHBO-ECOLI); Fasta hit to
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                                             in 172 aa overlap"
                                             /codon-start=1
                                             /transl-table=11
                                             /product="conserved hypothetical
                                             protein"
                                             /protein-id="CAD07791.1"
                                             /db-xref="GI:16504339"
                                             /db-xref="SPTREMBL:Q8XH07"
                                             /translation="MSKKIAVLITDEFEDSEFTS
                                             PAAEFRQAGHEVITIEKEAGKTVK
                                             GKKGEASVTIDKAIDDVRPDEFDALLLPGGHSPD
                                             YLRGDSRFVDFTRDFVNSGKPVFA
                                             ICHGPQLLISADVIRGRKLTAVKPIIIDVKNAGA
                                             EFYDQEVVVDKDQLVTSRTPDDLP
                                             AFNREALRLLGA"
misc-feature        88928..89386             /gene="STY3452"
                                             /note="Pfam match to entry PF01965
                                             ThiJ, ThiJ/PfpI family, score
                                             296.00, E-value 4.8e-85"
gene                complement(89417..89860  /gene="STY3453"
                    )
CDS                 complement(89417..89860  /gene="STY3453"
                    )
                                             /note="Orthologue of E. coli yhbP
                                             (YHBP-ECOLI); Fasta hit to
                                             YHBP-ECOLI (147 aa), 84% identity
                                             in 147 aa overlap"
                                             /codon-start=1
                                             /transl-table=11
                                             /product="conserved hypothetical
                                             protein"
                                             /protein-id="CAD07792.1"
                                             /db-xref="GI:16504340"
                                             /db-xref="SPTREMBL:Q8XEW3"
                                             /translation="MDTLTAIGRWLAKQHVVTWC
                                             VHHEGELWCANAFYLFDAQNVALY
                                             LLTDDKTRHAQMSGACAPVAGTVNGQPKTVARIR
                                             GVQFKGEIRRLEGQESDAARKAYL
                                             RRFPVARVLPAPVWEIRLDEIKFTDNTLGFGKKL
                                             HWLRDSRAQQA"
gene                89898..90215             /gene="STY3454"
CDS                 89898..90215             /gene="STY3454"
                                             /note="Orthologue of E. coli yhbQ
                                             (YHBQ-ECOLI); Fasta hit to
                                             YHBQ-ECOLI (100 aa), 81% identity
                                             in 100 aa overlap"
                                             /codon-start=1
                                             /transl-table=11
                                             /product="conserved hypothetical
                                             protein"
                                             /protein-id="CAD07793.1"
                                             /db-xref="GI:16504341"
                                             /db-xref="GOA:Q8XGW2"
                                             /db-xref="SWISS-PROT:Q8XGW2"
                                             /translation="MLMATMTPWYLYLIRTADNA
                                             LYTGITTDVARRYRQHQTGKGAKA
                                             LRGKGELTLAFAAQVGDRSLALRIEYRIKQLTKR
                                             QKERLVTEREAFEALLSSLQTPVL KND"
gene                complement(90202..90705  /gene="STY3455"
                    )
CDS                 complement(90202..90705  /gene="STY3455"
                    )
                                             /note="Similar to Escherichia coli
                                             hypothetical protein YhbS
                                             SW:YHBS-ECOLI (P45473) (167 aa)
                                             fasta scores: E(): 0, 96.4% id in
                                             167 aa and to Streptomyces
                                             coelicolor putative
                                             acetyltransferase SCF56.14C
                                             TR:Q9RD52 (EMBL:AL133424) (173 aa)
                                             fasta scores: E(): 7.7e-07, 30.9%
                                             id in 165 aa Orthologue of E. coli
                                             YHBS-ECOLI; Fasta hit to
                                             YHBS-ECOLI (167 aa), 96% identity
                                             in 167 aa overlap"
```

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                                        /transl-table=11
                                        /product="putative
                                        acetyltransferase"
                                        /protein-id="CAD07794.1"
                                        /db-xref="GI:16504342"
                                        /db-xref="GOA:Q8XF87"
                                        /db-xref="SPTREMBL:Q8XF87"
                                        /translation="MLIRVEIPIDAPGIDALLRR
                                        SFESDAEAKLVHDLREDGFLTLGL
                                        VATDDEGQVVGYVAFSPVDVQGEDLQWVGMAPLA
                                        VDEKYRGQGLARQLVYEGLDSLNE
                                        FGYAAVVTLGDPALYSRFGFELAAHYDLHCRWPG
                                        TESAFQVHRLAEDALEGVTGLVEY HDHFNRF"
misc-feature     complement(90337..90561 /gene="STY3455"
                 )
                                        /note="Pfam match to entry PF00583
                                        Acetyltransf, Acetyltransferase
                                        (GNAT) family, score 57.20,
                                        E-value 3.6e-13"
gene             complement(90699..91223 /gene="STY3456"
                 )
CDS              complement(90699..91223 /gene="STY3456"
                 )
                                        /note="Orthologue of E. coli yhbT
                                        (YHBT-ECOLI); Fasta hit to
                                        YHBT-ECOLI (174 aa), 91% identity
                                        in 174 aa overlap"
                                        /codon-start=1
                                        /transl-table=11
                                        /product="conserved hypothetical
                                        protein"
                                        /protein-id="CAD07795.1"
                                        /db-xref="GI:16504343"
                                        /db-xref="GOA:Q8Z3I5"
                                        /db-xref="SPTREMBL:Q8Z3I5"
                                        /translation="MLDKLRSRLVHAGPSLMSVP
                                        VKLTPFALKRQVLEQVLSWQFRQA
                                        LADGELEFLEGRWLSIHVRDIDLKWYTTVENEKL
                                        IVSQQADADVSFSADASDLLMIAA
                                        RKQDPDTLFFQRRLVIEGDTELGLYVKNLMDAIE
                                        LEQMPKALRIMLLQLADFVEAGMK
                                        NSPETKQTSVGEPC"
misc-feature     complement(90816..91136 /gene="STY3456"
                 )
                                        /note="Pfam match to entry PF02036
                                        SCP2, SCP-2 sterol transfer
                                        family, score 101.00, E-value
                                        2.3e-26"
gene             91440..92435            /gene="STY3457"
CDS              91440..92435            /gene="STY3457"
                                        /note="Orthologue of E. coli yhbU
                                        (YHBU-ECOLI); Fasta hit to
                                        YHBU-ECOLI (331 aa), 97% identity
                                        in 331 aa overlap"
                                        /codon-start=1
                                        /transl-table=11
                                        /product="putative protease"
                                        /protein-id="CAD07796.1"
                                        /db-xref="GI:16504344"
                                        /db-xref="GOA:Q8XEV5"
                                        /db-xref="SPTREMBL:Q8XEV5"
                                        /translation="MELLCPAGNLPALKAAIENG
                                        ADAVYIGLKDDTNARHFAGLNFTE
                                        KKLQEAVSFVHQHRRKLHIAINTFAHPDGYARWQ
                                        RAVDMAAQLGADALILADLAMLEY
                                        AAERYPHIERHVSVQASATNEEAIRFYHRNFDVH
                                        RVVLPRVLSIHQVKQLARVTPVPL
                                        EVFAFGSLCIMAEGRCYLSSYLTGESPNTVGACS
                                        PARFVRWQQTPQGLESRLNDVLID
                                        RYQDGENAGYPTLCKGRYLVDGERYHALEEPTSL
                                        NTLELLPELMAANIASVKIEGRQR
                                        SPAYVSQVAKVWRQAIDRCKAAPQNFVPQRDWME
                                        TLGAMSEGTQTTLGAYHRKWQ"
misc-feature     91659..92432            /gene="STY3457"
                                        /note="Pfam match to entry PF01136
```

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                                            U32, score 519.00, E-value
                                            3.4e-152"
misc-feature    91920..91976                /gene="STY3457"
                                            /note="PS01276 Peptidase family
                                            U32 signature"
gene            92444..93322                /gene="STY3458"
                                            /note="synonym: yhbV"
CDS             92444..93322                /gene="STY3458"
                                            /note="Orthologue of E. coli yhbV
                                            (YHBV-ECOLI); Fasta hit to
                                            YHBV-ECOLI (298 aa), 91% identity
                                            in 292 aa overlap"
                                            /codon-start=1
                                            /transl-table=11
                                            /product="conserved hypothetical
                                            protein"
                                            /protein-id="CAD07797.1"
                                            /db-xref="GI:16504345"
                                            /db-xref="SPTREMBL:Q8Z3I4"
                                            /translation="MKYSLGPVLYYWPKETLEDF
                                            YQQAAKSSADIIYLGEAVCSKRRA
                                            TKVGDWLEMAKSLAASGKQVALSTLALVQASSEL
                                            SELKRYVDNGDFLLEASDLGVVNL
                                            CAERKLPFVAGHALNCYNAVTLRRLLKEGMVRWC
                                            MPVELSRDWLVNLLNQCDELGIRN
                                            QFEVEVLSYGHLPLAYSARCFTARSEDRPKDECE
                                            TCCIKYPNGRDVLSQENQQVFVLN
                                            GIQTMSGYVYNLGNELTSMQGLVDIVRLSPLGTE
                                            TFAMLDAFRANENGGAPLPLAAHS
                                            DCNGYWKRLAGLELQA"
gene            93500..94507                /gene="STY3459"
CDS             93500..94507                /gene="STY3459"
                                            /note="Similar to Escherichia coli
                                            hypothetical protein YhbW
                                            SW:YHBW-ECOLI (P45529) (335 aa)
                                            fasta scores: E(): 0, 94.9% id in
                                            335 aa and to the N-terminus of
                                            several monooxygenases e.g.
                                            Photobacterium leiognathi alkanal
                                            monooxygenase beta chain luxB
                                            SW:LXB2-PHOLE (P29239) (326 aa)
                                            fasta scores: E(): 4.1e-05, 26.4%
                                            id in 193 aa Orthologue of E. coli
                                            yhbW (YHBW-ECOLI); Fasta hit to
                                            YHBW-ECOLI (335 aa), 95% identity
                                            in 335 aa overlap"
                                            /codon-start=1
                                            /transl-table=11
                                            /product="possible monooxygenase"
                                            /protein-id="CAD07798.1"
                                            /db-xref="GI:16504346"
                                            /db-xref="GOA:Q8Z3I3"
                                            /db-xref="SPTREMBL:Q8Z3I3"
                                            /translation="MTDKTIPFSVLDLAPIPEGS
                                            SAKEAFTHSLDLARLAEKRGYHRY
                                            WLAEHHNMTGIASAATSVLIGYLAANTTTLHLGS
                                            GGVMLPNHSPLVIAEQFGTLNTLY
                                            PGRIDLGLGRAPGSDQPTMRALRRHMSGDIDNFP
                                            RDVAELVDWFDARDPNPHVRPVPG
                                            YGEKIPIWLLGSSLYSAQLAAQLGLPFAFASHFT
                                            PDMLFQALHLYRTQFKPSARLEKP
                                            YAMVCINIIAADSNRDAEFLFTSMQQAFVKLRRG
                                            ETGQLPPPIENMETFWSPSEQYGV
                                            QQALSMSLVGDKAKVRHGLVSILRETQADEIMVN
                                            GQIFDHQARLHSFDLAMDVKQELL G"
misc-feature    93521..93781                /gene="STY3459"
                                            /note="Pfam match to entry PF00296
                                            bac-luciferase, Bacterial
                                            luciferase, score 7.20, E-value
                                            0.1"
gene            complement(94598..95842     /gene="STY3460"
                )
CDS             complement(94598..95842     /gene="STY3460"
                )
                                            /note="Fasta hit to TNAB-ECOLI
```

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                                      overlap Fasta hit to TYRP-ECOLI
                                      (403 aa), 35% identity in 401 aa
                                      overlap Orthologue of E. coli mtr
                                      (MTR-ECOLI); Fasta hit to
                                      MTR-ECOLI (414 aa), 95% identity
                                      in 414 aa overlap"
                                      /codon-start=1
                                      /transl-table=11
                                      /product="probable amino acid
                                      permease"
                                      /protein-id="CAD07799.1"
                                      /db-xref="GI:16504347"
                                      /db-xref="GOA:Q8Z3I2"
                                      /db-xref="SPTREMBL:Q8Z3I2"
                                      /translation="MATLTTTQTSPSLLGGVVII
                                      GGTIIGAGMFSLPVVMSGAWFFWS
                                      MAALVFTWFCMLHSGLMILEANLNYRIGSSFDTI
                                      TKDLLGKGWNVVNGISIAFVLYIL
                                      TYAYISASGSILHHTFAEMSLNVPARAAGFAFAL
                                      LVAFVVWLSTKAVSRMTAIVLGAK
                                      VITFFLTFGSLLGHVQPTTLFNVAESHASYTPYL
                                      LMTLPFCLASFGYHGNVPSLMKYY
                                      GKDPRTIVKCLIYGTLLALALYSVWLLGTMGNIP
                                      RPEFIGIAQKGGNIDVLVQALSGV
                                      LNSRSLDLLLVVFSNFAVASSFLGVTLGLFDYLA
                                      DLFGFDDSAMGRFKTALLTFLPPM
                                      IGGLLYPNGFLYAIGYAGLAATIWAAIVPALLAR
                                      KSRERFGSPKFRVWGGKPMIALIL
                                      VFGVGNAVIHILSSFNLLPVYQ"
misc-feature      complement(95720..95770  /gene="STY3460"
                  )

                                      /note="PS00594 Aromatic amino
                                      acids permeases signature"
gene              complement(95996..97936  /gene="STY3461"
                  )
CDS               complement(95996..97936  /gene="STY3461"
                  )
                                      /note="Similar to Escherichia coli
                                      ATP-dependent RNA helicase
                                      cold-shock dead-box protein A
                                      SW:DEAD-ECOLI () (646 aa) fasta
                                      scores: E(): 0, 97.7% id in 646
                                      aa"
                                      /codon-start=1
                                      /transl-table=11
                                      /product="ATP-dependent RNA
                                      helicase (dead-box protein)"
                                      /protein-id="CAD07800.1"
                                      /db-xref="GI:16504348"
                                      /db-xref="GOA:Q8Z3I1"
                                      /db-xref="SPTREMBL:Q8Z3I1"
                                      /translation="MMSYVDWPPLILRHTYYMAE
                                      FETTFADLGLKAPILEALTDLGYE
                                      KPSPIQAECIPHLLGGRDVLGMAQTGSGKTAAFS
                                      LPLLNNLDPELKAPQILVLAPTRE
                                      LAVQVAEAMTDFSKHMRGVNVVALYGGQRYDVQL
                                      RALRQGPQIVVGTPGRLLDHLKRG
                                      TLDLSKLSGLVLDEADEMLRMGFIEDVETIMAQI
                                      PEGHQTALFSATMPEAIRRITRRF
                                      MKEPQEVRIQSSVTTRPDISQSYWTVWGMRKNEA
                                      LVRFLEAEDFDAAIIFVRTKNATL
                                      EVAEALERNGYNSAALNGDMNQALREQTLERLKD
                                      GRLDILIATDVAARGLDVERISLV
                                      VNYDIPMDSESYVHRIGRTGRAGRAGRALLFVEN
                                      RERRLLRNIERTMKLTIPEVELPN
                                      AELLGKRRLEKFAAKVQQQLESSDLDQYRALLAK
                                      IQPSAEGEELDLETLAAALLKMAQ
                                      GERPLILPPDAPMRPKREFRDRDDRGPRDRNDRG
                                      PRGDREERPRRERRDVGDMQLYRI
                                      EVGRDDGVEVRHIVGAIANEGDISSRYIGNIKLF
                                      ASHSTIELPKGMPGEVLQHFTRTR
                                      ILNKPMNMQLLGDAVPHAGGERRGGGRSFSGERR
                                      EGGRNFSGERREGGRGDGRRFSGE
                                      RRESRGPRRDDSTGRRRFGGDA"
misc-feature      complement(96866..97111  /gene="STY3461"
```

		/note="Pfam match to entry PF00271 helicase-C, Helicases conserved C-terminal domain, score 125.60, E-value 9.5e-34"
misc-feature	complement(97217..97831)	/gene="STY3461"
		/note="Pfam match to entry PF00270 DEAD, DEAD/DEAH box helicase, score 232.80, E-value 1.1e-72"
misc-feature	complement(97400..97426)	/gene="STY3461"
		/note="PS00039 DEAD-box subfamily ATP-dependent helicases signature"
misc-feature	complement(97715..97738)	/gene="STY3461"
		/note="PS00017 ATP/GTP-binding site motif A (P-loop)"
gene	complement(98064..98948)	/gene="STY3462"
CDS	complement(98064..98948)	/gene="STY3462"

/note="Orthologue of E. coli yhbM
(YHBM-ECOLI); Fasta hit to
YHBM-ECOLI (294 aa), 97% identity
in 294 aa overlap. Contains 3x
PFAM hits to TPR repeat domain."
/codon-start=1
/transl-table=11
/product="conserved hypothetical
protein"
/protein-id="CAD07801.1"
/db-xref="GI:16504349"
/db-xref="GOA:Q8XG77"
/db-xref="SPTREMBL:Q8XG77"
/translation="MKPFLRWCFVATALTLAGCS
NSAWRKSEVLAVPLQPTLQQEVIL
ARMEQILASRALTDDERAQLLYERGVLYDSLGLR
ALARNDFSQALAIRPDMPEVFNYL
GIYLTQAGNFDAAYEAFDSVLELDPTYNYAHLNR
GIALYYGGRDKLAQDDLLAFYQDD
PNDPYRSLWLYLVEQKLNEKQAKEALKARFEKSD
KEQWGWNIVEFYLGDISEATLMER
LKADATDNTSLAEHLSETNFYLGKYYLSLGDLDS
ATALFKLAVANNVHNFVEHRYALL
ELSLLGQDQDDLAESDQQ"

misc-feature	complement(98148..98249)	/gene="STY3462"
		/note="Pfam match to entry PF00515 TPR, TPR Domain, score 11.30, E-value 2.9"
misc-feature	complement(98562..98663)	/gene="STY3462"
		/note="Pfam match to entry PF00515 TPR, TPR Domain, score 32.70, E-value 8.3e-06"
misc-feature	complement(98664..98765)	/gene="STY3462"
		/note="Pfam match to entry PF00515 TPR, TPR Domain, score 26.00, E-value 0.00088"
gene	complement(99058..101193)	/gene="STY3463"
		/note="synonym: pnp"
CDS	complement(99058..101193)	/gene="STY3463"

/note="Orthologue of E. coli pnp
(PNP-ECOLI); Fasta hit to
PNP-ECOLI (711 aa), 97% identity
in 711 aa overlap"
/codon-start=1
/transl-table=11
/product="polynucleotide
phosphorylase"
/protein-id="CAD07802.1"
/db-xref="GI:16504350"

```
                                    /db-xref="SPTREMBL:Q8Z3I0"
                                    /translation="MLNPIVREFQYGQHTVTLET
                                    GMMARQATAAVMVSMDDTAVFVTV
                                    VGQKKAKPGQDFFPLTVNYQERTYAAGRIPGSFF
                                    RREGRPSEGETLIARLIDRPVRPL
                                    FPEGFVNEVQVIATVVSVNPQVNPDIVAMIGASA
                                    ALSLSGIPFNGPIGAARVGYINDQ
                                    YVLNPTQDELKESKLDLVVAGTEAAVLMVESEAE
                                    LLSEDTMLGAVVFGHEQQQVVIQA
                                    INDLVKEAGKPRWDWQPEAVNDALNARVAALAES
                                    RLSDAYRITDKQERYAQVDVIKSE
                                    TIEQLIAEDETLDANELGEILHAIEKNVVRSRVL
                                    AGEPRIDGREKDMIRGLDVRTGVL
                                    PRTHGSALFTRGETQALVTATLGTARDAQVLDEL
                                    MGERTDSFLFHYNFPPYSVGETGM
                                    VGSPKRREIGHGRLAKRGVLAVMPDMDKFPYTVR
                                    VVSEITESNGSSSMASVCGASLAL
                                    MDAGVPIKAAVAGIAMGLVKEGDNYVVLSDILGD
                                    EDHLGDMDFKVAGSRDGISALQMD
                                    IKIEGITKEIMQVALNQAKGARLHILGVMEQAIN
                                    APRGDISEFAPRIHTIKISTDKIK
                                    DVIGKGGSVIRALTEETGTTIEIEDDGTVKIAAT
                                    DGEKAKYAIRRIEEITAEIEVGRI
                                    YNSKVTRIVDFGAFVAIGGGKEGLVHISQIADKR
                                    VEKVTDYLQMGQEVPVKVLEVDRQ
                                    GRVRLSIKEATEQSQPAAAPEAPASEQAE"
misc-feature      complement(99124..99342  /gene="STY3463"
                  )
                                    /note="Pfam match to entry PF00575
                                    S1, S1 RNA binding domain,  score
                                    92.80, E-value 5.2e-24"
misc-feature      complement(99385..99525  /gene="STY3463"
                  )
                                    /note="Pfam match to entry PF00013
                                    KH-domain, KH domain,  score 47.50,
                                    E-value 3e-10"
misc-feature      complement(99607..10025  /gene="STY3463"
                  1)
                                    /note="Pfam match to entry PF01138
                                    RNase-PH, 3' exoribonuclease
                                    family,  score 301.50, E-value
                                    1e-86"
misc-feature      complement(100561..1011  /gene="STY3463"
                  84)
                                    /note="Pfam match to entry PF01138
                                    RNase-PH, 3' exoribonuclease
                                    family,  score 239.00, E-value
                                    6.6e-68"
gene              complement(101435..1017  /gene="STY3464"
                  04)
                                    /note="synonym: rpsO"
CDS               complement(101435..1017  /gene="STY3464"
                  04)
                                    /note="Orthologue of E. coli rpsO
                                    (RS15-ECOLI); Fasta hit to
                                    RS15-ECOLI (88 aa),  98% identity
                                    in 88 aa overlap"
                                    /codon-start=1
                                    /transl-table=11
                                    /product="30S ribosomal subunit
                                    protein S15"
                                    /protein-id="CAD07803.1"
                                    /db-xref="GI:16504351"
                                    /db-xref="GOA:Q8XFF9"
                                    /db-xref="SWISS-PROT:Q8XFF9"
                                    /translation="MSLSTEATAKIVSEFGRDAN
                                    DTGSTDVQVALLTAQINHLQGHFA
                                    EHKKDHHSRRGLLRMVSQRRKLLDYLKRKDVARY
                                    TALIERLGLRR"
misc-feature      complement(101441..1016  /gene="STY3464"
                  38)
                                    /note="Pfam match to entry PF00312
                                    Ribosomal-S15, Ribosomal protein
                                    S15,  score 133.80, E-value
                                    1.7e-36"
```

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                        90)                     /note="PS00362 Ribosomal protein
                                                S15 signature"
gene            complement(101855..1027  /gene="STY3465"
                        99)
                                                /note="synonym: truB"
CDS             complement(101855..1027  /gene="STY3465"
                        99)
                                                /note="Orthologue of E. coli truB
                                                (TRUB-ECOLI); Fasta hit to
                                                TRUB-ECOLI (314 aa), 94% identity
                                                in 314 aa overlap"
                                                /codon-start=1
                                                /transl-table=11
                                                /product="tRNA pseudouridine 55
                                                synthase (psi55 synthase) (p35
                                                protein)"
                                                /protein-id="CAD07804.1"
                                                /db-xref="GI:16504352"
                                                /db-xref="GOA:Q8Z3H9"
                                                /db-xref="SPTREMBL:Q8Z3H9"
                                                /translation="MSRPRRRGRDIHGVLLLDKP
                                                QGMSSNDVLQKVKRIYNANRAGHT
                                                GALDPLATGMLPICLGEATKFSQYLLDSDKRYRV
                                                IARLGQRTDTSDADGQIVQERPVT
                                                FSAEQLASALETFRGDIEQIPSMYSALKYQGRKL
                                                YEYARQGIEVPREARPITVYELLF
                                                IRHEGNELELEVHCSKGTYIRTIIDDLGEKLGCG
                                                AHVTYLRRLTVSKYPVDRMVTLEH
                                                LQTLVAQAEQQGVPAAQLLDPLLMPMDSPASDYP
                                                VVNLPLTSSVYFKNGNPVRTTGAP
                                                LKGLVRVTEGEDDKFIGMGEIDDEGRVAPRRLVV
                                                EYPA"
misc-feature    complement(102260..1027  /gene="STY3465"
                        12)
                                                /note="Pfam match to entry PF01509
                                                TruB-N, TruB family
                                                pseudouridylate synthase (N
                                                terminal domain), score 326.70,
                                                E-value 2.7e-94"
gene            complement(102799..1032  /gene="STY3466"
                        00)
                                                /note="synonym: rbfA"
CDS             complement(102799..1032  /gene="STY3466"
                        00)
                                                /note="Orthologue of E. coli rbfA
                                                (RBFA-ECOLI); Fasta hit to
                                                RBFA-ECOLI (132 aa), 96% identity
                                                in 132 aa overlap"
                                                /codon-start=1
                                                /transl-table=11
                                                /product="ribosome-binding factor
                                                A (P15B protein)"
                                                /protein-id="CAD07805.1"
                                                /db-xref="GI:16504353"
                                                /db-xref="GOA:Q8Z3H8"
                                                /db-xref="SWISS-PROT:Q8Z3H8"
                                                /translation="MAKEFGRPQRVAQEMQKEIA
                                                LILQREIKDPRVGMMTTVSGVEMS
                                                RDLAYAKVFVTFLNDQDEAAVKNGIKALQEASGF
                                                IRSLLGKAMRLRIVPELTFFYDNS
                                                LVEGMRMSNLVTNVVKHDEERRVNPDDSKED"
misc-feature    complement(102862..1031  /gene="STY3466"
                        82)
                                                /note="Pfam match to entry PF02033
                                                RBFA, Ribosome-binding factor A,
                                                score 222.50, E-value 6.4e-63"
misc-feature    complement(102901..1029  /gene="STY3466"
                        66)
                                                /note="PS01319 Ribosome-binding
                                                factor A signature"
gene            complement(103421..1060  /gene="STY3467"
                        99)
                                                /note="synonym: infB"
CDS             complement(103421..1060  /gene="STY3467"
```

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                                        /note="Orthologue of E. coli infB
                                        (IF2-ECOLI); Fasta hit to
                                        IF2-ECOLI (890 aa), 96% identity
                                        in 892 aa overlap"
                                        /codon-start=1
                                        /transl-table=11
                                        /product="protein chain initiation
                                        factor 2"
                                        /protein-id="CAD07806.1"
                                        /db-xref="GI:16504354"
                                        /db-xref="GOA:Q8Z3H7"
                                        /db-xref="SWISS-PROT:Q8Z3H7"
                                        /translation="MTDLTLKALAAERQVSVDRL
                                        VQQFADAGIRKSADDSVSAQEKQT
                                        LLAHLNREAVSGPDKLTLQRKTRSTLNIPGTGGK
                                        SKSVQIEVRKKRTFVKRDPQEAER
                                        LAAEEQAQREAEEQARREAEEQAKREAQQKAERE
                                        AAEQAKREAAEKAKREAAEKDKVS
                                        NQQTDDMTKTAQAEKARRENEAAELKRKAEEEAR
                                        RKLEEEARRVAEEARRMAEENKWT
                                        ATPEPVEDTSDYHVTTSQHARQAEDENDREVEGG
                                        RGRGRNAKAARPAKKGKHAESKAD
                                        REEARAAVRGGKGGKRKGSSLQQGFQKPAQAVNR
                                        DVVIGETITVGELANKMAVKGSQV
                                        IKAMMKLGAMATINQVIDQETAQLVAEEMGHKVI
                                        LRRENELEEAVMSDRDTGAAAEPR
                                        APVVTIMGHVDHGKTSLLDYIRSTKVASGEAGGI
                                        TQHIGAYHVETDNGMITFLDTPGH
                                        AAFTSMRARGAQATDIVVLVVAADDGVMPQTIEA
                                        IQHAKAAGVPVVVAVNKIDKPEAD
                                        PDRVKNELSQYGILPEEWGGESQFVHVSAKAGTG
                                        IDELLDAILLQAEVLELKAVRKGM
                                        ASGAVIESFLDKGRGPVATVLVREGTLHKGDIVL
                                        CGFEYGRVRAMRNELGQEVLEAGP
                                        SIPVEILGLSGVPAAGDEVTVVRDEKKAREVALY
                                        RQGKFREVKLARQQKSKLENMFVN
                                        MTEGEVHEVNIVLKADVQGSVEAISDSLLKLSTD
                                        EVKVKIIGSGVGGITETDATLAAA
                                        SNAILVGFNVRADASARKVIESESLDLRYYSVIY
                                        NLIDEVKAAMSGMLSPELKQQIIG
                                        LAEVRDVFKSPKFGAIAGCMVTEGTIKRHNPIRV
                                        LRDNVVIYEGELESLRRFKDDVNE
                                        VRNGMECGIGVKNYNDVRVGDMIEVFEIIEIQRT
                                        IA"
misc-feature     complement(103451..1038 /gene="STY3467"
                 52)
                                        /note="Pfam match to entry PF02131
                                        IF2, Initiation factor 2, score
                                        311.60, E-value 9e-90"
misc-feature     complement(103508..1035 /gene="STY3467"
                 76)
                                        /note="PS01176 Initiation factor 2
                                        signature"
misc-feature     complement(103898..1049 /gene="STY3467"
                 29)
                                        /note="Pfam match to entry PF00009
                                        GTP-EFTU, Elongation factor Tu
                                        family, score 262.10, E-value
                                        5.5e-77"
misc-feature     complement(104879..1049 /gene="STY3467"
                 02)
                                        /note="PS00017 ATP/GTP-binding
                                        site motif A (P-loop)"
gene             complement(106124..1076 /gene="STY3468"
                 26)
                                        /note="synonym: nusA"
CDS              complement(106124..1076 /gene="STY3468"
                 26)
                                        /note="Orthologue of E. coli nusA
                                        (NUSA-ECOLI); Fasta hit to
                                        NUSA-ECOLI (495 aa), 94% identity
                                        in 500 aa overlap"
                                        /codon-start=1
                                        /transl-table=11
                                        /product="L factor"
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                                        /db-xref="GI:16504355"
                                        /db-xref="GOA:Q8Z3H6"
                                        /db-xref="SPTREMBL:Q8Z3H6"
                                        /translation="MNKEILAVVEAVSNEKALPR
                                        EKIFEALESALATATKKKYEQEID
                                        VRVEIDRKSGDFDTFRRWLIVEEVTMPTKEITLE
                                        AARFEDESLNVGDYVEDQIESVTF
                                        DRITTQTAKQVIVQKVREAERAMVVDQFRDQEGE
                                        IVTGVVKKVNRDNISLEIKSEGMA
                                        GNAEAVILREDMLPRENFRPGDRIRGVLYAVRPE
                                        ARGAQLFVTRSKPEMLIELFRIEV
                                        PEIGEEVIEIKAAARDPGSRAKIAVKTNDKRIDP
                                        VGACVGMRGARVQAVSTELGGERI
                                        DIVLWDDNPAQFVINAMAPADVASIVVDEDKHTM
                                        DIAVEAGNLAQAIGRNGQNVHLAS
                                        QLSGWELNVMTVDDLQAKHQAEAHAAIEIFTKYL
                                        DIDEEFATVLVEEGFSTLEELAYV
                                        PMKELLEIDGLDEPTVEALRERAKNALATLAQDQ
                                        EASLGDNKPADDLLNLEGLDRDMA
                                        FKLAARGVCTLEDLADQGIDDLADIEGLTDEKAG
                                        ELIMAARNICWFGDEA"
misc-feature    complement(107018..1072   /gene="STY3468"
                36)
                                          /note="Pfam match to entry PF00575
                                          S1, S1 RNA binding domain, score
                                          32.60, E-value 2.2e-07"
gene            complement(107654..1080   /gene="STY3469"
                76)
CDS             complement(107654..1080   /gene="STY3469"
                76)
                                          /note="Orthologue of E. coli yhbC
                                          (YHBC-ECOLI); Fasta hit to
                                          YHBC-ECOLI (140 aa), 95% identity
                                          in 140 aa overlap"
                                          /codon-start=1
                                          /transl-table=11
                                          /product="conserved hypothetical
                                          protein"
                                          /protein-id="CAD07808.1"
                                          /db-xref="GI:16504356"
                                          /db-xref="SPTREMBL:Q8XFC7"
                                          /translation="MITAPVEALGYELVGIEFIR
                                          GRTSTLRIYIDSEDGINVDDCADV
                                          SHQVSAVLDVEDPISVAYNLEVSSPGLDRPMFTA
                                          DHYARFQGEEVALVLRMAVQNRRK
                                          WQGIIKAVDGEMITVTVEGKDEVFALSNIQKANL
                                          VPHF"
tRNA            complement(108314..1083   /product="tRNA-Met"
                90)
                                          /note="tRNA Met anticodon CAT,
                                          Cove score 86.07"
gene            108668..110077            /gene="STY3470"
                                          /note="synonym: argG"
CDS             108668..110077            /gene="STY3470"
                                          /note="Orthologue of E. coli argG
                                          (ASSY-ECOLI); Fasta hit to
                                          ASSY-ECOLI (446 aa), 96% identity
                                          in 446 aa overlap"
                                          /codon-start=1
                                          /transl-table=11
                                          /product="argininosuccinate
                                          synthetase"
                                          /protein-id="CAD07809.1"
                                          /db-xref="GI:16504357"
                                          /db-xref="GOA:Q8Z3H5"
                                          /db-xref="SWISS-PROT:Q8Z3H5"
                                          /translation="MHKNALKQKPISLSVNQAGF
                                          YSMTTILKHLPAGQRIGIAFSGGL
                                          DTSAALLWMRQKGAVPYAYTANLGQPDEDDYDAI
                                          PRRAMEYGAENARLIDCRKQLVAE
                                          GIAAIQCGAFHNTTGGLTYFNTTPLGRAVTGTML
                                          VAAMKEDGVNIWGDGSTYKGNDIE
                                          RFYRYGLLTNAELQIYKPWLDTDFIDELGGRHEM
                                          SEFMIACGFDYKMSVEKAYSTDSN
                                          MLGATHEAKDLEFLNSSVKIVNPIMGVKFWDESV
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                                        GTSMAAESRRNGLSSSTLANALTR
                                        PWPKGELIIAKALGTEPWVIWPSRYHDPRTHEFI
                                        DRTRLMRARNKDKQNVE"
gene               complement(123421..1246 /gene="STY3486"
                   80)
                                        /note="synonym: murA"
CDS                complement(123421..1246 /gene="STY3486"
                   80)
                                        /note="Orthologue of E. coli murA
                                        (MURA-ECOLI); Fasta hit to
                                        MURA-ECOLI (419 aa), 97% identity
                                        in 419 aa overlap"
                                        /codon-start=1
                                        /transl-table=11
                                        /product="UDP-N-acetylglucosamine
                                        1-carboxyvinyltransferase"
                                        /protein-id="CAD07824.1"
                                        /db-xref="GI:16504372"
                                        /db-xref="GOA:Q8XF63"
                                        /db-xref="SWISS-PROT:Q8XF63"
                                        /translation="MDKFRVQGPTTLQGEVTISG
                                        AKNAALPILFAALLAEEPVEIQNV
                                        PKLKDVDTSMKLLSQLGAKVERNGSVHIDASQVN
                                        VFCAPYDLVKTMRASIWALGPLVA
                                        RFGQGQVSLPGGCTIGARPVDLHITGLEQLGATI
                                        KLEEGYVKASVEGRLKGAHIVMDK
                                        VSVGATVTIMCAATLAEGTTIIENAAREPEIVDT
                                        ANFLVTLGAKIAGQGTDRITIEGV
                                        ERLGGGVYRVLPDRIETGTFLVAAAISRGKILCR
                                        NAQPDTLDAVLAKLRDAGADIEVG
                                        EDWISLDMHGKRPKAVNVRTAPHPAFPTDMQAQF
                                        TLLNLVAEGTGFITETVFENRFMH
                                        VPELSRMGARAEIESNTVICHGVETLSGAQVMAT
                                        DLRASASLVLAGCIAEGTTIVDRI
                                        YHIDRGYERIEDKLRALGANIERVKGE"
misc-feature       complement(123463..1246 /gene="STY3486"
                   65)
                                        /note="Pfam match to entry PF00275
                                        EPSP-syntase, EPSP synthase
                                        (3-phosphoshikimate
                                        1-carboxyvinyltransferase), score
                                        617.60, E-value 7.1e-182"
gene               complement(124734..1250 /gene="STY3487"
                   27)
CDS                complement(124734..1250 /gene="STY3487"
                   27)
                                        /note="Similar to Escherichia coli
                                        protein YrbA SW:YRBA-ECOLI
                                        (P43781; P76672) (84 aa) fasta
                                        scores: E(): 0, 97.6% id in 84 aa.
                                        Weakly similar to several
                                        BolA-like proteins involved in the
                                        general stress response e.g.and to
                                        Pseudomonas fluorescens BolA
                                        protein TR:Q9XAV4 (EMBL:AJ243174)
                                        (99 aa) fasta scores: E():
                                        1.3e-07, 37.5% id in 72 aa. Note
                                        codon 14 offers an alternative
                                        translational start site."
                                        /codon-start=1
                                        /transl-table=11
                                        /product="conserved hypothetical
                                        protein"
                                        /protein-id="CAD07825.1"
                                        /db-xref="GI:16504373"
                                        /db-xref="GOA:Q8XFL8"
                                        /db-xref="SPTREMBL:Q8XFL8"
                                        /translation="MLGCFHYLTNKEPMENHEIQ
                                        SVLMNALSLQEVHVSGDGSHFQVI
                                        AVGEMFDGMSRVKKQQTVYGPLMEYIADNRIHAV
                                        SIKAYTPAEWARDRKLNGF"
misc-feature       complement(124764..1249 /gene="STY3487"
                   88)
                                        /note="Pfam match to entry PF01722
                                        BolA, BolA-like protein, score
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gene	complement(125176..1254 72)	/gene="STY3488"
CDS	complement(125176..1254 72)	/gene="STY3488"
		/note="Similar to the C-terminus of Escherichia coli hypothetical 14.4 kDa protein in YrbB SW:YRBB-ECOLI (P45389) (129 aa) fasta scores: E(): 1.3e-25, 69.1% id in 97 aa. Also similar to several anti-sigma factor antagonists e.g. Listeria monocytogenes anti-sigma B factor antagonist RsbV SW:RSBV-LISMO (O85016) (114 aa) fasta scores: E(): 0.38, 25.6% id in 90 aa" /codon-start=1 /transl-table=11 /product="possible anti-sigma factor antagonist" /protein-id="CAD07826.1" /db-xref="GI:16504374" /db-xref="SPTREMBL:Q8XGD1" /translation="MTPQLTWTREADTLVLAGEL DQDVLAPLWDARVEAMNGVTRIDL SQISRVDTGGLALLAHLVNQAKKQGNAVSLSGVN DKVYALAQLYNLPEDVLPRM"
misc-feature	complement(125179..1254 63)	/gene="STY3488"
		/note="Pfam match to entry PF01740 STAS, STAS domain, score 29.50, E-value 7.6e-05"
gene	complement(125472..1261 07)	/gene="STY3489"
CDS	complement(125472..1261 07)	/gene="STY3489"
		/note="Orthologue of E. coli yrbC (YRBC-ECOLI); Fasta hit to YRBC-ECOLI (211 aa), 94% identity in 211 aa overlap. Contains a possible N-terminal signal sequence" /codon-start=1 /transl-table=11 /product="possible exported protein" /protein-id="CAD07827.1" /db-xref="GI:16504375" /db-xref="SPTREMBL:Q8XF31" /translation="MFKRLMMVALLVIAPLSAAT AADQSNPYKLMNEAAQKTFDRLKN EQPKIRANPDYLRDVVDQELLPYVQVKYAGALVL GRYYKEATPAQREAYFAAFREYLK QAYGQALAMYHGQTYQIAPEQPLGDATIVPIRVT IIDPNGRPPVRLDFQWRKNTQTGN WQAYDMIAEGVSMITTKQNEWSDLLRTKGIDGLT AQLKSISQQKITLDEKQ"
gene	complement(126126..1266 77)	/gene="STY3490"
CDS	complement(126126..1266 77)	/gene="STY3490"
		/note="Orthologue of E. coli YRBD-ECOLI; Fasta hit to YRBD-ECOLI (183 aa), 87% identity in 183 aa overlap. Contains a possible N-terminal signal sequence" /codon-start=1 /transl-table=11 /product="possible exported protein" /protein-id="CAD07828.1" /db-xref="GI:16504376" /db-xref="SPTREMBL:Q8XG30" /translation="MQTKKNEIWVGVFLLVALLA

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                                           TFDNIGGLKVRSPVRIGGVVVGRVEDISLDPKTY
                                           LPRVTLDIEERYNHIPDTSSLSIR
                                           TSGLLGEQYLALNVGFEDPELGTSILKDGSTIQD
                                           TKSAMVLEDMIGQFLYNSKGDDNK
                                           NSGDAPAATEGHTEATTPAGETK"
gene                complement(126682..1274  /gene="STY3491"
                    64)
CDS                 complement(126682..1274  /gene="STY3491"
                    64)
                                           /note="Orthologue of E. coli yrbE
                                           (YRBE-ECOLI); Fasta hit to
                                           YRBE-ECOLI (260 aa), 96% identity
                                           in 260 aa overlap. Contains
                                           possible membrane spanning
                                           hydrophobic domains."
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                                           protein"
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                                           VRQLYNVGVLSMLIIIVSGVFIGMVLGLQGYLVL
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                                           VAALLFAGRAGSALTAEIGLMRATEQLSSMEMMA
                                           VDPLRRVISPRFWAGVISLPLLTI
                                           IFVAVGIWGGSLVGVSWKGIDAGFFWSAMQNAVD
                                           WRMDLVNCLIKSVVFAITVTWIAL
                                           FNGYDAIPTSAGISRATTRTVVHASLAVLGLDFV
                                           LTALMFGN"
gene                complement(127472..1282  /gene="STY3492"
                    84)
CDS                 complement(127472..1282  /gene="STY3492"
                    84)
                                           /note="Fasta hit to ARTP-ECOLI
                                           (242 aa), 30% identity in 234 aa
                                           overlap Fasta hit to YHBG-ECOLI
                                           (240 aa), 33% identity in 228 aa
                                           overlap Fasta hit to GLTL-ECOLI
                                           (241 aa), 30% identity in 242 aa
                                           overlap Fasta hit to TAUB-ECOLI
                                           (255 aa), 31% identity in 228 aa
                                           overlap Fasta hit to YECC-ECOLI
                                           (250 aa), 34% identity in 229 aa
                                           overlap Fasta hit to GLNQ-ECOLI
                                           (240 aa), 32% identity in 245 aa
                                           overlap Fasta hit to PSTB-ECOLI
                                           (257 aa), 31% identity in 256 aa
                                           overlap Orthologue of E. coli
                                           YRBF-ECOLI; Fasta hit to
                                           YRBF-ECOLI (269 aa), 95% identity
                                           in 266 aa overlap"
                                           /codon-start=1
                                           /transl-table=11
                                           /product="possible ABC-transport
                                           protein, ATP-binding component"
                                           /protein-id="CAD07830.1"
                                           /db-xref="GI:16504378"
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                                           FDNVAYPLREHTNLPAPLLKSVVMMKLEAVGLRG
                                           AAKLMPSELSGGMARRAALARAIA
                                           LEPDLIMFDEPFVGQDPITMGVLVKLISELNSAL
                                           GVTCVVVSHDVPEVLSIADHAWIM
                                           ADKKIVAHGSAQALQENTDPRVRQFLDGIADGPV
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misc-feature        complement(127622..1281  /gene="STY3492"
                    85)
                                           /note="Pfam match to entry PF00005
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		/note="PS00211 ABC transporters family signature"
misc-feature	complement(128141..1281 64)	/gene="STY3492"
		/note="PS00017 ATP/GTP-binding site motif A (P-loop)"
gene	128497..129474	/gene="STY3493"
CDS	128497..129474	/gene="STY3493"
		/note="Similar to Escherichia coli hypothetical protein YrbG SW:YRBG-ECOLI (P45394) (325 aa) fasta scores: E(): 0, 87.3% id in 324 aa. Also similar in parts to Eukaryotic sodium/calcium exchange proteins e.g. Drosophila melanogaster potassium-dependent sodium/calcium exchanger TR:Q9U6A0 (EMBL:AF190455) (856 aa) fasta scores: E(): 9.2e-07, 30.1% id in 153 aa. Contains multiple possible membrane spanning hydrophobic domains Orthologue of E. coli yrbG (YRBG-ECOLI); Fasta hit to YRBG-ECOLI (325 aa), 87% identity in 324 aa overlap"
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		/transl-table=11
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		/db-xref="GI:16504379"
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		/db-xref="SPTREMBL:Q8Z3G7"
		/translation="MLLAMALLIIGLLLVAYGAD RLVFAASILCRTFGIPPLIIGMTV VSIGTSLPEIIVSVAASLHGQLDLAVGAALGSNI TNILLILGLAALVRPFTVHSDVLR RELPLMLFVSVVAGSVLHDGQLSRSDGIFLLLLA VLWLLFIVKIARLAERQGNDSLTR EQLAELPREDGLPVAFLWLGIALVIMPMATRMVI DNATVLANYFAMSELTLGLTVIAV GTSLPELATAIAGVRKGENDIAVGNLIGANIFNL AIVLGLPALIAPGEINPLAFGRDY SVMLLVSVVFALLCWRHPRQIGRGAGILLTGGFI VWLAMLYWLSPLLVG"
misc-feature	128533..128949	/gene="STY3493"
		/note="Pfam match to entry PF01699 Na-Ca-Ex, Sodium/calcium exchanger protein, score 171.70, E-value 1.2e-47"
misc-feature	129046..129468	/gene="STY3493"
		/note="Pfam match to entry PF01699 Na-Ca-Ex, Sodium/calcium exchanger protein, score 163.10, E-value 4.9e-45"
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CDS	129488..130474	/gene="STY3494"
		/note="Fasta hit to GUTQ-ECOLI (308 aa), 46% identity in 308 aa overlap Orthologue of E. coli yrbH (YRBH-ECOLI); Fasta hit to YRBH-ECOLI (328 aa), 92% identity in 328 aa overlap"
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		/db-xref="SPTREMBL:Q8Z3G6"
		/translation="MSHLALQPGFDFQQAGKEVL

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                                          MARAADVHLCVKVPKEACPLGLAP
                                          TSSTTATLVMGDALAVALLKARGFTAEDFALSHP
                                          GGALGRKLLLRVSDIMHTGDEIPH
                                          VNKHATLRDALLEITRKNLGMTVICDESMKIDGI
                                          FTDGDLRRMFDMGGDMRQLGIAEV
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                                          DQLLGVLHMHDLLRAGVV"
misc-feature      129614..130018          /gene="STY3494"
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                                          E-value 7.1e-43"
misc-feature      130115..130276          /gene="STY3494"
                                          /note="Pfam match to entry PF00571
                                          CBS, CBS domain, score 38.80,
                                          E-value 1.2e-07"
misc-feature      130310..130468          /gene="STY3494"
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                                          E-value 1.9e-07"
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CDS               130495..131061          /gene="STY3495"
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                                          in 188 aa overlap"
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                                          /transl-table=11
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                                          LIAFSDLLEKLAIAPENVAYVGDDLIDWPVMEKV
                                          GLSVAVADAHPLLIPRADYVTHIA
                                          GGRGAVREVCDLLLLAQGKLDEAKGQSI"
gene              131058..131633          /gene="STY3496"
CDS               131058..131633          /gene="STY3496"
                                          /note="Orthologue of E. coli yrbK
                                          (YRBK-ECOLI); Fasta hit to
                                          YRBK-ECOLI (191 aa), 91% identity
                                          in 191 aa overlap. Contains a
                                          possible N-terminal signal
                                          sequence"
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                                          protein"
                                          /protein-id="CAD07834.1"
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                                          EHTDTVVYSPEGALSYRLIAQHVEYFSDQAVSWF
                                          TQPVLTTFDKDKVPTWSIKADKAK
                                          LTNDRMLYLYGHVEVNALVPDAQLRRITTDNAQI
                                          NLVTQDVTSNDLVTLYGTTFNSSG
                                          LKMRGNLRSKNAELIEKVRTSYEIQNKQTQP"
gene              131638..132156          /gene="STY3497"
CDS               131638..132156          /gene="STY3497"
                                          /note="Orthologue of E. coli yhbN
                                          (YHBN-ECOLI); Fasta hit to
                                          YHBN-ECOLI (185 aa), 92% identity
                                          in 185 aa overlap. Due to the
                                          overlap, lacks the very N-terminal
                                          12 aa of the E. coli orthologue."
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                                          ELAKDFVVLTGNAYLEQLDSNITGDKITYLVKEQ
                                          KMQAFSEKGKRVTTVLVPSQLQDK
                                          NKGQTPAQKKSN"
gene         132163..132888               /gene="STY3498"
CDS          132163..132888               /gene="STY3498"
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                                          overlap Fasta hit to YCFV-ECOLI
                                          (233 aa), 30% identity in 203 aa
                                          overlap Fasta hit to ZNUC-ECOLI
                                          (251 aa), 33% identity in 233 aa
                                          overlap Fasta hit to LIVF-ECOLI
                                          (237 aa), 35% identity in 229 aa
                                          overlap Fasta hit to FECE-ECOLI
                                          (255 aa), 31% identity in 237 aa
                                          overlap Fasta hit to TAUB-ECOLI
                                          (255 aa), 32% identity in 238 aa
                                          overlap Fasta hit to LIVG-ECOLI
                                          (255 aa), 32% identity in 249 aa
                                          overlap Fasta hit to FTSE-ECOLI
                                          (222 aa), 30% identity in 216 aa
                                          overlap Fasta hit to BTUD-ECOLI
                                          (249 aa), 31% identity in 231 aa
                                          overlap Fasta hit to PHNC-ECOLI
                                          (262 aa), 31% identity in 249 aa
                                          overlap Fasta hit to YECC-ECOLI
                                          (250 aa), 31% identity in 239 aa
                                          overlap Fasta hit to P76909 (246
                                          aa), 33% identity in 204 aa
                                          overlap Fasta hit to YRBF-ECOLI
                                          (269 aa), 34% identity in 228 aa
                                          overlap Fasta hit to YABJ-ECOLI
                                          (232 aa), 30% identity in 215 aa
                                          overlap Fasta hit to YHDZ-ECOLI
                                          (252 aa), 31% identity in 237 aa
                                          overlap Orthologue of E. coli yhbG
                                          (YHBG-ECOLI); Fasta hit to
                                          YHBG-ECOLI (240 aa), 97% identity
                                          in 240 aa overlap"
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                                          GIGYLPQEASIFRRLSVFDNLMAV
                                          LQIRDDLTAEQREDRANELMEEFHIEHLRDSMGQ
                                          ALSGGERRRVEIARALAANPKFIL
                                          LDEPFAGVDPISVIDIKRIIEHLRDSGLGVLITD
                                          HNVRETLAVCERAYIVSQGHLIAH
                                          GTPTEILQDEHVKRVYLGEDFRL"
misc-feature 132247..132801               /gene="STY3498"
                                          /note="Pfam match to entry PF00005
                                          ABC-tran, ABC transporter, score
                                          219.90, E-value 3.7e-62"
misc-feature 132268..132291               /gene="STY3498"
                                          /note="PS00017 ATP/GTP-binding
                                          site motif A (P-loop)"
misc-feature 132574..132618               /gene="STY3498"
                                          /note="PS00211 ABC transporters
                                          family signature"
gene         132936..134369               /gene="STY3499"
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CDS	132936..134369	/gene="STY3499" /note="Orthologue of E. coli rpoN (RP54-ECOLI); Fasta hit to RP54-ECOLI (477 aa), 94% identity in 477 aa overlap" /codon-start=1 /transl-table=11 /product="RNA polymerase sigma-54 factor (sigma-N)" /protein-id="CAD07837.1" /db-xref="GI:16504385" /db-xref="GOA:Q8Z3G3" /db-xref="SPTREMBL:Q8Z3G3" /translation="MKQGLQLRLSQQLAMTPQLQ QAIRLLQLSTLELQQELQQALENN PLLEQTDLHDEIDTQQPQDDDPLDTADALEQKEM PEELPLDASWDEIYTAGTPSGPSG DYIDDELPVYQGETTQSLQDYLMWQVELTPFSDT DRAIATSIVDAVDDTGYLTVSLDE IRESMGDVEVDLDEVEAVLKRIQRFDPVGVAAKD LRDCLLIQLSQFDKSTPWLEEARL IICDHLDLLANHDFRTLMRVTRLKEEVLKEAVNL IQSLDPRPGQSIQTGEPEYVIPDV LVRKHNGRWTVELNSDSIPRLQINQHYAAMCNSA RNDADSQFIRSNLQDAKWLIKSLE SRNDTLLRVSRCIVEQQQAFFEQGEEYMKPMVLA DIAQAVEMHESTISRVTTQKYLHS PRGIFELKYFFSSHVNTEGGGEASSTAIRALVKK LIAAENPAKPLSDSKLTSLLSEQG IMVARRTVAKYRESLSIPPSNQRKQLV"
misc-feature	132936..134360	/gene="STY3499" /note="Pfam match to entry PF00309 Sigma54-factors, Sigma-54 factors family, score 938.70, E-value 1.5e-278"
misc-feature	134025..134084	/gene="STY3499" /note="PS00717 Sigma-54 factors family signature 1"
misc-feature	134298..134321	/gene="STY3499" /note="PS00718 Sigma-54 factors family signature 2"
gene	134392..134679	/gene="STY3500"
CDS	134392..134679	/gene="STY3500" /note="Orthologue of E. coli yhbH (RP5M-ECOLI); Fasta hit to RP5M-ECOLI (95 aa), 95% identity in 95 aa overlap" /codon-start=1 /transl-table=11 /product="probable sigma(54) modulation protein" /protein-id="CAD07838.1" /db-xref="GI:16504386" /db-xref="SPTREMBL:Q8Z3G2" /translation="MQLNITGHNVEITEALREFV TTKFAKLEQYFERINQVYVVLKVE KVTHISDATLHVNGGEIHASAEGQDMYAAIDGLI DKLARQLTKHKDKLKQY"
gene	134797..135288	/gene="ptsN" /note="synonym: STY3501"
CDS	134797..135288	/gene="ptsN" /EC-number="2.7.1.69" /note="Similar to Escherichia coli nitrogen regulatory IIA protein PtsN or RpoP SW:PTSN-ECOLI (P31222) (163 aa) fasta scores: E(): 0, 95.1% id in 163 aa" /codon-start=1 /transl-table=11 /product="nitrogen regulatory IIA protein" /protein-id="CAD07839.1" /db-xref="GI:16504387" /db-xref="GOA:Q8XEZ0" /db-xref="SPTREMBL:Q8XEZ0"

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                                     phosphoenolpyruvate-dependent
                                     sugar phosphotransferase system,
                                     EIIA 2, score 97.50, E-value
                                     5e-26"
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     CDS            135334..136188   /gene="STY3502"
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                                     YHBJ-ECOLI; Fasta hit to
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                                     TMVFESFGFKHGIPIDADYVFDVRFLPNPHWDPK
                                     LRPMTGLDKPVAAFLDRHTEVHNF
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     CDS            136185..136457   /gene="STY3503"
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                                     Orthologue of E. coli ptsO
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                                     in 90 aa overlap"
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                                     VIALFNSGFDED"
     misc-feature   136188..136421   /gene="STY3503"
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                                     PTS-HPr, PTS HPr component
                                     phosphorylation sites, score
                                     138.00, E-value 1.7e-37"
     misc-feature   136224..136247   /gene="STY3503"
                                     /note="PS00369 PTS HPR component
                                     histidine phosphorylation site
                                     signature"
     misc-feature   136305..136352   /gene="STY3503"
                                     /note="PS00589 PTS HPR component
                                     serine phosphorylation site
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gene	136702..137334	/gene="STY3504"
CDS	136702..137334	/gene="STY3504" /note="Orthologue of E. coli YRBL-ECOLI; Fasta hit to YRBL-ECOLI (210 aa), 77% identity in 210 aa overlap" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAD07842.1" /db-xref="GI:16504390" /db-xref="SPTREMBL:Q8XFU2" /translation="MILLSKQTPLGAGRHRKCYT HPDNARRCIKVIYNRDHGGDKEIR RELSYYAHLSRYLTDWSAIPRYYGTVETDCGTGY VYDMITDFNGAPSITLTEFAAQCR YEEDVAVLRRLLKKLKRYLLDNHIVTMSLKPQNI LCQRISESEVVPVVCDNLGESTFI PLATWSTWCCERKLERVWQRFIAQPALAVALERD AQPKDKKRLALTSHEA"
gene	complement(137409..13813 7)	/gene="mtgA" /note="synonym: STY3505"
CDS	complement(137409..13813 7)	/gene="mtgA" /EC-number="2.4.2.-" /note="Similar to Escherichia coli monofunctional biosynthetic peptidoglycan transglycosylase mtgA SW:MTGA-ECOLI (P46022) (242 aa) fasta scores: E(): 0, 83.9% id in 242 aa" /codon-start=1 /transl-table=11 /product="monofunctional biosynthetic peptidoglycan transglycosylase" /protein-id="CAD07843.1" /db-xref="GI:16504391" /db-xref="GOA:Q8Z3G0" /db-xref="SPTREMBL:Q8Z3G0" /translation="MSKRRIAPLTFLRRLLLRIL AALAVFWGGGIALFSVVPVPFSAV MAERQISAWLGGEFGYVAHSDWVSMADISPWMGL AVIAAEDQKFPEHWGFDVPAIEKA LAHNERNESRIRGASTLSQQTAKNLFLWDGRSWV RKGLEAGLTLGIETVWSKKRILTV YLNIAEFGDGIFGVEAAAQRYFHKPASRLSVSEA ALLAAVLPNPLRYKANAPSGYVRS RQAWIMRQMRQLGGESFMTRNQLN"
misc-feature	complement(137499..13800 05)	/gene="mtgA" /note="Pfam match to entry PF00912 Transglycosyl, Transglycosylase, score 300.60, E-value 1.9e-86"
gene	complement(138134..13878 7)	/gene="STY3506"
CDS	complement(138134..13878 7)	/gene="STY3506" /note="Similar to Escherichia coli sigma cross-reacting protein 27A to which antibodies against region 2.2 peptide of RNA polymerase sigma subunit bind, YhbL SW:S27A-ECOLI (P26428; P76673) (217 aa) fasta scores: E(): 0, 88.9% id in 217 aa. Also significantly similar to the C-terminus of Homo sapiens ES1 proteins: SW:ES1-HUMAN () (268 aa) fasta scores: E(): 4.8e-32, 45.3%

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                                              /db-xref="SPTREMBL:Q8Z3F9"
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                                              NFASKGSECRVDSDVVALAKAMHQSGKPLGFICI
                                              APAMLPKIFDFPLRLTIGTDIDTA
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                                              AQDIAQAASGIDKLVSRVLVLAE"
gene                    complement(139014..1413  /gene="STY3507"
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CDS                     complement(139014..1413  /gene="STY3507"
                        50)
                                              /note="Orthologue of E. coli arcB
                                              (ARCB-ECOLI); Fasta hit to
                                              ARCB-ECOLI (776 aa), 94% identity
                                              in 778 aa overlap"
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                                              /transl-table=11
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                                              control sensor protein"
                                              /protein-id="CAD07845.1"
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                                              KLNVQLKDNIAQLNQEIADREKAEAELQETFEQL
                                              KVEIKEREEAQIQLEQQSSFLRSF
                                              LDASPDLVFYRNEDKEFSGCNRAMELLTGKSEKQ
                                              LVHLKPEDVYSPEAAEKVIETDEK
                                              VFRHNVSLTYEQWLDYPDGRKACFEIRKVPYYDR
                                              VGKRHGLMGFGRDITERKRYQDAL
                                              ERASRDKTTFISTISHELRTPLNGIVGLSRILLD
                                              TDLTAEQEKYLKTIHVSAVTLGNI
                                              FNDIIDMDKMERRKVQLDNQPVDFTSFMADLENL
                                              SGLQAQQKGLRFVLEPTLPLPHKV
                                              ITDGTRLRQILWNLISNAVKFTQQGQVTVRARYD
                                              EGDMLHFEVEDSGIGIPQDEQDKI
                                              FAMYYQVKDSHGGKPATGTGIGLAVSRRLAKNMG
                                              GDITVSSLPGKGSTFTLTVHAPAV
                                              AEEVEDAFDEDDMPLPALHVLLVEDIELNVIVAR
                                              SVLEKLGNSVDVAMTGKAALEMFA
                                              PGEYDLVLLDIQLPDMTGLDIARELTRRHTREDL
                                              PPLVALTANVLKDKKEYLDAGMDD
                                              VLSKPLSVPALTAMIKKFWDATDKEESTVTPEES
                                              DKAQALLDIPMLEQYIELVGPKLI
                                              TDGLAVFEKMMLGYLSVLESNLTARDKKGVVEEG
                                              HKIKGAAGSVGLRHLQQLGQQIQS
                                              PDLPAWEDNVVEWIEEMKQEWQHDVAVLKAWVAN
                                              AEKK"
misc-feature            complement(139434..1397  /gene="STY3507"
                        75)
                                              /note="Pfam match to entry PF00072
                                              response-reg, Response regulator
                                              receiver domain, score 118.80,
                                              E-value 1.1e-31"
misc-feature            complement(139839..1404  /gene="STY3507"
                        77)
                                              /note="Pfam match to entry PF00512
                                              signal, Histidine kinase, score
                                              266.70, E-value 3e-76"
misc-feature            complement(140694..1408  /gene="STY3507"
                        88)
                                              /note="Pfam match to entry PF00989
                                              PAS, PAS domain, score 47.70,
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gene	complement(141443..1423	/gene="STY3508"
	72)	
CDS	complement(141443..1423	/gene="STY3508"
	72)	

/note="Orthologue of E. coli yhcC
(YHCC-ECOLI); Fasta hit to
YHCC-ECOLI (309 aa), 95% identity
in 307 aa overlap"
/codon-start=1
/transl-table=11
/product="conserved hypothetical
protein"
/protein-id="CAD07846.1"
/db-xref="GI:16504394"
/db-xref="SPTREMBL:Q8XFV9"
/translation="MQLQKLVNMFGGDLLRRYGQ
KVHKLTLHGGFSCPNRDGTIGRGG
CTFCNVASFADEAQQHHSIAEQLAHQAHLVNRAK
RYLAYFQAYTSTFAEVQVLRSMYQ
QAVSQASIVGLCVGTRPDCVPQAVVDLLCEYKDQ
GYEVWLELGLQTAHDKTLRRINRG
HDFACYQRTTRIARERGLKVCAHLIVGLPGEGQA
ECLQTMERVVETGVDGIKLHPLHI
VKGSTMAKAWEAGRLNGIELDDYTLTAGEMIRHT
PPEVIYHRISASARRPTLLAPLWC
ENRWTGMVELDKYLNEHGVQGSALARPWIPPVA"

gene	143044..147504	/gene="STY3510"
		/note="synonym: gltB"
CDS	143044..147504	/gene="STY3510"

/EC-number="1.4.1.13"
/note="Similar to Escherichia coli
glutamate synthase [NADPH] large
chain precursor GltB SW:GLTB-ECOLI
(P09831) (1517 aa) fasta scores:
E(): 0, 95.4% id in 1486 aa and to
Pseudomonas aeruginosa glutamate
synthase large subunit GltB
TR:P95456 (EMBL:U81261) (1482 aa)
fasta scores: E(): 0, 60.9% id in
1476 aa"
/codon-start=1
/transl-table=11
/product="glutamate synthase
[NADPH] large chain precursor"
/protein-id="CAD07847.1"
/db-xref="GI:16504395"
/db-xref="GOA:Q8Z3F7"
/db-xref="SPTREMBL:Q8Z3F7"
/translation="MLYDKSLEKDNCGFGLIAHI
EGEPSHKVVRTAIHALARMQHRGA
ILADGKTGDGCGLLLQKPDRFFRIVAEERGWRLA
KNYAVGMIFLNKDPELAAASRHIV
EEELQQETLSIVGWRDVPTNEGVLGEIALSSLPR
IEQIFVNAPAGWRPRDMERRLFIA
RRRIEKRLQDDKDFYVCSLSNLVNIYKGLCMPAD
LPRFYLDLADLRLESAICLFHQRF
STNTVPRWPLAQPFRYLAHNGEINTITGNRQWAR
ARTYKFQTPLIPDLQSAAPFVNET
GSDSSSLDNMLELLLAGGMDIIRAMRLLVPPAWQ
NNPDMDQDLRAFFDFNSMHMEPWD
GPAGIVMSDGRFAACNLDRNGLRPARYVITKDKL
ITCASEVGIWDYQPDEVVEKGRVG
PGELMVIDTRGGRILHSAETDDDLKSRHPYKAWM
EKNVRRLVPFEELPDEEVGSRELD
DDLLASYQKQFNYSAEELDSVIRVLGENGQEAVG
SMGDDTPFAVLSSQPRIIYDYFRQ
QFAQVTNPPIDPLREAHVMSLATSIGREMNVFCE
AEGQAHRLSFKSPILLYSDFKQLT
TMSEHHYRADWLDITFDVTETTLDATVKALCDKA
EQMVRNGTVLLVLSDRNIGKNRLP
VPAPMAVGAVQTRLVDQSLRCDANIIVETGSARD
PHHFAVLLGFGATAIYPYLAYETL
GRLIDTQAIAKNYRTVMQNYRNGINKGLYKIMSK
MGISTIASYRCSKLFEAVGLHDDV
VNLCFQGVVSRIGGASFDDFQQDLLNLSKRAWLA

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                                        VVRTLQQAVQSGEYSDYQEYAKLVNERPAATLRD
                                        LLAIHPDGEAVTIDEVEPASELFK
                                        RFDTAAMSIGALSPEAHEALAEAMNSLGGNSNSG
                                        EGGEDPARYGTNKVSRIKQVASGR
                                        FGVTPAYLVNADVIQIKVAQGAKPGEGGQLPGDK
                                        VTPYIAKLRYSVPGVTLISPPPHH
                                        DIYSIEDLAQLIFDLKQVNPKAMISVKLVSEPGV
                                        GTIATGVAKAYADLITIAGYDGGT
                                        GASPLSSVKYAGCPWELGLVETQQALVANGLRHK
                                        IRLQVDGGLKTGVDIIKAAILGAE
                                        SFGFGTGPMVALGCKYLRICHLNNCATGVATQDE
                                        KLRKNHYHGLPFKVTNYFEFIARE
                                        VRELMASLGVTRLVDLIGRTDLLKELEGFTAKQQ
                                        KLALSRLLETAEPHPGKALYCTEN
                                        NPPFDNGVLNAQLLQQAKPFVDARQSKTFWFDIR
                                        NTDRSVGASLSGYIAQTHGDQGLA
                                        SDPIKAHFSGTAGQSFGVWNAGGVELYLTGDAND
                                        YVGKGMAGGLIAIRPPVGSAFLSH
                                        KASIIGNTCLYGATGGRLYAAGRAGERFGVRNSG
                                        AITVVEGIGDNGCEYMTGGIVCVL
                                        GKTGVNFGAGMTGGFAYVLDEDGEFRKRVNPELV
                                        EVLDVDSLAIHEEHLRGLITEHVQ
                                        HTGSQRGEEILSRWSSFSTQFALVK
                                        PKSSDVKALLGHRSRSAAELRVQAQ"
```

misc-feature	143173..143196	/gene="STY3510" /note="PS00017 ATP/GTP-binding site motif A (P-loop)"
misc-feature	145420..146514	/gene="STY3510" /note="Pfam match to entry PF01645 Glu-synthase, Conserved region in glutamate synthase, score 820.90, E-value 4.4e-243"
misc-feature	146740..147333	/gene="STY3510" /note="Pfam match to entry PF01493 DUF14, Domain of unknown function DUF14, score 360.20, E-value 2.1e-104"
gene	147514..148932	/gene="STY3511" /note="synonym: gltD"
CDS	147514..148932	/gene="STY3511" /note="Fasta hit to P76440 (412 aa), 33% identity in 443 aa overlap Orthologue of E. coli gltD (GLTD-ECOLI); Fasta hit to GLTD-ECOLI (471 aa), 95% identity in 471 aa overlap" /codon-start=1 /transl-table=11 /product="glutamate synthase (NADPH) small chain" /protein-id="CAD07848.1" /db-xref="GI:16504396" /db-xref="GOA:Q8Z3F6" /db-xref="SPTREMBL:Q8Z3F6" /translation="MSQNVYQFIDLQRVDPPKKP LKLRKIEFVEIYEPFSEGQAKAQA DRCLSCGNPYCEWKCPVHNYIPNWLKLANEGRIF EAAELSHQTNTLPEVCGRVCPQDR LCEGSCTLHDEFGAVTIGNIERYINDKAFEMGWR PDMTGVRQTDKRVAIIGAGPAGLA CADVLTRNGVKAVVFDRHPEIGGLLTFGIPAFKL EKEVMTRRREIFTGMGIEFKLNTE VGRDVQLEDLLKDYDAVFLGVGTYQSMRGGLENE DADGVFDALPFLIANTKQIMGFGE TSDEPYVSMEGKRVVVLGGGDTAMDCVRTSIRQG ATHVTCAYRRDEENMPGSRREVKN AREEGVEFQFNVQPLGIEVNANGKVSGVKMVRTE MGEPDAKGRRRAEIVAGSEHVVPA DAVVMAFGFRPHSMEWLAKHSVELDSQGRIIAPE RSDNAFQTSNPKIFAGGDIVRGSD LVVTAIAEGRKAADGIMNYLEV"
misc-feature	147958..148848	/gene="STY3511" /note="Pfam match to entry PF00070 pyr-redox, Pyridine nucleotide-disulphide

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                                          E-value 2e-33"
gene            149140..150243           /gene="STY3512"
CDS             149140..150243           /gene="STY3512"
                                         /note="Orthologue of E. coli yhcG
                                         (YHCG-ECOLI); Fasta hit to
                                         YHCG-ECOLI (375 aa), 77% identity
                                         in 363 aa overlap"
                                         /codon-start=1
                                         /transl-table=11
                                         /product="conserved hypothetical
                                         protein"
                                         /protein-id="CAD07849.1"
                                         /db-xref="GI:16504397"
                                         /db-xref="SPTREMBL:Q8Z3F5"
                                         /translation="MTNPTLAPQSDEYQQIHDGI
                                         IRLVDTARTETVRSINAIMTATYW
                                         EIGRRIVEFEQGGEARAAYGTQLIERLSVDLSQR
                                         YKRGFSNRNLWQIRTFYLCFQHIE
                                         IPQTLSAESSNLIPLAKTFPLPWSAYVRLLSVKD
                                         NDARTFYEKETLRNGWSVRQLDRQ
                                         IATQFYERTLLSHDKSAMLQQPAPAEPNVLPEQA
                                         IRDPFILEFLNLKDEYSESDLEDA
                                         LLSHLMDFMLELGDDFAFVGRQRRLRIDDSWFRV
                                         DLLFFHRRLRCLLLVDLKVGKFGY
                                         ADAGQMNMYLNYAKEHWTMPGENPPVGLVLCAGK
                                         GAGEAHYALTGLPNTIMASEYKVQ
                                         LPDEKLLTDELIRSQTMLETQLTRGGSLTTEKN"
gene            150360..151613           /gene="STY3513"
                                         /note="synonym: codB"
CDS             150360..151613           /gene="STY3513"
                                         /note="Similar to Escherichia coli
                                         cytosine permease codB
                                         SW:CODB-ECOLI (P25525) (419 aa)
                                         fasta scores: E(): 0, 82.5% id in
                                         416 aa"
                                         /codon-start=1
                                         /transl-table=11
                                         /product="cytosine permease"
                                         /protein-id="CAD07850.1"
                                         /db-xref="GI:16504398"
                                         /db-xref="GOA:Q8Z3F4"
                                         /db-xref="SPTREMBL:Q8Z3F4"
                                         /translation="MSQDNNYSQGPVPQAARKGV
                                         IPLTFVMLGLTFFSASMWTGGTLG
                                         TGLTYHDFFLAVFFGNLLLGIYTAFLGYIGAKTG
                                         LSTHLLARYSFGVKGSWLPSLLLG
                                         STQVGWFGVGVAMFAIPVSKATGIDANILIAVSG
                                         LLMTLTIFFGISALTILSIVAVPA
                                         IVILGSYSVWLAVSGVGGLEHLKTIVPQTPLDFS
                                         SALALVVGSFVSAGTLTADFVRFG
                                         RHAKSAVLIAMVAFFLGNSLMFIFGAAGAAAVGQ
                                         ADISDVMIAQGLLLPAIVVLGLNI
                                         WTTNDNALYASGLGFANITGLSSRTLSVVNGIIG
                                         TVCALWLYNNFVGWLTFLSSAIPP
                                         IGGVIIADYLVNRRRYADFNTVRFIPVNWIAILS
                                         VALGIAAGHYVPGIVPVNAVLGGV
                                         FSYILLNPLFNRSLAKSPEVSHAEQ"
misc-feature    150390..151553           /gene="STY3513"
                                         /note="Pfam match to entry PF02133
                                         Transp-cyt-pur, Permeases for
                                         cytosine/purines, uracil,
                                         thiamine, allantoin, score 322.90,
                                         E-value 3.6e-93"
gene            151600..152880           /gene="STY3514"
                                         /note="synonym: codA"
CDS             151600..152880           /gene="STY3514"
                                         /note="Orthologue of E. coli codA
                                         (CODA-ECOLI); Fasta hit to
                                         CODA-ECOLI (426 aa), 84% identity
                                         in 426 aa overlap"
                                         /codon-start=1
                                         /transl-table=11
                                         /product="cytosine deaminase"
                                         /protein-id="CAD07851.1"
                                         /db-xref="GI:16504399"
```

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                                        /translation="MQNNNITIRQTRLQGHEGLW
                                        QITIENGRFSRIEPQEATSLPQGE
                                        VLDAEGGLAIPPFVEPHIHLDTTQTAGEPSWNQS
                                        GTLFEGIERWAERKAMLTHEDVKA
                                        RAMQTLKWQMANGIQYVRTHVDVSDPTLTALKAM
                                        LEVKQEVAPWVDLQIVAFPQEGIL
                                        SYPNGEALLEEAVRLGADVIGAIPHFEFTREYGV
                                        ESLHKTFALAQKYDRLIDVHCDEI
                                        DDEQSRFVETVAALAHRDGMGARVTASHTTAMHS
                                        YNGAYASRLFRLLKMSGINFVANP
                                        LVNIHLQGRFDTYPKRRGVTRVKEMLEAGINVCF
                                        GHDDVFDPWYPLGTANMLQVLHMG
                                        LHVCQLMGYGQINDGLNLITTHSAKTLHLQDYGL
                                        SVGNAANLVILPAENGFDAVRRQT
                                        PARYSIRHRRVIAETVPSQTTLHLTQPEAVTFKR
                                        "
gene             complement(152962..1534    /gene="STY3515"
                 29)
CDS              complement(152962..1534    /gene="STY3515"
                 29)
                                        /note="Fasta hit to YJGK-ECOLI
                                        (150 aa), 32% identity in 148 aa
                                        overlap Orthologue of E. coli
                                        YHCH-ECOLI; Fasta hit to
                                        YHCH-ECOLI (154 aa), 81% identity
                                        in 154 aa overlap"
                                        /codon-start=1
                                        /transl-table=11
                                        /product="conserved hypothetical
                                        protein"
                                        /protein-id="CAD07852.1"
                                        /db-xref="GI:16504400"
                                        /db-xref="GOA:Q8Z3F2"
                                        /db-xref="SPTREMBL:Q8Z3F2"
                                        /translation="MMMGEVQSLPSCGLHPRLLD
                                        ALTLALAARPQEKAPGRYELQGDN
                                        IFMNVMQLTTQMPAGKKAELHEQYIDIQLLLTGV
                                        ERIAFGMSGAARQCEEMHVEEDYQ
                                        LCSQIADEQTITLQAGMFAVFMPGEPHKPGCAVG
                                        EPDDIKKVVVKVRASLLAA"
gene             complement(153426..1543    /gene="STY3516"
                 01)
CDS              complement(153426..1543    /gene="STY3516"
                 01)
                                        /note="Similar to several
                                        including: Escherichia coli
                                        hypothetical protein YhcI
                                        SW:YHCI-ECOLI (P45425) (291 aa)
                                        fasta scores: E(): 0, 74.9% id in
                                        291 aa and toseveral kinases e.g.
                                        Streptomyces coelicolor
                                        glucokinase SW:GLK-STRCO () (317
                                        aa) fasta scores: E(): 8.1e-18,
                                        31.8% id in 314 aa Fasta hit to
                                        YCFX-ECOLI (303 aa), 30% identity
                                        in 306 aa overlap Orthologue of E.
                                        coli yhcI (YHCI-ECOLI); Fasta hit
                                        to YHCI-ECOLI (291 aa), 75%
                                        identity in 291 aa overlap"
                                        /codon-start=1
                                        /transl-table=11
                                        /product="possible kinase"
                                        /protein-id="CAD07853.1"
                                        /db-xref="GI:16504401"
                                        /db-xref="GOA:Q8Z3F1"
                                        /db-xref="SWISS-PROT:Q8Z3F1"
                                        /translation="MTTLAIDIGGTKLAAALIDN
                                        NLRISQRRELPTPASKTPDALREA
                                        LKALVEPLRAEARQVAIASTGIIQEGMLLALNPH
                                        NLGGLLHFPLVQTLETIAGLPTLA
                                        VNDAQAAAWAEYHALPDDIRDMVFITVSTGVGGG
                                        VVCDGKLLTGKGGLAGHLGHTLAD
                                        PHGPVCGCGRVGCVEAIASGRGMAAAARDDLAGC
                                        DAKTLFIRAGEGHQQARHLVSQSA
                                        QVIARMIADVKAITDCQCVVIGGSVGLAEGYLEQ
```

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                                      AGLLGAALLAQGDTL"
misc-feature    complement(153753..1542  /gene="STY3516"
                89)
                                      /note="Pfam match to entry PF00480
                                      ROK, ROK family, score 236.10,
                                      E-value 3.8e-69"
misc-feature    complement(153834..1539  /gene="STY3516"
                17)
                                      /note="PS01125 ROK family
                                      signature"
gene            complement(154298..1549  /gene="STY3518"
                77)
                                      /pseudo
CDS             complement(154298..1549  /gene="STY3518"
                77)
                                      /note="Similar to several
                                      including: Escherichia coli
                                      hypothetical protein YhcJ
                                      SW:YHCJ-ECOLI (P45426) (229 aa)
                                      fasta scores: E(): 9e-28, 72.5% id
                                      in 109 aa and to Clostridium
                                      perfringens putative
                                      N-acetylmannosamine-6-p epimerase
                                      nanE TR:Q9S4L0 (EMBL:AF130859)
                                      (221 aa) fasta scores: E():
                                      8.5e-11, 48.8% id in 80 aa.
                                      Contains a frameshift mutation
                                      following codon 96."
                                      /pseudo
                                      /codon-start=1
                                      /transl-table=11
                                      /product="conserved hypothetical
                                      protein (pseudogene)"
gene            complement(155024..1565  /gene="STY3519"
                14)
                                      /note="synonym: nanT"
CDS             complement(155024..1565  /gene="STY3519"
                14)
                                      /note="Fasta hit to YJHB-ECOLI
                                      (405 aa), 35% identity in 452 aa
                                      overlap Orthologue of E. coli nanT
                                      (NANT-ECOLI); Fasta hit to
                                      NANT-ECOLI (496 aa), 95% identity
                                      in 496 aa overlap"
                                      /codon-start=1
                                      /transl-table=11
                                      /product="putative sialic acid
                                      transporter"
                                      /protein-id="CAD07855.1"
                                      /db-xref="GI:16504402"
                                      /db-xref="GOA:Q8XFJ3"
                                      /db-xref="SPTREMBL:Q8XFJ3"
                                      /translation="MSTSTQNIPWYRHLNRAQWR
                                      AFSAAWLGYLLDGFDFVLIALVLT
                                      EVQSEFGLTTVQAASLISAAFISRWFGGLLLGAM
                                      GDRYGRRLAMVSSIILFSVGTLAC
                                      GFAPGYTTMFIARLVIGMGMAGEYGSSATYVIES
                                      WPKHLRNKASGFLISGFSVGAVVA
                                      AQVYSLVVPVWGWRALFFIGILPIIFALWLRKNI
                                      PEAEDWKEKHAGKAPVRTMVDILY
                                      RGEHRIINILMTFAAAAALWFCFAGNLQNAAIVA
                                      GLGLLCAVIFISFMVQSSGKRWPT
                                      GVMLMLVVLFAFLYSWPIQALLPTYLKTELAYDP
                                      HTVANVLFFSGFGAAVGCCVGGFL
                                      GDWLGTRKAYVCSLLASQILIIPVFAIGGTNVWV
                                      LGLLLFFQQMLGQGIAGILPKLIG
                                      GYFDTDQRAAGLGFTYNVGALGGALAPILGALIA
                                      QRLDLGTALASLSFSLTFVVILLI
                                      GLDMPSRVQRWLRPEALRTHDAIDDKPFSGAVPL
                                      GSGKGAFVKTKS"
misc-feature    complement(155114..1564  /gene="STY3519"
                57)
                                      /note="Pfam match to entry PF00083
                                      sugar-tr, Sugar (and other)
                                      transporter, score 41.30, E-value
```

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gene            complement(156630..1575   /gene="STY3520"
                23)
                                          /note="synonym: nanA"
CDS             complement(156630..1575   /gene="STY3520"
                23)
                                          /note="Orthologue of E. coli nanA
                                          (NPL-ECOLI); Fasta hit to
                                          NPL-ECOLI (296 aa), 91% identity
                                          in 295 aa overlap"
                                          /codon-start=1
                                          /transl-table=11
                                          /product="N-acetylneuraminate
                                          lyase"
                                          /protein-id="CAD07856.1"
                                          /db-xref="GI:16504403"
                                          /db-xref="GOA:Q8Z3F0"
                                          /db-xref="SWISS-PROT:Q8Z3F0"
                                          /translation="MAKALQGVMAALLTPFDHQQ
                                          QLDSESLRRLVRFNIGQGIDGLYV
                                          GGSTGEAFVQSLAEREQVLEIVAEEAKGKITLIA
                                          HVGTVSTAESQQLASAAKRYGFDA
                                          VSAVTPFYYPFSFEEHCDHYRAIIDSADGLPMVV
                                          YNIPALSGVKLTLDQINTLVTLPG
                                          VNALKQTSGDLFQMEQIRRAHPDLVLYNGYDEIF
                                          ASGLLAGADGGIGSTYNIMGWRYQ
                                          GIVQALREGDVAKAQRLQTECNKVIDLLIKTGVF
                                          RGLKTVLHYMDVVSVPLCRKPFAP
                                          VDEKYLPALKALAQQLMEEKA"
misc-feature    complement(156693..1574   /gene="STY3520"
                51)
                                          /note="Pfam match to entry PF00701
                                          DHDPS, Dihydrodipicolinate
                                          synthetase family, score 441.70,
                                          E-value 6.3e-129"
misc-feature    complement(157023..1571   /gene="STY3520"
                15)
                                          /note="PS00666 Dihydrodipicolinate
                                          synthetase signature 2"
misc-feature    complement(157350..1574   /gene="STY3520"
                03)
                                          /note="PS00665 Dihydrodipicolinate
                                          synthetase signature 1"
gene            complement(157658..1584   /gene="STY3521"
                49)
CDS             complement(157658..1584   /gene="STY3521"
                49)
                                          /note="Similar to several proposed
                                          regulatory proteins e.g.
                                          Escherichia coli hypothetical
                                          transcriptional regulator YhcK
                                          SW:YHCK-ECOLI (P45427) (263 aa)
                                          fasta scores: E(): 0, 87.5% id in
                                          263 aa and to Streptomyces
                                          coelicolor putative
                                          transcriptional regulator SCF55.06
                                          TR:Q9RJQ8 (EMBL:AL132991) (253 aa)
                                          fasta scores: E(): 6.6e-11, 27.2%
                                          id in 254 aa"
                                          /codon-start=1
                                          /transl-table=11
                                          /product="putative GntR-family
                                          transcriptional regulator"
                                          /protein-id="CAD07857.1"
                                          /db-xref="GI:16504404"
                                          /db-xref="GOA:Q8XFH8"
                                          /db-xref="SWISS-PROT:Q8XFH8"
                                          /translation="MDVMNAFDSQAEDSPTSLGR
                                          SLRRRPLARKKLSEMVEEELEQMI
                                          RRHEFGEGEQLPSERELMAFFNVGRPSVREALAA
                                          LKRKGLVQINNGERARVSRPSADT
                                          IISELSGMAKDFLTHPGGIAHFEQLRLFFESSLV
                                          RYAAEHATDEQIALLTKALEINSQ
                                          SLDDNALFIRSDVEFHRVLAEIPGNPIFMAIHVA
                                          LLDWLIAARPSVPDRELHEHNNVS
                                          YQQHIVIVDAIRQRDPDKADRALQTHLNSVSATW
```

misc-feature	complement(158165..1583 44)	/gene="STY3521"
		/note="Pfam match to entry PF00392 gntR, Bacterial regulatory proteins, gntR family, score 94.50, E-value 1.1e-27"
misc-feature	complement(158213..1582 87)	/gene="STY3521"
		/note="PS00043 Bacterial regulatory proteins, gntR family signature"
gene	complement(158558..1590 58)	/gene="STY3522"
		/note="synonym: sspB"
CDS	complement(158558..1590 58)	/gene="STY3522"
		/note="Orthologue of E. coli sspB (SSPB-ECOLI); Fasta hit to SSPB-ECOLI (165 aa), 89% identity in 167 aa overlap" /codon-start=1 /transl-table=11 /product="stringent starvation protein B" /protein-id="CAD07858.1" /db-xref="GI:16504405" /db-xref="SPTREMBL:Q8XGT9" /translation="MDLSQLTPRRPYLLRAFYEW LLDNQLTPHLVVDVMLPGVHVPME YARDGQIVLNIAPRAVGNLELSNDEVRFNARFGG VPRQVSVPLAAVLAIYARENGAGT MFEPEAAYDEDVVSLNDDDNTAGAESETVMSVID GDKPDHDDDSSPDDEPPPPRGGRP ALRVVK"
gene	complement(159064..1597 02)	/gene="STY3523"
		/note="synonym: sspA"
CDS	complement(159064..1597 02)	/gene="STY3523"
		/note="Orthologue of E. coli sspA (SSPA-ECOLI); Fasta hit to SSPA-ECOLI (211 aa), 98% identity in 210 aa overlap" /codon-start=1 /transl-table=11 /product="stringent starvation protein A" /protein-id="CAD07859.1" /db-xref="GI:16504406" /db-xref="SPTREMBL:Q8Z3E9" /translation="MAVAANKRSVMTLFSGPTDI YSHQVRIVLAEKGVSFEIEHVEKD NPPQDLIDLNPNQSVPTLVDRELTLWESRIIMEY LDERFPHPPLMPVYPVARGESRLY MHRIEKDWYTLMNVIVNGSASEVDSARKQLREEL LAIAPVFGQKPYFLSDEFSLVDCY LAPLLWRLPQLGIEFSGAGAKELKGYMTRVFERD SFLASLTEAEREMRLGRG"
misc-feature	complement(159121..1596 72)	/gene="STY3523"
		/note="Pfam match to entry PF00043 GST, Glutathione S-transferases., score 166.00, E-value 1.9e-49"
gene	complement(160017..1604 09)	/gene="STY3524"
		/note="synonym: rpsI"
CDS	complement(160017..1604 09)	/gene="STY3524"
		/note="Orthologue of E. coli rpsI (RS9-ECOLI); Fasta hit to RS9-ECOLI (129 aa), 99% identity in 129 aa overlap" /codon-start=1 /transl-table=11 /product="30S ribosomal subunit protein S9"

```
                                       /db-xref="GI:16504407"
                                       /db-xref="GOA:Q8XFX5"
                                       /db-xref="SWISS-PROT:Q8XFX5"
                                       /translation="MAENQYYGTGRRKSSAARVF
                                       IKPGNGKIVINQRSLEQYFGRETA
                                       RMVVRQPLELVDMVEKLDLYITVKGGGISGQAGA
                                       IRHGITRALMEYDESLRGELRKAG
                                       FVTRDARQVERKKVGLRKARRRPQFSKR"
     misc-feature    complement(160020..1603   /gene="STY3524"
                     82)
                                       /note="Pfam match to entry PF00380
                                       Ribosomal-S9, Ribosomal protein
                                       S9/S16, score 249.10, E-value
                                       7.2e-77"
     misc-feature    complement(160149..1602   /gene="STY3524"
                     05)
                                       /note="PS00360 Ribosomal protein
                                       S9 signature"
     gene            complement(160425..1608   /gene="STY3525"
                     53)
                                       /note="synonym: rplM"
     CDS             complement(160425..1608   /gene="STY3525"
                     53)
                                       /note="Orthologue of E. coli rplM
                                       (RL13-ECOLI); Fasta hit to
                                       RL13-ECOLI (142 aa), 100% identity
                                       in 142 aa overlap"
                                       /codon-start=1
                                       /transl-table=11
                                       /product="50S ribosomal subunit
                                       protein L13"
                                       /protein-id="CAD07861.1"
                                       /db-xref="GI:16504408"
                                       /db-xref="GOA:P02410"
                                       /db-xref="SWISS-PROT:P02410"
                                       /translation="MKTFTAKPETVKRDWYVVDA
                                       TGKTLGRLATELARRLRGKHKAEY
                                       TPHVDTGDYIIVLNADKVAVTGNKRTDKVYYHHT
                                       GHIGGIKQATFEEMIARRPERVIE
                                       IAVKGMLPKGPLGRAMFRKLKVYAGNEHNHAAQQ
                                       PQVLDI"
     misc-feature    complement(160428..1608   /gene="STY3525"
                     11)
                                       /note="Pfam match to entry PF00572
                                       Ribosomal-L13, Ribosomal protein
                                       L13, score 305.00, E-value
                                       9.2e-88"
     misc-feature    complement(160473..1605   /gene="STY3525"
                     41)
                                       /note="PS00783 Ribosomal protein
                                       L13 signature"
     gene            complement(161154..1622   /gene="STY3526"
                     78)
     CDS             complement(161154..1622   /gene="STY3526"
                     78)
                                       /note="Orthologue of E. coli yhcM
                                       (YHCM-ECOLI); Fasta hit to
                                       YHCM-ECOLI (375 aa), 85% identity
                                       in 373 aa overlap"
                                       /codon-start=1
                                       /transl-table=11
                                       /product="putative ATP/GTP-binding
                                       protein"
                                       /protein-id="CAD07862.1"
                                       /db-xref="GI:16504409"
                                       /db-xref="SPTREMBL:Q8Z3E8"
                                       /translation="MQSLSPTSRYLQALNEGTHQ
                                       PDDVQKEAVDRLETLYQALTAKKS
                                       SATPPGGLIARLGKLLGKNEPDAQIPVRGLYMWG
                                       GVGRGKTWLMDLFYHSLPGERKLR
                                       LHFHRFMLRVHEELTALQGQIDPLDIIADRFKTE
                                       TDVLCFDEFFVTDITDAMLLGGLM
                                       KALFARGITLVATSNIPPEELYRNGLQRARFLPA
                                       IDAIKQHCDIMNVDAGVDYRLRTL
                                       TQAHLWLTPLNDETRRQMDKLWLALAGAAREHAP
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		TLCVEARSQHDYIALSRLFHTVLLFDVPVMTPLM ENEARRFIALVDEFYERHVKLVVS AAAPLYEIYQGERLKFEFQRCLSRLQEMQSAEYL KREHMP"
misc-feature	complement(162024..1620 47)	/gene="STY3526"
		/note="PS00017 ATP/GTP-binding site motif A (P-loop)"
gene	162465..162869	/gene="STY3527"
CDS	162465..162869	/gene="STY3527" /note="Orthologue of E. coli yhcB (YHCB-ECOLI); Fasta hit to YHCB-ECOLI (134 aa), 96% identity in 132 aa overlap" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAD07863.1" /db-xref="GI:16504410" /db-xref="SPTREMBL:Q8Z3E7" /translation="MFMTWEYALIGLVVGIIIGA VAMRFGNRKLRQQQALQYELEKNK AELEEYREELVSHFARSAELLDTMAHDYRQLYQY MAKSSSSLLPEMSAESNPFRNRLA ESEASNDQAPVQMPRDYSEGASGLLRSGAKRD"
gene	163026..164393	/gene="degQ" /note="synonym: STY3528"
CDS	163026..164393	/gene="degQ" /EC-number="3.4.21.-" /note="Similar to Escherichia coli protease DegQ SW:DEGQ-ECOLI (P39099) (455 aa) fasta scores: E(): 0, 90.1% id in 455 aa" /codon-start=1 /transl-table=11 /product="serine protease" /protein-id="CAD07864.1" /db-xref="GI:16504411" /db-xref="GOA:Q8Z3E6" /db-xref="SPTREMBL:Q8Z3E6" /translation="MKKHTQLLSALALSVGLTLS APFPALASIPGQVPGQATLPSLAP MLEKVLPAVVSVKVEGTATQSQKVPEEFKKFFGE DLPDQPSQPFEGLGSGVIIDAAKG YVLTNNHVINQAQKISIQLNDGREFDAKLIGGDD QSDIALLQIQNPSKLTQIAIADSD KLRVGDFAVAVGNPFGLGQTATSGIISALGRSGL NLEGLENFIQTDASINRGNSGGAL LNLNGELIGINTAILAPGGGSIGIGFAIPSNMAQ TLAQQLIQFGEIKRGLLGIKGTEM TADIAKAFKLNVQRGAFVSEVLPNSGSAKAGVKS GDVIISLNGKPLNSFAELRSRIAT TEPGTKVKLGLLRDGKPLEVEVTLDSNTSSSASA EMIAPALQGATLSDGQLKDGTKGV KVDSVEKSSPAAQAGLQKDDVIIGVNRDRISSIA EMRKVMAAKPSIIALQVVRGNENI YLLLR"
misc-feature	163302..163790	/gene="degQ" /note="Pfam match to entry PF00089 trypsin, Trypsin, score 75.70, E-value 3.5e-23"
misc-feature	163797..164069	/gene="degQ" /note="Pfam match to entry PF00595 PDZ, PDZ domain (Also known as DHR or GLGF)., score 79.80, E-value 5.5e-20"
misc-feature	164118..164363	/gene="degQ" /note="Pfam match to entry PF00595 PDZ, PDZ domain (Also known as DHR or GLGF)., score 54.40, E-value 2.5e-12"
misc-feature	164309..164332	/gene="degQ" /note="PS00017 ATP/GTP-binding site motif A (P-loop)"
gene	164486..165556	/gene="degS"

CDS	164486..165556	/gene="degS"

/EC-number="3.4.21.-"
/note="Similar to Escherichia coli
protease degs precursor degs or
hhob or htrH SW:DEGS-ECOLI
(P31137) (355 aa) fasta scores:
E(): 0, 91.6% id in 356 aa"
/codon-start=1
/transl-table=11
/product="serine protease"
/protein-id="CAD07865.1"
/db-xref="GI:16504412"
/db-xref="GOA:Q8XEX3"
/db-xref="SPTREMBL:Q8XEX3"
/translation="MFVKLLRSVAIGLIVGAILL
AVMPSLRKINPIAVPQFDSTDETP
ASYNFAVRRAAPAVVNVYNRSMNSTAHNQLEIRT
LGSGVIMDQRGYIITNKHVINDAD
QIIVALQDGRVFEALLVGSDSLTDLAVLKINATG
GLPTIPINTKRTPHIGDVVLAIGN
PYNLGQTITQGIISATGRIGLNPTGRQNFLQTDA
SINHGNSGGALVNSLGELMGINTL
SFDKSNDGETPEGLGFAIPFQLATKIMDKLIRDG
RVIRGYIGIGGREIAPLHAQQGSG
MDPIQGIVVNEVTPNGPAALAGIQVNDLIISVNN
KPAVSALETMDQVAEIRPGSVIPV
VVMRDDKQLTFQVTVQEYPASN"

| misc-feature | 164669..165217 | /gene="degS" |

/note="Pfam match to entry PF00089
trypsin, Trypsin, score 92.90,
E-value 1.2e-28"

| misc-feature | 165227..165502 | /gene="degS" |

/note="Pfam match to entry PF00595
PDZ, PDZ domain (Also known as DHR
or GLGF)., score 64.60, E-value
2.1e-15"

| repeat-unit | 166341..169683 | /note="repeat element rep12" |
| gene | complement(166342..1676 43) | /gene="oadB" |

/note="synonym: STY3531"

| CDS | complement(166342..1676 43) | /gene="oadB" |

/EC-number="4.1.1.3"
/note="Similar to Salmonella
typhimurium oxaloacetate
decarboxylase beta chain OadB
SW:DCOB-SALTY (Q03031) (433 aa)
fasta scores: E(): 0, 98.2% id in
433 aa"
/codon-start=1
/transl-table=11
/product="oxaloacetate
decarboxylase beta chain"
/protein-id="CAD07866.1"
/db-xref="GI:16504413"
/db-xref="GOA:Q8Z3E5"
/db-xref="SPTREMBL:Q8Z3E5"
/translation="MESLNALLQGMGLMHLGAGQ
AIMLLVSLLLLWLAIAKKFEPLLL
LPIGFGGLLSNIPEAGMALTALESLLAHHDAGQL
AVIAAKLNCAPDVHAIKEALALAL
PSVQNQMENLAVDMGYTPGVLALFYKVAIGSGVA
PLVIFMGVGAMTDFGPLLANPRTL
LLGAAAQFGIFATVLGALTLNYFGLIAFTLPQAA
AIGIIGGADGPTAIYLSGKLAPEL
LGAIAVAAYSYMALVPLIQPPIMRALTSEKERKI
RMVQLRTVSKREKILFPVVLLLLV
ALLLPDAAPLLGMFCFGNLMRESGVVERLSDTVQ
NGLINIVTIFLGLSVGAKLVADKF
LQPQTLGILLLGVIAFGIGTAAGVLMAKLLNLCS
KNKINPLIGSAGVSAVPMAARVSN
KVGLESNPQNFLLMHAMGPNVAGVIGSAIAAGVM
LKYVLAM"

| gene | complement(167656..1694 31) | /gene="oadA" |

CDS	complement(167656..1694 31)	/gene="oadA"

/EC-number="4.1.1.3"
/note="Similar to Salmonella
typhimurium oxaloacetate
decarboxylase alpha chain OadA
SW:DCOA-SALTY (Q03030) (590 aa)
fasta scores: E(): 0, 98.6% id in
590 aa"
/codon-start=1
/transl-table=11
/product="oxaloacetate
decarboxylase alpha chain"
/protein-id="CAD07867.1"
/db-xref="GI:16504414"
/db-xref="GOA:Q8XGX8"
/db-xref="SPTREMBL:Q8XGX8"
/translation="MTIAITDVVLRDAHQSLFAT
RLRLDDMLPIAAQLDDVGYGSLEC
WGGATFDACIRFLGEDPWLRLRELKKAMPKTPLQ
MLLRGQNLLGYRHYADDVVERFVE
RAVKNGMDVFRVFDAMNDPRNMKAALQAVRSHGA
HAQGTLSYTTSPAHTLQTWLDLTE
QLLETGVDSIAIKDMSGILTPMAAFELVSEIKKR
FEVRLHLHCHATTGMAEMALLKAI
EAGVDGVDTAISSMSATYGHPATEALVATLAGTE
HDTGLDILKLENIAAYFREVRKKY
HAFEGQLKGYDSRILVAQVPGGMLTNLESQLKQQ
NAADRLDQVLAEIPRVREDLGFIP
LVTPTSQIVGTQAVLNVLTGERYKTIAKETAGIL
KGEYGHTPVPVNAALQARVLEGSA
PVTCRPADLLKPELAELEADVRRQAQEKGITLAG
NAIDDVLTVALFPQIGLKFLENRH
NPAAFEPLPQAEAAQPVAKAEKPAASGIYTVEVE
GKAFVVRVSDGGDISQLTTAVPAA
SSAPVQAAAPAGAGTPVTAPLAGNIWKVIATEGQ
SVAEGDVLLILEAMKMETEIRAAQ
AGTVRGIAVKSGDAVSVGDTLMTLA"

misc-feature	complement(167662..1678 65)	/gene="oadA"

/note="Pfam match to entry PF00364
biotin-lipoyl, Biotin-requiring
enzymes, score 101.10, E-value
2.2e-26"

misc-feature	complement(167740..1677 93)	/gene="oadA"

/note="PS00188 Biotin-requiring
enzymes attachment site"

misc-feature	complement(168577..1694 07)	/gene="oadA"

/note="Pfam match to entry PF00682
HMGL-like, HMGL-like, score
326.40, E-value 3.4e-94"

gene	complement(169447..1696 89)	/gene="oadG"

/note="synonym: STY3533"

CDS	complement(169447..1696 89)	/gene="oadG"

/EC-number="4.1.1.3"
/note="Similar to Salmonella
typhimurium oxaloacetate
decarboxylase gamma chain oadG
SW:DCOG-SALTY (Q03032) (83 aa)
fasta scores: E(): 3.7e-22, 85.5%
id in 83 aa."
/codon-start=1
/transl-table=11
/product="oxaloacetate
decarboxylase gamma chain"
/protein-id="CAD07868.1"
/db-xref="GI:16504415"
/db-xref="GOA:Q8Z3E4"
/db-xref="SWISS-PROT:Q8Z3E4"
/translation="MTNAALLLGEGFTLMLLGMG
FVLAFLFLLIFAIRGMSAVITRFF

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                                        NA"
gene            complement(169845..1704  /gene="STY3534"
                62)
                                         /note="synonym: ttdB"
CDS             complement(169845..1704  /gene="STY3534"
                62)
                                         /note="Orthologue of E. coli ttdB
                                         (TTDB-ECOLI); Fasta hit to
                                         TTDB-ECOLI (201 aa), 67% identity
                                         in 203 aa overlap"
                                         /codon-start=1
                                         /transl-table=11
                                         /product="tartrate dehydratase"
                                         /protein-id="CAD07869.1"
                                         /db-xref="GI:16504416"
                                         /db-xref="GOA:Q8XEV4"
                                         /db-xref="SPTREMBL:Q8XEV4"
                                         /translation="MTKKILTTPIKDEDLADIKA
                                         GDIIYLNGHIVTCRDVAHRRLIEG
                                         GRELPVDVRGGAILHAGPIVRPIKGEDDKFEMVS
                                         VGPTTSMRMEKFEKEFIAQTGVKL
                                         IVGKGGMGKGTEEGCAEHKALHCVFPAGCAVVAA
                                         VCVEEIEDAQWRDLGMPETLWVCR
                                         VKEFGPLIVSIDTHGNNLFEQNKIIFNQRKEIVA
                                         DEICQNVSFIK"
gene            complement(170462..1713  /gene="STY3535"
                61)
                                         /note="synonym: ttdA"
CDS             complement(170462..1713  /gene="STY3535"
                61)
                                         /note="Orthologue of E. coli ttdA
                                         (TTDA-ECOLI); Fasta hit to
                                         TTDA-ECOLI (303 aa), 54% identity
                                         in 294 aa overlap"
                                         /codon-start=1
                                         /transl-table=11
                                         /product="tartrate dehydratase"
                                         /protein-id="CAD07870.1"
                                         /db-xref="GI:16504417"
                                         /db-xref="GOA:Q8XFJ9"
                                         /db-xref="SPTREMBL:Q8XFJ9"
                                         /translation="MSKSEQISHMTDVMAKFVGY
                                         TGKVLPDDVTAKLEDLHKKETSKL
                                         ADVIFTTMIENQRLAKELDRPSCQDTGVIQFLVE
                                         CGTNFPLIGELEALLREAVIKATV
                                         DSPLRHNSVETFDEYNTGKNVGKGTPTVFWEIVP
                                         NSDQCSIYTYMAGGGCSLPGKAMV
                                         LMPGAGYEGVTRFVLDVMTSYGLNACPPLLVGVG
                                         VATSVETAALLSKKALMRPIGSHN
                                         ENERAASLEKMLEDGINKIGLGPQGMSGNTSVMG
                                         VNIENTARHPSTIGVAVNVGCWSH
                                         RKGHIVFDKDLNYTITSHSGVNF"
gene            complement(171394..1727  /gene="STY3536"
                46)
CDS             complement(171394..1727  /gene="STY3536"
                46)
                                         /note="Similar to Methanobacterium
                                         thermoautotrophicum
                                         sodium/dicarboxylate or sulfate
                                         cotransporter mth788 TR:O26881
                                         (EMBL:AE000857) (443 aa) fasta
                                         scores: E(): 2.1e-31, 29.9% id in
                                         428 aa. Contains multiple possible
                                         membrane spanning hydrophobic
                                         domains"
                                         /codon-start=1
                                         /transl-table=11
                                         /product="possible membrane
                                         transport protein"
                                         /protein-id="CAD07871.1"
                                         /db-xref="GI:16504418"
                                         /db-xref="GOA:Q8Z3E3"
                                         /db-xref="SPTREMBL:Q8Z3E3"
                                         /translation="MTYFLYGNNFSSSILDTISY
                                         IIDWIIINMEPITLTLCLLVFAIV
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                                     FIDTNVILFVAMFIVGGALFETGM
                                     ANKVGGVITRFAKTEKQLIFTIMVVVGLMSGVLS
                                     NTGTAAVLIPVVIGVAAKSGFSRS
                                     RLLMPLVFAAALGGNLSLIGAPGNLIAQSALQNI
                                     GGGFGFFEYAKIGLPMLICGILYF
                                     LTIGYRFLPNNATGGEVGSVGEQRDYSHVPQWKQ
                                     RLSLVVLIATILGMIFEKKIGVSL
                                     AVTGCIGALVLVVSGVLTEKQAYKAIDSQTIFIF
                                     GGTLALAKALEMTGAGKLVADYVI
                                     GMLGQNSSPFMLLIAVFALSVVMTNFMSNTATTA
                                     LLVPVSLSIAAGMGADPRAVLMAT
                                     VIGGSCAYATPIGMPANMMVLSAGGYKFVDYAKA
                                     GIPLIIVSTIVSLILLPILFPFHP "
misc-feature     complement(171424..1718   /gene="STY3536"
                 31)
                                     /note="Pfam match to entry PF00939
                                     Na-sulph-symp, Sodium:sulfate
                                     symporter transmembrane region,
                                     score 29.30, E-value 1.1e-07"
misc-feature     complement(172444..1726   /gene="STY3536"
                 41)
                                     /note="Pfam match to entry PF00939
                                     Na-sulph-symp, Sodium:sulfate
                                     symporter transmembrane region,
                                     score 7.40, E-value 0.19"
gene             complement(172873..1734   /gene="STY3537"
                 78)
CDS              complement(172873..1734   /gene="STY3537"
                 78)
                                     /note="Similar to Streptomyces
                                     coelicolor putative GntR-family
                                     transcriptional regulator
                                     scgd3.11C TR:Q9XA67
                                     (EMBL:AL096822) (216 aa) fasta
                                     scores: E(): 7.4e-11, 33.2% id in
                                     189 aa"
                                     /codon-start=1
                                     /transl-table=11
                                     /product="possible transcriptional
                                     regulator"
                                     /protein-id="CAD07872.1"
                                     /db-xref="GI:16504419"
                                     /db-xref="SPTREMBL:Q8Z3E2"
                                     /translation="MLRKAILSRELVEGQEITLE
                                     GIAGMVGVSSMPVREAFQILAADG
                                     LIKVRPNKGAVVLGINEQTIREHYEIRALLESEA
                                     VAKASRPGTDISRIAEVHYAAEKA
                                     LAENNSAEYSDLNQAFHMEIWNVAGNEKMKMLLC
                                     NMWNGLSMGHKVTEEEYAVISIQE
                                     HKSILQALELHDETLARQRMREHIIRSMENMLTR
                                     YVGDPSA"
gene             complement(173525..1741   /gene="STY3538"
                 54)
CDS              complement(173525..1741   /gene="STY3538"
                 54)
                                     /note="Similar to the DNA-binding
                                     domains of several regulatory
                                     proteins e.g. Pseudomonas putida
                                     VanR protein vanR TR:Q9R9S9
                                     (EMBL:AJ252091) (237 aa) fasta
                                     scores: E(): 9.7e-06, 46.4% id in
                                     69 aa"
                                     /codon-start=1
                                     /transl-table=11
                                     /product="possible GntR-family
                                     transcriptional regulator"
                                     /protein-id="CAD07873.1"
                                     /db-xref="GI:16504420"
                                     /db-xref="GOA:Q8Z3E1"
                                     /db-xref="SPTREMBL:Q8Z3E1"
                                     /translation="MKKIQRTQTRDHITQMLRYE
                                     ILSGNIKAGEELAQGSIAEQLGLS
                                     RMPVREALQSLEQEGFLIRLPNRHMQVAHLEADR
                                     VSHIFRVIAAMAAEMFSLIPSEVG
                                     DALLIRAQALAVAEDKSCELECHAMLISYVNNRY
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                                      QESAQLFAELADVIRQGRRDEIGQVMQRYFLSLA
                                      EIMRQHMKDWESAEA"
     misc-feature    complement(173960..1741  /gene="STY3538"
                     18)
                                      /note="Pfam match to entry PF00392
                                      gntR, Bacterial regulatory
                                      proteins, gntR family, score
                                      44.90, E-value 2.5e-12"
     gene            complement(174274..1752  /gene="STY3539"
                     12)
                                      /note="synonym: mdh"
     CDS             complement(174274..1752  /gene="STY3539"
                     12)
                                      /note="Orthologue of E. coli mdh
                                      (MDH-ECOLI); Fasta hit to
                                      MDH-ECOLI (312 aa), 95% identity
                                      in 312 aa overlap"
                                      /codon-start=1
                                      /transl-table=11
                                      /product="malate dehydrogenase"
                                      /protein-id="CAD07874.1"
                                      /db-xref="GI:16504421"
                                      /db-xref="GOA:Q8Z3E0"
                                      /db-xref="SPTREMBL:Q8Z3E0"
                                      /translation="MKVAVLGAAGGIGQALALLL
                                      KNQLPSGSELSLYDIAPVTPGVAV
                                      DLSHIPTAVKIKGFSGEDATPALEGADVVLISAG
                                      VARKPGMDRSDLFNVNAGIVKNLV
                                      QQIAKTCPKACVGIITNPVNTTVAIAAEVLKKAG
                                      VYDKNKLFGVTTLDIIRSNTFVAE
                                      LKGKLPTEVEVPVIGGHSGVTILPLLSQIPGVSF
                                      TEQEAAELTKRIQNAGTEVVEAKA
                                      GGGSATLSMGQAAARFGLSLVRALQGEKGVVECA
                                      YVEGDGQYARFFSQPLLLGKNGVE
                                      ERKSIGTLSTFEQHSLDAMLDTLKKDIQLGEDFI
                                      NK"
     misc-feature    complement(174292..1752  /gene="STY3539"
                     09)
                                      /note="Pfam match to entry PF00056
                                      ldh, lactate/malate dehydrogenase,
                                      score 474.50, E-value 8.5e-139"
     misc-feature    complement(174739..1747  /gene="STY3539"
                     77)
                                      /note="PS00068 Malate
                                      dehydrogenase active site
                                      signature"
     gene            175626..176096   /gene="argR"
                                      /note="synonym: STY3540"
     CDS             175626..176096   /gene="argR"
                                      /note="Similar to Salmonella
                                      typhimurium arginine repressor
                                      argR SW:ARGR-SALTY (P37170) (156
                                      aa) fasta scores: E(): 0, 100.0%
                                      id in 156 aa, and to Escherichia
                                      coli arginine repressor argr or
                                      xerA SW:ARGR-ECOLI (P15282) (156
                                      aa) fasta scores: E(): 0, 94.9% id
                                      in 156 aa Orthologue of E. coli
                                      argR (ARGR-ECOLI); Fasta hit to
                                      ARGR-ECOLI (156 aa), 95% identity
                                      in 156 aa overlap"
                                      /codon-start=1
                                      /transl-table=11
                                      /product="arginine repressor"
                                      /protein-id="CAD07875.1"
                                      /db-xref="GI:16504422"
                                      /db-xref="GOA:P37170"
                                      /db-xref="SWISS-PROT:P37170"
                                      /translation="MRSSAKQEELVRAFKALLKE
                                      EKFSSQGEIVLALQDQGFENINQS
                                      KVSRMLTKFGAVRTRNAKMEMVYCLPAELGVPTT
                                      SSPLKNLVLDIDYNDAVVVIHTSP
                                      GAAQLIARLLDSLGKAEGILGTIAGDDTIFTTPA
                                      SGFSVRDLYEAILELFEQEL"
     misc-feature    175641..176093   /gene="argR"
```

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                                          Arg-repressor, Arginine repressor,
                                          score 391.80, E-value 6.7e-114"
     gene        176461..176724           /gene="STY3542"
     CDS         176461..176724           /gene="STY3542"
                                          /note="Fasta hit to YCFR-ECOLI (85
                                          aa), 34% identity in 88 aa overlap
                                          Fasta hit to YJFN-ECOLI (100 aa),
                                          34% identity in 93 aa overlap
                                          Fasta hit to YAHO-ECOLI (91 aa),
                                          31% identity in 91 aa overlap
                                          Fasta hit to YJFY-ECOLI (91 aa),
                                          33% identity in 87 aa overlap
                                          Fasta hit to YBIJ-ECOLI (86 aa),
                                          47% identity in 88 aa overlap
                                          Orthologue of E. coli YHCN-ECOLI;
                                          Fasta hit to YHCN-ECOLI (87 aa),
                                          78% identity in 87 aa overlap"
                                          /codon-start=1
                                          /transl-table=11
                                          /product="conserved hypothetical
                                          protein"
                                          /protein-id="CAD07876.1"
                                          /db-xref="GI:16504423"
                                          /db-xref="SPTREMBL:Q8Z3D9"
                                          /translation="MKIKTTVATLSILSVLSFGA
                                          FAAEPISAEQAQNREAIESVSVSA
                                          IGSSPMDMNAMLSKKADEQGATAYHITEARSGSN
                                          WHATAELYK"
     gene        176828..177094           /gene="STY3543"
     CDS         176828..177094           /gene="STY3543"
                                          /note="Fasta hit to YCFR-ECOLI (85
                                          aa), 34% identity in 89 aa overlap
                                          Fasta hit to YJFN-ECOLI (100 aa),
                                          34% identity in 93 aa overlap
                                          Fasta hit to YJFY-ECOLI (91 aa),
                                          30% identity in 86 aa overlap
                                          Fasta hit to YKGI-ECOLI (83 aa),
                                          35% identity in 80 aa overlap
                                          Fasta hit to YBIJ-ECOLI (86 aa),
                                          37% identity in 90 aa overlap
                                          Paralogue of E. coli YHCN-ECOLI;
                                          Fasta hit to YHCN-ECOLI (87 aa),
                                          53% identity in 88 aa overlap"
                                          /codon-start=1
                                          /transl-table=11
                                          /product="conserved hypothetical
                                          protein"
                                          /protein-id="CAD07877.1"
                                          /db-xref="GI:16504424"
                                          /db-xref="SPTREMBL:Q8XEN2"
                                          /translation="MKTKYIIASLGLATLLSFGA
                                          NAAVHQVNAEQAQNLQPMGTISVS
                                          QIGSTPMDMRQEIVAKAEKAGANSYRIIELKEGD
                                          NWHATAELYK"
     gene        complement(177154..1774  /gene="STY3544"
                 26)
     CDS         complement(177154..1774  /gene="STY3544"
                 26)
                                          /note="Orthologue of E. coli
                                          YHCO-ECOLI; Fasta hit to
                                          YHCO-ECOLI (90 aa), 77% identity
                                          in 90 aa overlap"
                                          /codon-start=1
                                          /transl-table=11
                                          /product="conserved hypothetical
                                          protein"
                                          /protein-id="CAD07878.1"
                                          /db-xref="GI:16504425"
                                          /db-xref="SPTREMBL:Q8XFF0"
                                          /translation="MNVYTFDFNDIKNQSDFYRE
                                          FTQTFGLASEKVSDLDTLWDAVMS
                                          DILPLPLEIEFVHLPDKLRRRYGALILLFDEAEE
                                          ELEGRLRFNVRH"
     gene        complement(177598..1795  /gene="STY3545"
                 65)
```

CDS	complement(177598..1795 65)	/gene="STY3545"

/note="Orthologue of E. coli yhcP
(YHCP-ECOLI); Fasta hit to
YHCP-ECOLI (655 aa), 92% identity
in 655 aa overlap. Contains
multiple possible membrane
spanning hydrophobic domains and a
possible N-terminal signal
sequence."
/codon-start=1
/transl-table=11
/product="putative membrane
protein"
/protein-id="CAD07879.1"
/db-xref="GI:16504426"
/db-xref="SPTREMBL:Q8Z3D8"
/translation="MGIFSIANQHIRFAVKLACA
IVLALFIGFHFQLETPRWAVLTAA
IVAAGPAFAAGGEPYSGAIRYRGMLRIIGTFIGC
IAALIIIISMIRAPLLMILVCCVW
AGFCTWISSLVRIENSYAWGLSGYTALIIVITIQ
TEPLLTPQFALERCSEIVIGIGCA
ILADLLFSPRSIKQEVDRELDCLLVAQYQLMQLC
IKHGDSEEVDNAWGDLVRRTAALE
GMRSNLNMESSRWVRANRRLKALNTLSLTLITQS
CETYLIQNTRPELITDTFRELFET
PVETVQDVHRQLKRMRRVIVWTGERETPVTLYSW
VGAATRYLLLKRGVISNTKISATE
EEILQGEPVVKVESAERHHAMVNFWRTTLSCILG
TLFWLWTGWTSGNGAMVMIAVVTS
LAMRLPNPRMVCIDFIYGTLAALPLGLLYFLVII
PNTQQSMLLLCLSLAVLGFFIGIE
VQKRRLGSMGALASTINIIVLDNPMTFHFIQFLD
SALGQIVGCMLAFIVILLVRDKSK
DRTGRVLLNQFVSAAVSAMTTNVVRRKENRLPAL
YQQLFLLMNKFPGDLPKFRLALTM
IIAHQRLRDAPIPVNEDLSVFHRQLRRTADHVIS
AGSDDKRRRYFGQLLDELDIYQEK
LRIWEAPPQVTEPVKRLTGMLHKYQNALTDS"

gene	complement(179571..1805 03)	/gene="STY3546"

/note="synonym: yhcQ"

CDS	complement(179571..1805 03)	/gene="STY3546"

/note="Fasta hit to YDHJ-ECOLI
(299 aa), 39% identity in 286 aa
overlap Fasta hit to YJCR-ECOLI
(343 aa), 30% identity in 337 aa
overlap Orthologue of E. coli yhcQ
(YHCQ-ECOLI); Fasta hit to
YHCQ-ECOLI (310 aa), 93% identity
in 310 aa overlap. Contains a
possible N-terminal signal
sequence."
/codon-start=1
/transl-table=11
/product="possible exported
protein"
/protein-id="CAD07880.1"
/db-xref="GI:16504427"
/db-xref="GOA:Q8XF83"
/db-xref="SPTREMBL:Q8XF83"
/translation="MKTLTRKLSRTAITLVLVIL
AFIAIFRAWVYYTESPWTRDARFS
ADVVAIAPDVAGLITHVNVHDNQLVKKDQVLFTI
DQPRYQKALAEAEADVAYYQVLAQ
EKRQEAGRRNRLGVQAMSREEIDQANNVLQTVLH
QLAKAQATRDLAKLDLERTVIRAP
ADGWVTNLNVYAGEFITRGSTAVALVKKNSFYVQ
AYMEETKLEGVRPGYRAEITPLGS
NRVLKGTVDSVAAGVTNASSTSDAKGMATIDSNL
EWVRLAQRVPVRIRLDEQQGNLWP
AGTTATVVITGKQDRDASQDSFFRKLAHRLREFG
"

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                                        /note="Pfam match to entry PF00529
                                        HlyD, HlyD family secretion
                                        protein, score 135.20, E-value
                                        1.2e-36"
gene            complement(180511..1807 /gene="STY3546a"
                14)
CDS             complement(180511..1807 /gene="STY3546a"
                14)
                                        /note="Similar to Escherichia coli
                                        hypothetical protein YhcR
                                        SW:YHCR-ECOLI (P46478) (90 aa)
                                        fasta scores: E(): 5.6e-29, 98.5%
                                        id in 67 aa"
                                        /codon-start=1
                                        /transl-table=11
                                        /product="conserved hypothetical
                                        protein"
                                        /protein-id="CAD07881.1"
                                        /db-xref="GI:16504428"
                                        /db-xref="SPTREMBL:Q8XEK3"
                                        /translation="MSLFPVIVVFGLSFPPIFFE
                                        LLLSLAIFWLVRRMLVPTGIYDFV
                                        WHPALFNTALYCCLFYLISRLFV"
gene            180896..181825          /gene="STY3547"
CDS             180896..181825          /gene="STY3547"
                                        /note="Fasta hit to YHJC-ECOLI
                                        (299 aa), 31% identity in 293 aa
                                        overlap Fasta hit to YAFC-ECOLI
                                        (304 aa), 31% identity in 290 aa
                                        overlap Fasta hit to YEAT-ECOLI
                                        (307 aa), 30% identity in 293 aa
                                        overlap Orthologue of E. coli
                                        YHCS-ECOLI; Fasta hit to
                                        YHCS-ECOLI (309 aa), 95% identity
                                        in 309 aa overlap"
                                        /codon-start=1
                                        /transl-table=11
                                        /product="probable LysR-family
                                        transcriptional regulator"
                                        /protein-id="CAD07882.1"
                                        /db-xref="GI:16504429"
                                        /db-xref="GOA:Q8XFH1"
                                        /db-xref="SPTREMBL:Q8XFH1"
                                        /translation="MERLKRMSVFAKVVEFGSFT
                                        AAARQLQMSVSSISQTVAKLEDEL
                                        QVKLLNRSTRSIGLTEAGKIYYQGCRRMLHEVQD
                                        VHEQLYAFNNTPIGTLRIGCSSTM
                                        AQNVLAGLTAKLLKEYPGLAVNLVTGIPAPDLIA
                                        DGLDVVIRVGALQDSSLFSRRLGA
                                        MPMVVCAAKPYLAQYGVPEKPADLSSHSWLEYSV
                                        RPDNEFELIAPEGISTRLIPQGRF
                                        VTNDPMTLRWLTAGTGIAYVPLMWVIDEINRGD
                                        LEILLPRYQSDPRPVYALYTEKDK
                                        LPLKVQVVINALTDYFVDVAHLFQGMHGRGKEK"
misc-feature    180905..181324          /gene="STY3547"
                                        /note="Pfam match to entry PF00126
                                        HTH-1, Bacterial regulatory
                                        helix-turn-helix protein, lysR
                                        family, score 170.30, E-value
                                        3.1e-47"
misc-feature    180947..181039          /gene="STY3547"
                                        /note="PS00044 Bacterial
                                        regulatory proteins, lysR family
                                        signature"
gene            complement(181948..1833 /gene="tldD"
                93)
                                        /note="synonym: STY3548"
CDS             complement(181948..1833 /gene="tldD"
                93)
                                        /note="Similar to Escherichia coli
                                        protein TldD which suppresses the
                                        inhibitory activity of the carbon
                                        storage regulator CsrA
                                        SW:TLDD-ECOLI (P46473) (481 aa)
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                                          481 aa"
                                          /codon-start=1
                                          /transl-table=11
                                          /product="TldD protein"
                                          /protein-id="CAD07883.1"
                                          /db-xref="GI:16504430"
                                          /db-xref="SPTREMBL:Q8XFQ3"
                                          /translation="MSLNLVSEQLLAANGLNHQD
                                          LFAILGQLAERRLDYGDLYFQSSY
                                          HESWVLEDRIIKDGSYNIDQGVGVRAISGEKTGF
                                          AYADQISLLALEQSAQAARTIVRE
                                          NGEGKVKTLAAVAHQPLYTTLDPLQSMSREEKLD
                                          ILRRVDKAAREADKRVQEVNASLT
                                          GVYELILVAATDGTLAADVRPLVRLSVSVQVEED
                                          GKRERGASGGGGRFGYEYFLADLD
                                          GEVRADAWAKEAVRMALVNLSAVAAPAGTLPVVL
                                          GAGWPGVLLHEAVGHGLEGDFNRR
                                          GTSVFSGQIGEQVASALCTVVDDGTMMNRRGSVA
                                          IDDEGTPGQYNVLIENGVLKGYMQ
                                          DKLNARLMGAAPTGNGRRESYAHLPMPRMTNTYM
                                          LAGQSTPQEIIESVEYGIYAPNFG
                                          GGQVDITSGKFVFSTSEAYLIENGKVTTPVKGAT
                                          LIGSGIETMQQISMVGNDLKLDNG
                                          VGVCGKEGQSLPVGVGQPTLKVDNLTVGGTA"
misc-feature        complement(182398..1832  /gene="tldD"
                    94)
                                          /note="Pfam match to entry PF01523
                                          PmbA-TldD, Putative modulator of
                                          DNA gyrase, score 385.30, E-value
                                          6.3e-112"
gene                complement(183538..1873  /gene="STY3549"
                    38)
CDS                 complement(183538..1873  /gene="STY3549"
                    38)
                                          /note="This CDS is similar to two
                                          adjoining E. coli hypothetical
                                          proteins. The N-terminus is
                                          similar to yhdR SW:YHDR-ECOLI
                                          (P46476) (282 aa) fasta scores:
                                          E(): 0, 82.0% id in 272 aa and the
                                          C-terminus is similar to yhdP
                                          SW:YHDP-ECOLI (P46474; P76676;
                                          P46475) (986 aa) fasta scores:
                                          E(): 0, 79.9% id in 987 aa.
                                          Contains a possible N-terminal
                                          signal sequence."
                                          /codon-start=1
                                          /transl-table=11
                                          /product="possible exported
                                          protein"
                                          /protein-id="CAD07884.1"
                                          /db-xref="GI:16504431"
                                          /db-xref="SPTREMBL:Q8Z3D7"
                                          /translation="MRRLPGILLLTGAALIVIAA
                                          LLVSGLRLALPHLDAWRPAILNKI
                                          ESVTGVPVAASQLSASWQNFGPTLEAHNIHAALK
                                          DGGELSIKRVTLALDVWQSLLHMR
                                          WQFRDLTFWQLNFRTNTPLQSSDGEGIETSRLSD
                                          LFLRQFDHFDLRDSQISFLTLSGQ
                                          RAELAIPQLTWLNGKERHRAEGEVSLSSLTGQHG
                                          VMQVRMDLRDDDGLLNNGRVWLQA
                                          DDIDVKPWLGKWMQDNVALQTARFSLEGWMTLSK
                                          GEIAGGDVWLKQGGASWLGDNTTH
                                          TLSVDNLTAQISREQPGWQFYIPDTRITLDGKPW
                                          PSGALTVAWLPQQDVGGENHTRSD
                                          ELRIRASNLELAGLEALRPLAAKLSPVLGEIWQA
                                          TQPSGKIATLALDIPLQATEKTRF
                                          QASWENLAWKQWKLLPGAEHFSGTLAGSVEDGQM
                                          KVAMQQAKMPYETVFRAPLEIENG
                                          VATLSWLKNENGFQLDGRDIDVKAKAVHARGGFR
                                          YLQPTGDEPWLGILAGISTDDGSQ
                                          AWRYFPENLMGKALVDYLSGAIQGGEADNATLVY
                                          GGNPHLFPYKHNEGQFEVLVPLRN
                                          ATFAFQPDWPALKNLNIELDFLNDGLWMRSDSVD
                                          LGGVKASKLAAAIPDYSKEKLLID
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                                        DVNARLHLDIPLDGEQVTAEGDVS
                                        LRNNSLFIKPLNSTLKNLNGKFSFVNGALKSGPL
                                        TANWFNQPLNLDFSTTEGAKAYQV
                                        AVNLNGNWQPTRMGVLPPQLNDALSGSVTWNGKV
                                        GIDLPYHADTTYHIELNGDLRNVS
                                        SHLPSPLNKPAGEAIPVNIQADGNLKSFALTGSA
                                        GSKNHFNSRWLLNQKLTLDRAIWT
                                        TDSRTIPPLPAQQGVELNLPALDGAQWLALFQKG
                                        AADNVSSSAEFPQRVTLRTPALSL
                                        GGQQWNNLSVVSAPSLNGTKIEAQGREVNATLLM
                                        RNHAPWLANIKYLYYNPGVAKTHA
                                        SSPTPTSPLASANTISFRGWPDLQLRCEECWLWG
                                        QKYGRIDGDFAIKGNTLTLANGLI
                                        DTGFARLKANGEWVNAPGNERTSLKGSLHGSNLD
                                        TAAGFFGISTPIQNASFNVDYDLH
                                        WRNPPCQPEEATLNGILRTRLGKGEFTDLSSGHA
                                        GQLLRLLSFDALLRKLRFDFRDTF
                                        SEGFYFDSIHSTAWIKDGVLHTDDTLVDGLEADI
                                        AMKGSVDLVRRRLDMEAVVAAEIS
                                        ATVGVAAAFAVNPIVGAAVFAASKVLGPLWSKVS
                                        ILRYRITGPVDAPQINEVLRQPRK ESQQ"
gene              complement(187449..1889    /gene="rnG"
                  18)
                                           /note="synonym: STY3550"
CDS               complement(187449..1889    /gene="rnG"
                  18)
                                           /EC-number="3.1.4.-"
                                           /note="Similar to Escherichia coli
                                           ribonuclease G cafA r rnG
                                           SW:RNG-ECOLI (P25537; P76677) (488
                                           aa) fasta scores: E(): 0, 96.7% id
                                           in 488 aa"
                                           /codon-start=1
                                           /transl-table=11
                                           /product="ribonuclease G"
                                           /protein-id="CAD07885.1"
                                           /db-xref="GI:16504432"
                                           /db-xref="GOA:Q8XGR0"
                                           /db-xref="SPTREMBL:Q8XGR0"
                                           /translation="MTAELLVNVTPSETRVAYID
                                           GGILQEIHIEREARRGIVGNIYKG
                                           RVSRVLPGMQAAFVDIGLDKAAFLHASDIMPHTE
                                           CVAGDEQKQFTVRDISELVRQGQD
                                           LMVQVVKDPLGTKGARLTTDITLPSRYLVFMPGA
                                           SHVGVSQRIESESERERLKKVVAE
                                           YCDEQGGFIIRTAAEGVCEEDLASDAAYLKRVWT
                                           KVMERKKRPQTRYQMYGELALAQR
                                           VLRDFADAQLDRIRVDSRLTYESLLEFTAEYIPE
                                           MTSKLEHYSGHQPIFDLYDVENEI
                                           QRALERKVELKSGGYLIIDQTEAMTTVDINTGAF
                                           VGHRNLDDTIFNTNIEATQAIARQ
                                           LRLRNLGGIIIIDFIDMNNEDHRRRVLHSLEQAL
                                           SKDRVKTSINGFSPLGLVEMTRKR
                                           TRESVEHVLCNECPTCHGRGTVKTVETVCYEIMR
                                           EIVRVHHAYDSDRFLVYASPAVAE
                                           ALKGEESHALAEVEIFVGKQVKVQVEPLYNQEQF
                                           DVVMM"
misc-feature      complement(188553..1888    /gene="rnG"
                  16)
                                           /note="Pfam match to entry PF00575
                                           S1, S1 RNA binding domain, score
                                           68.20, E-value 3.3e-17"
gene              complement(188908..1895    /gene="STY3551"
                  01)
                                           /note="synonym: yhdE"
CDS               complement(188908..1895    /gene="STY3551"
                  01)
                                           /note="Fasta hit to YCEF-ECOLI
                                           (207 aa), 38% identity in 185 aa
                                           overlap Orthologue of E. coli yhdE
                                           (YHDE-ECOLI); Fasta hit to
                                           YHDE-ECOLI (197 aa), 85% identity
                                           in 197 aa overlap"
                                           /codon-start=1
                                           /transl-table=11
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                                       protein"
                                       /protein-id="CAD07886.1"
                                       /db-xref="GI:16504433"
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                                       /translation="MTTLYLASGSPRRQELLIQL
                                       GFSFEQVVPGIEEQRRVQESAQQY
                                       VVRLAREKAQAGVALVPRDLPVLGADTIVVLNGE
                                       VLEKPRDAAHAAEMLRLLSGNTHQ
                                       VMTAVALADSQQTLDCLVVTEVTFRTLSAQDITG
                                       YVASGEPLDKAGAYGIQGRGGCFV
                                       RKINGSYHAVVGLPLVETYELLSHFNALRDKRDK
                                       HDG"
gene               complement(189510..1900  /gene="STY3552"
                   01)
                                       /note="synonym: mreD"
CDS                complement(189510..1900  /gene="STY3552"
                   01)
                                       /note="Orthologue of E. coli mreD
                                       (MRED-ECOLI); Fasta hit to
                                       MRED-ECOLI (162 aa), 94% identity
                                       in 162 aa overlap"
                                       /codon-start=1
                                       /transl-table=11
                                       /product="rod shape-determining
                                       protein"
                                       /protein-id="CAD07887.1"
                                       /db-xref="GI:16504434"
                                       /db-xref="SPTREMBL:Q8XGG6"
                                       /translation="MVASYRSQGRWVIWLSFLIA
                                       LLLQIMPWPDDIIVFRPNWVLLIL
                                       LYWILALPHRVNVGTGFVMGAILDLISGSTLGVR
                                       ALSMSIVAYLVALKFQLFRNLALW
                                       QQALVVMLLSLAVDIIVFWAEFLVINVSFRPEVF
                                       WSSVVNGVLWPWLFLLMRKVRQQF AVQ"
gene               complement(190001..1910  /gene="STY3553"
                   53)
                                       /note="synonym: mreC"
CDS                complement(190001..1910  /gene="STY3553"
                   53)
                                       /note="Orthologue of E. coli mreC
                                       (MREC-ECOLI); Fasta hit to
                                       MREC-ECOLI (367 aa), 91% identity
                                       in 349 aa overlap"
                                       /codon-start=1
                                       /transl-table=11
                                       /product="rod shape-determining
                                       protein"
                                       /protein-id="CAD07888.1"
                                       /db-xref="GI:16504435"
                                       /db-xref="SPTREMBL:Q8Z3D6"
                                       /translation="MKPIFSRGPSLQIRLILAVL
                                       VALGVIIADSRLGTFSQIRTYMDT
                                       AVSPFYFISNGPRELLDSVSQTLASRDQLELENR
                                       ALRQELLLKNSDLLMLGQYKQENA
                                       RLRELLGSPLRQDEQKMVTQVISTVNDPYSDQVV
                                       IDKGSVNGVYEGQPVISDKGVVGQ
                                       VVAVAKLTSRVLLICDATHALPIQVLRNDIRVIA
                                       AGNGCTDDLQLEHLPANTDIRVGD
                                       VLVTSGLGGRFPEGYPVAVVSSVKLDTQRAYTVI
                                       QARPTAGLQRLRYLLLLWGADRNG
                                       ANPMTPEEVHRVANERLMQMMPQVLPSPDAMGPP
                                       APVPDPATGITQPSAGQTTPVSTQ
                                       SSPSGATTPSARAPGG"
gene               complement(191118..1921  /gene="mreB"
                   61)
                                       /note="synonym: STY3554"
CDS                complement(191118..1921  /gene="mreB"
                   61)
                                       /note="Similar to Escherichia coli
                                       rod shape-determining protein MreB
                                       mreb SW:MREB-ECOLI (P13519;
                                       P76678) (347 aa) fasta scores:
                                       E(): 0, 100.0% id in 347 aa"
                                       /codon-start=1
                                       /transl-table=11
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                                      protein"
                                      /protein-id="CAD07889.1"
                                      /db-xref="GI:16504436"
                                      /db-xref="GOA:P13519"
                                      /db-xref="SWISS-PROT:P13519"
                                      /translation="MLKKFRGMFSNDLSIDLGTA
                                      NTLIYVKGQGIVLNEPSVVAIRQD
                                      RAGSPKSVAAVGHDAKQMLGRTPGNIAAIRPMKD
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                                      FMRPSPRVLVCVPVGATQVERRAIRESAQGAGAR
                                      EVFLIEEPMAAAIGAGLPVSEATG
                                      SMVVDIGGGTTEVAVISLNGVVYSSSVRIGGDRF
                                      DEAIINYVRRNYGSLIGEATAERI
                                      KHEIGSAYPGDEVREIEVRGRNLAEGVPRGFTLN
                                      SNEILEALQEPLTGIVSAVMVALE
                                      QCPPELASDISERGMVLTGGGALLRNLDRLLMEE
                                      TGIPVVVAEDPLTCVARGGGKALE
                                      MIDMHGGDLFSEE"
gene            complement(192469..1944  /gene="STY3555"
                09)
                                         /note="synonym: yhdA"
CDS             complement(192469..1944  /gene="STY3555"
                09)
                                         /note="Orthologue of E. coli yhdA
                                         (YHDA-ECOLI); Fasta hit to
                                         YHDA-ECOLI (646 aa), 84% identity
                                         in 646 aa overlap. Contains a
                                         possible N-terminal signal
                                         sequence."
                                         /codon-start=1
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                                         /product="putative lipoprotein"
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                                         /db-xref="GI:16504437"
                                         /db-xref="GOA:Q8Z3D5"
                                         /db-xref="SPTREMBL:Q8Z3D5"
                                         /translation="MRLTTKFSAFITLLTGLTIF
                                         VTLIGCSLSFYNAVQYKYVSRVQA
                                         TATAIDTHLVTHDIVSLTPQIDELMIASDIVRVD
                                         LLQGERSVYSHSRARGYRPAGTSD
                                         MYRELVVPLIKHPGMSLRLVYQDPMGNYFHSLIT
                                         TAPLTLAIGFIVLILFLSVRWLQR
                                         QLSGQELLEIRSTRILNGERGANVRGSVYEWPAR
                                         TSSALDVLLSEIQFAHEQRSRLDT
                                         LIRSYAAQDTKTGLGNRLFFDNQLATLLEDQEKV
                                         GVHGVVMMIRLPDFNLLRDSLGGN
                                         QAEEQMFMLINLLSTFIMRYPGSLLARYHRSDFA
                                         VLLPHRTLKEAESIAGQLLKAVDA
                                         LPANKMLDRDDMVHIGICAWRSGQSTDQVMEHAE
                                         AAARNAALQGGNSWAIYDDTLPEK
                                         GRGNVRWRTLIEQMLNRGGPRLYQKPAVTREGRV
                                         HHRELMCRIYDGKEEVSSAEYMPM
                                         VLQFGLSEEYDRLQISRLITLLGYWPDENLAMQL
                                         TVESLIRPRFQRWLRDTLMQCEKS
                                         QRNRIIIELAEADVCQHISRLQPILRLVNALGVR
                                         VAVTQAGLTLVSTSWIKALNVELL
                                         KLHPSLVRNIEKRTENQLLVQSLVEACAGTPTQV
                                         YATGVRSRGEWQTLTKRGVAGGQG
                                         DFFASSQLLDTNVKKYSQRYSV"
misc-feature    complement(192505..1932  /gene="STY3555"
                27)
                                         /note="Pfam match to entry PF00563
                                         DUF2, Domain of unknown function
                                         2, score 392.30, E-value 4.6e-114"
misc-feature    complement(193267..1937  /gene="STY3555"
                61)
                                         /note="Pfam match to entry PF00990
                                         DUF9, Domain of unknown function
                                         DUF9, score 109.70, E-value
                                         5.7e-29"
misc-feature    complement(194332..1943  /gene="STY3555"
                64)
                                         /note="PS00013 Prokaryotic
                                         membrane lipoprotein lipid
                                         attachment site"
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CDS	194613..195587	/note="synonym: yhdH" /gene="STY3556" /note="Orthologue of E. coli yhdH (YHDH-ECOLI); Fasta hit to YHDH-ECOLI (324 aa), 89% identity in 323 aa overlap" /codon-start=1 /transl-table=11 /product="possible oxidoreductase" /protein-id="CAD07891.1" /db-xref="GI:16504438" /db-xref="GOA:Q8XG63" /db-xref="SPTREMBL:Q8XG63" /translation="MQALILEQQDGKTLASVQHL EESQLPAGDVTVDVHWSSLNYKDA LAITGKGKIIRHFPMIPGIDFAGTVHASEDPRFH AGQEVLLTGWGVGENHWGGLAERA RVKGDWLVALPAGLSSRNAMIIGTAGFTAMLCVM ALEDAGIRPQDGEVVVTGASGGVG STAVALLHKLGYQVAAVSGRESTHGYLKSLGANR ILSRDEFAESRPLEKQLWAGAIDT VGDKVLAKVLAQMNYGGCVAACGLAGGFALPTTV MPFILRNVRLQGVDSVMTPPARRA EAWARLVKDLPESFYAQAATEITLADAPKFADAI INNQVQGRTLVKIK"
misc-feature	194652..195581	/gene="STY3556" /note="Pfam match to entry PF00107 adh-zinc, Zinc-binding dehydrogenases, score 118.50, E-value 1.2e-31"
misc-feature	194964..195011	/gene="STY3556" /note="PS00038 Myc-type, 'helix-loop-helix' dimerization domain signature"
gene	195700..196704	/gene="STY3557"
CDS	195700..196704	/gene="STY3557" /note="Orthologue of E. coli P76342; Fasta hit to P76342 (334 aa), 88% identity in 334 aa overlap" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAD07892.1" /db-xref="GI:16504439" /db-xref="GOA:Q8XES1" /db-xref="SWISS-PROT:Q8XES1" /translation="MKKIRPLTEADVTAESAFFM QRRQVLKALGISAAALSLPSTAQA DLFSWFKGNDRPKAPAGKPLEFSQPAAWRSDLAL TPEDKVTGYNNFYEFGLDKADPAA NAGSLKTEPWTLKISGEVAKPFTLDYDDLTHRFP LEERIYRMRCVEAWSMVVPWIGFP LYKLLAQAQPTSHAKYVAFETLYAPDDMPGQKDR FIGGGLKYPYVEGLRLDEAMHPLT LMTVGVYGKALPPQNGAPIRLIVPWKYGFKGIKS IVSIKLTRERPPTTWNLSAPNEYG FYANVNPHVDHPRWSQATERFIGSGGILDVQRQP TLLFNGYANEVASLYRGLNLRENF "
gene	196705..197304	/gene="STY3558"
CDS	196705..197304	/gene="STY3558" /note="Orthologue of E. coli P76343; Fasta hit to P76343 (211 aa), 85% identity in 195 aa overlap" /codon-start=1 /transl-table=11 /product="putative membrane protein" /protein-id="CAD07893.1" /db-xref="GI:16504440" /db-xref="GOA:Q8Z3D4" /db-xref="SWISS-PROT:Q8Z3D4" /translation="MRLTVKQITWLKVCLHLAGF

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                                              HFTGRTALKFLLATLLVSPLARYAKQPLLIRTRR
                                              LLGLWCFVWATLHLTSYALLELGI
                                              HNLALLGSELISRPYLTLGIISWLVLLALTLTST
                                              QFAQRKLGKRWQTLHNVVYLVAIL
                                              APIHYLWSVKILSPQPVIYAALALALLALRYRKF
                                              RQWWR"
gene            197698..198168                /gene="STY3559"
                                              /note="synonym: accB"
CDS             197698..198168                /gene="STY3559"
                                              /note="Orthologue of E. coli accB
                                              (BCCP-ECOLI); Fasta hit to
                                              BCCP-ECOLI (156 aa), 93% identity
                                              in 156 aa overlap"
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                                              /transl-table=11
                                              /product="biotin carboxyl carrier
                                              protein"
                                              /protein-id="CAD07894.1"
                                              /db-xref="GI:16504441"
                                              /db-xref="GOA:Q8XGD9"
                                              /db-xref="SPTREMBL:Q8XGD9"
                                              /translation="MDIRKIKKLIELVEESGISE
                                              LEISEGEESVRISRTTANAGFPVM
                                              QQAYAAPMMQQPALSNAVAPAATPAMEAPAAAEI
                                              SGHIVRSPMVGTFYRTPSPDAKAF
                                              IEVGQKVNVGDTLCIVEAMKMMNQIEADKAGTVK
                                              AILVESGQPVEFDEPLVVIE"
misc-feature    197938..198162                /gene="STY3559"
                                              /note="Pfam match to entry PF00364
                                              biotin-lipoyl, Biotin-requiring
                                              enzymes, score 131.30, E-value
                                              1.7e-35"
misc-feature    198031..198084                /gene="STY3559"
                                              /note="PS00188 Biotin-requiring
                                              enzymes attachment site"
gene            198179..199528                /gene="STY3560"
                                              /note="synonym: accC"
CDS             198179..199528                /gene="STY3560"
                                              /note="Orthologue of E. coli accC
                                              (ACCC-ECOLI); Fasta hit to
                                              ACCC-ECOLI (449 aa), 97% identity
                                              in 449 aa overlap"
                                              /codon-start=1
                                              /transl-table=11
                                              /product="biotin carboxylase"
                                              /protein-id="CAD07895.1"
                                              /db-xref="GI:16504442"
                                              /db-xref="GOA:Q8XF58"
                                              /db-xref="SPTREMBL:Q8XF58"
                                              /translation="MLDKIVIANRGEIALRILRA
                                              CKELGIKTVAVHSSADRDLKHVLL
                                              ADETVCIGPAPSVKSYLNIPAIISAAEITGAVAI
                                              HPGYGFLSENANFAEQVERSGFIF
                                              IGPKADTIRLMGDKVSAITAMKKAGVPTVPGSDG
                                              PLGDDMNANRAHAKRIGYPVIIKA
                                              SGGGGGRGMRVVRSDAELAQSISMTKAEAKAAFS
                                              NDMVYMEKYLENPRHIEIQVLADG
                                              QGNAIYLAERDCSMQRRHQKVVEEAPAPGITPEL
                                              RRYIGERCAKACVDIGYRGAGTFE
                                              FLFENGEFYFIEMNTRIQVEHPVTEMITGVDLIK
                                              EQLRIAAGQPLSITQDEVVVRGHA
                                              VECRINAEDPNTFLPSPGKITRFHAPGGFGVRWE
                                              SHIYAGYTVPPYYDSMIGKLICYG
                                              ENRDVAIARMKNALQELIIDGIKTNIDLQTRIMN
                                              DEHFQHGGTNIHYLEKKLGLQEK"
misc-feature    198188..199288                /gene="STY3560"
                                              /note="Pfam match to entry PF00289
                                              CPSase-L-chain,
                                              Carbamoyl-phosphate synthase
                                              (CPSase), score 710.50, E-value
                                              7.6e-210"
misc-feature    198638..198682                /gene="STY3560"
                                              /note="PS00866 Carbamoyl-phosphate
                                              synthase subdomain signature 1"
misc-feature    199034..199057                /gene="STY3560"
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gene	199637..199879	synthase subdomain signature 2" /gene="STY3561"
CDS	199637..199879	/gene="STY3561" /note="Similar to Escherichia coli hypothetical protein YhdT SW:YHDT-ECOLI (P45566) (80 aa) fasta scores: E(): 5.2e-30, 85.0% id in 80 aa, and to Haemophilus influenzae hypothetical protein HI0974.1 SW:YHDT-HAEIN (P46455) (85 aa) fasta scores: E(): 9.1e-12, 41.0% id in 78 aa" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAD07896.1" /db-xref="GI:16504443" /db-xref="SPTREMBL:Q8Z3D3" /translation="MDARFVQAHKEARWALWLTL CYLAAWLVAAYLSGDSPGITGLPH WFEMACLLTPLVFILLCWAMVKFIYRDIPLEDDD AA"
gene	199869..201320	/gene="STY3562" /note="synonym: panF"
CDS	199869..201320	/gene="STY3562" /note="Orthologue of E. coli panF (PANF-ECOLI); Fasta hit to PANF-ECOLI (483 aa), 94% identity in 483 aa overlap" /codon-start=1 /transl-table=11 /product="sodium/pantothenate symporter (pantothenate permease)" /protein-id="CAD07897.1" /db-xref="GI:16504444" /db-xref="GOA:Q8Z3D2" /db-xref="SPTREMBL:Q8Z3D2" /translation="MQLEVILPLVAYLVVVFGVS IYAMRKRTAGTFLNEYFLGSRSMG GIVLAMTLTATYISASSFIGGPGAAYKYGLGWVL LAMIQLPAVWLSLGILGKKFAILA RRYNAVTLNDMLFARYQSRLLVWLASLSLLVAFI GAMTVQFIGGARLLETAAGIPYET GLLIFGVSIALYTAFGGFRASVLNDTLQGLVMLV GTIVLLVGVVHAAGGLHQAVDTLH ALDPKLVTPQGADDILSPAFMTSFWVLVCFGVIG LPHTAVRCISYKDSKAVHRGIIIG TIVVAILMFGMHLAGALGRAVLPDLTVPDLVIPT LMVKVLPPFAAGIFLAAPMAAIMS TINAQLLQSSATIIKDLYLNLRPDQMQNEIRLKR MSAAITLLLGALLLLAAWKPPEMI IWLNLLAFGGLEAVFLWPLVLGLYWERANAAGAL SAMIVGGVLYALLATFNIQYLGFH PIVPALLLSLLAFLIGNRFGSSASQATVLSTDK"
misc-feature	199974..201164	/gene="STY3562" /note="Pfam match to entry PF00474 SSF, Sodium:solute symporter family, score 663.00, E-value 1.5e-195"
misc-feature	200331..200408	/gene="STY3562" /note="PS00456 Sodium:solute symporter family signature 1"
misc-feature	201108..201170	/gene="STY3562" /note="PS00457 Sodium:solute symporter family signature 2"
gene	201332..202213	/gene="STY3563" /note="synonym: prmA"
CDS	201332..202213	/gene="STY3563" /note="Orthologue of E. coli prmA (PRMA-ECOLI); Fasta hit to PRMA-ECOLI (293 aa), 96% identity in 292 aa overlap" /codon-start=1 /transl-table=11

```
                                        methyltransferase"
                                        /protein-id="CAD07898.1"
                                        /db-xref="GI:16504445"
                                        /db-xref="GOA:Q8XGI2"
                                        /db-xref="SPTREMBL:Q8XGI2"
                                        /translation="MPWIQLKLNTTGANAEELSD
                                        ALMEAGAVSITFQDTHDTPVFEPL
                                        PGETRLWGDTDVIGLFDAETDMKDVVAILEQHPL
                                        LGAGFAHKIEQLEDKDWEREWMDN
                                        FHPMRFGERLWICPSWRDIPDENAVNVMLDPGLA
                                        FGTGTHPTTSLCLQWLDGLDLNGK
                                        TVIDFGCGSGILAIAALKLGAAKAIGIDIDPQAI
                                        QASRDNAERNGVSDRLELYLPKDQ
                                        PEAMKADVVVANILAGPLRELAPLISVLPVEGGL
                                        LGLSGILASQAESVCDAYAELFTL
                                        DPVVEKEEWCRITGRKK"
gene          202993..203838            /gene="STY3564"
                                        /note="synonym: yhdG"
CDS           202993..203838            /gene="STY3564"
                                        /note="Fasta hit to YOHI-ECOLI
                                        (315 aa), 31% identity in 255 aa
                                        overlap Orthologue of E. coli yhdG
                                        (YHDG-ECOLI); Fasta hit to
                                        YHDG-ECOLI (321 aa), 96% identity
                                        in 281 aa overlap"
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                                        protein"
                                        /protein-id="CAD07899.1"
                                        /db-xref="GI:16504446"
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                                        /db-xref="SPTREMBL:Q8Z3D1"
                                        /translation="MMSSNPQVWESDKSRLRMVH
                                        VDEPGIRTVQIAGSDPVEMADAAR
                                        INVESGAQIIDINMGCPAKKVNRKLAGSALLQYP
                                        DLVKSILIGVVNAVDVPVTLKIRT
                                        GWAPEHRNCVEIAQLAEDCGIQALTIHGRTRACL
                                        FNGEAEYDSIRAVKQKVSIPIIAN
                                        GDITNPHKARAVLDYTGADALMIGRAAQGRPWIF
                                        REIQHYLDTGELLPPLPLAEVKRL
                                        LCTHVRELHDFYGQAKGYRIARKHVSWYLQEHAP
                                        DDQFRRTFNAIEDASEQLEALEAY FENFA"
misc-feature  202993..203835            /gene="STY3564"
                                        /note="Pfam match to entry PF01207
                                        UPF0034, Uncharacterized protein
                                        family UPF0034, score 416.60,
                                        E-value 2.4e-121"
misc-feature  203152..203208            /gene="STY3564"
                                        /note="PS01136 Uncharacterized
                                        protein family UPF0034 signature"
gene          203864..204160            /gene="STY3565"
                                        /note="synonym: fis"
CDS           203864..204160            /gene="STY3565"
                                        /note="Orthologue of E. coli fis
                                        involved in regulation and
                                        activation of upstream rRNA
                                        promoters and Hin-mediated DNA
                                        inversion (FIS-ECOLI); Fasta hit
                                        to FIS-ECOLI (98 aa), 100%
                                        identity in 98 aa overlap"
                                        /codon-start=1
                                        /transl-table=11
                                        /product="Fis DNA-binding protein"
                                        /protein-id="CAD07900.1"
                                        /db-xref="GI:16504447"
                                        /db-xref="GOA:P11028"
                                        /db-xref="SWISS-PROT:P11028"
                                        /translation="MFEQRVNSDVLTVSTVNSQD
                                        QVTQKPLRDSVKQALKNYFAQLNG
                                        QDVNDLYELVLAEVEQPLLDMVMQYTRGNQTRAA
                                        LMMGINRGTLRKKLKKYGMN"
gene          204246..205130            /gene="STY3566"
                                        /note="synonym: yhdJ"
CDS           204246..205130            /gene="STY3566"
```

(YHDJ-ECOLI); Fasta hit to
YHDJ-ECOLI (294 aa), 80% identity
in 283 aa overlap"
/codon-start=1
/transl-table=11
/product="putative
adenine-specific DNA-modification
methylase"
/protein-id="CAD07901.1"
/db-xref="GI:16504448"
/db-xref="GOA:Q8XF74"
/db-xref="SPTREMBL:Q8XF74"
/translation="MKAECEPQYFGDESKKIIHG
DALTELKKLPSESIDLIFADPPYN
IGKDFDGMVESWDEASFLAWLYECIDECHRVLKK
HGTMYIMNSTENMPYIDLKCRTLF
TIKSRIVWSYDSSGVQAKKYFGSMYEPILMMVKN
PKSYTFNRDAILVETTTGAKRALI
DYRKNPPQPYNQKKVPGNVWSFPRVRYLMDEYEN
HPTQKPSALLKRIILASSNPSDTV
LDPFAGSFTTGAVAAASGRKFIGIELNNEYVKMG
LRRLSVTSHYSENELAKVKKRKTQ
NLSKKQRNVGINALSSEK"

misc-feature	204354..204374	/gene="STY3566"

/note="PS00092 N-6
Adenine-specific DNA methylases
signature"

misc-feature	204459..205013	/gene="STY3566"

/note="Pfam match to entry PF01555
N6-N4-Mtase, DNA methylase, score
203.70, E-value 2.9e-57"

gene	205528..207138	/gene="STY3568"
CDS	205528..207138	/gene="STY3568"

/note="Similar in parts to several
e.g. Synechocystis sp nitrogen
fixation positive activator
protein nifL TR:P72843
(EMBL:D90901) (840 aa) fasta
scores: E(): 0, 44.1% id in 279
aa. Contains multiple possible
membrane spanning hydrophobic
domains and a possible N-terminal
signal sequence. Contains
C-terminal deletion relative to S.
typhimurium"
/codon-start=1
/transl-table=11
/product="putative exported
protein"
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/db-xref="GI:16504449"
/db-xref="GOA:Q8Z3D0"
/db-xref="SPTREMBL:Q8Z3D0"
/translation="MPVSEYNHILVAVSFAVAIF
ASYTALNMAGRVAGSARSNARIWL
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TGLSMLIAIGSSLFALWLVSAEKL
RLRRLLPGALVMGLGISAMHYTGMAALQFASIIV
WNSAWVALSIIIALLASCGALWLT
FRLRNEGTDVALRRAGAAVLMGIAIAGMHYAGMK
AAHFPQNWPMEHRGVDSNWLAVLV
SVVALTILGITLLVSLFDARLQARTALLASSLAQ
ANQELAQLALHDTLTRLPNRVLLE
DRLEQAISKANRESTSFALLFMDLDGFKAVNDAY
GHDIGDKLLVAVTHRLNQPLSGQF
TLARIGGDEFVLLAEVSAPDEAASLASALVHSID
APFTIDPYELVVTLSVGIALYPLD
GKNERELMFNADAAMYHTKHTGRNGYHFFQPSMN
MLAQTQLQLMNDLWLALERQELRL
VYQPKFQAPAGPIVGFEALLRWYHPKQGVLNPDQ
FLPLAEKTGLIVTIGSWVIDEACR
QLREWHLQGYALWSVAVTGNGKWSGLPD"

misc-feature	206287..206778	/gene="STY3568"

/note="Pfam match to entry PF00990
DUF9, Domain of unknown function

		8.2e-59"
gene	207104..207529	/gene="acrE"
		/note="synonym: STY3569"
		/pseudo
CDS	207104..207529	/gene="acrE"
		/note="This CDS appears to be a gene remnant which is highly similar to the very C-terminus of Escherichia coli acriflavin resistance protein E precursor acrE or envC SW:ACRE-ECOLI (P24180) (385 aa) fasta scores: E(): 0, 88.8% id in 134 aa"
		/pseudo
		/codon-start=1
		/transl-table=11
		/product="acriflavin resistance protein E (pseudogene)"
		/db-xref="PSEUDO:CAD07903.1"
		/db-xref="REMTREMBL:CAD07903"
gene	207541..210655	/gene="acrF"
		/note="synonym: STY3570"
		/pseudo
CDS	207541..210655	/gene="acrF"
		/note="Similar to Escherichia coli acriflavin resistance protein f acrF or envD SW:ACRF-ECOLI (P24181) (1034 aa) fasta scores: E(): 0, 89.7% id in 906 aa. There is a frameshift mutation after codon 906. The sequence has been checked and is believed to be correct Fasta hit to ACRB-ECOLI (1049 aa), 80% identity in 907 aa overlap Fasta hit to YHIV-ECOLI (1037 aa), 70% identity in 906 aa overlap Fasta hit to ACRD-ECOLI (1037 aa), 63% identity in 907 aa overlap Paralogue of E. coli acrF (ACRF-ECOLI); Fasta hit to ACRF-ECOLI (1034 aa), 90% identity in 906 aa overlap"
		/pseudo
		/codon-start=1
		/transl-table=11
		/product="acriflavin resistance protein F (pseudogene)"
misc-feature	207541..210258	/gene="acrF"
		/note="Pfam match to entry PF00873 ACR-tran, AcrB/AcrD/AcrF family, score 1760.20, E-value 0"
		/pseudo
misc-feature	210290..210628	/gene="acrF"
		/note="Pfam match to entry PF00873 ACR-tran, AcrB/AcrD/AcrF family, score 232.80, E-value 4.8e-66"
		/pseudo
gene	210892..211113	/gene="STY3572"
		/note="synonym: yhdV"
CDS	210892..211113	/gene="STY3572"
		/note="Orthologue of E. coli yhdV (YHDV-ECOLI); Fasta hit to YHDV-ECOLI (73 aa), 99% identity in 73 aa overlap. Contains a possible N-terminal signal sequence"
		/codon-start=1
		/transl-table=11
		/product="possible lipoprotein"
		/protein-id="CAD07905.1"
		/db-xref="GI:16504450"
		/db-xref="SPTREMBL:Q8XG38"
		/translation="MKRLIPVALLTTLLAGCAHD SPCVPVYDDQGRLVHTNTCMKGTT QDNWETAGAIAGGAAAVAGLTMGIIALSK"

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                                  trk system potassium uptake
                                  protein TrkH SW:TRKH-ECOLI
                                  (P21166; P76769) (483 aa) fasta
                                  scores: E(): 0, 97.1% id in 483 aa
                                  Fasta hit to TRKG-ECOLI (485 aa),
                                  41% identity in 481 aa overlap"
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                                  /transl-table=11
                                  /product="trk system potassium
                                  uptake protein"
                                  /protein-id="CAD07907.1"
                                  /db-xref="GI:16504452"
                                  /db-xref="GOA:Q8Z3C8"
                                  /db-xref="SPTREMBL:Q8Z3C8"
                                  /translation="MHFRAITRIVGLLVILFSGT
                                  MILPGLVALIYRDGAGGAFTQTFF
                                  VALAIGSILWWPNRREKGELKSREGFLIVVLFWT
                                  VLGSVGALPFIFSESPNLTITDAF
                                  FESFSGLTTTGATTLVGLDSLPHAILFYRQMLQW
                                  FGGMGIIVLAVAILPVLGVGGMQL
                                  YRAEMPGPLKDNKMRPRIAETAKTLWLIYVLLTV
                                  ACALALWFAGMPAFDAIGHSFSTI
                                  AIGGFSTHDASVGYFDSPTINTIIAIFLLISGCN
                                  YGLHFSLLSGRSLKVYWRDPEFRM
                                  FIGVQLTLVVICTLVLWFHNIYDSALTTLNQAFF
                                  QVVSMATTAGFTTDSIARWPLFLP
                                  VLLLCSAFIGGCAGSTGGGLKVIRILLLFKQGNR
                                  ELKRLVHPNAVYSIKLGNRALPER
                                  ILEAVWGFFSAYALVFIVSMLAIIATGVDDFSAF
                                  ASVVATLNNLGPGLGVVADNFASM
                                  NPVAKWILIANMLFGRLEVFTLLVLFTPTFWRE"
gene            complement(219869..2204   /gene="STY3575"
                83)
                                  /note="synonym: yigZ"
CDS             complement(219869..2204   /gene="STY3575"
                83)
                                  /note="Orthologue of E. coli yigZ
                                  (YIGZ-ECOLI); Fasta hit to
                                  YIGZ-ECOLI (205 aa), 91% identity
                                  in 204 aa overlap"
                                  /codon-start=1
                                  /transl-table=11
                                  /product="conserved hypothetical
                                  protein"
                                  /protein-id="CAD07908.1"
                                  /db-xref="GI:16504453"
                                  /db-xref="GOA:Q8Z3C7"
                                  /db-xref="SPTREMBL:Q8Z3C7"
                                  /translation="MDSWLIPAAPVTVVEEIKKS
                                  RFITLLAHTDGVEAAKAFVELVRA
                                  EHPDARHHCAAWVAGAPDDSQQLGFSDDGEPAGT
                                  AGKPMLAQLMGSGVGEITAVVVRY
                                  YGGILLGTGGLVKAYGGGVNQALRQLATQRKTPL
                                  TEYTLQCEYGQLAGIEALLGQFAG
                                  KIVSSDYQASVRLRVALPFAHVNAFSTKLADFSR
                                  GSLQLLAIEE"
misc-feature    complement(219872..2204   /gene="STY3575"
                11)
                                  /note="Pfam match to entry PF01205
                                  UPF0029, Uncharacterized protein
                                  family UPF0029, score 326.60,
                                  E-value 2.9e-94"
misc-feature    complement(220157..2202   /gene="STY3575"
                46)
                                  /note="PS00910 Uncharacterized
                                  protein family UPF0029 signature"
gene            complement(220483..2218   /gene="STY3576"
                14)
                                  /note="synonym: pepQ"
CDS             complement(220483..2218   /gene="STY3576"
                14)
                                  /note="Orthologue of E. coli pepQ
                                  (PEPQ-ECOLI); Fasta hit to
                                  PEPQ-ECOLI (443 aa), 96% identity
                                  in 443 aa overlap"
```

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                                    /transl-table=11
                                    /product="proline dipeptidase"
                                    /protein-id="CAD07909.1"
                                    /db-xref="GI:16504454"
                                    /db-xref="GOA:Q9L6L4"
                                    /db-xref="SPTREMBL:Q9L6L4"
                                    /translation="MESLAALYKNHIVTLQERTR
                                    DVLARFKLDALLIHSGELFNVFLD
                                    DHPYPFKVNPQFKAWVPVTQVPNCWLLVDGVNKP
                                    KLWFYLPVDYWHNVEPLPTSFWTE
                                    EVEVVALPKADGIGSQLPAARGNIGYIGPVPERA
                                    LQLDIAASNINPKGVIDYLHYYRA
                                    YKTDYELACMREAQKMAVSGHRAAEEAFRSGMSE
                                    FDINLAYLTATGHRDTDVPYSNIV
                                    ALNEHAAVLHYTKLDHQAPSEMRSFLLDAGAEYN
                                    GYAADLTRTWSAKSDNDYAHLVKD
                                    VNDEQLALIATMKAGVSYVDYHIQFHQRIAKLLR
                                    KHQIITDMSEEAMVENDLTGPFMP
                                    HGIGHPLGLQVHDVAGFMQDDSGTHLAAPSKYPY
                                    LRCTRVLQPRMVLTIEPGIYFIES
                                    LLAPWREGPFSKHFNWQKIEALKPFGGIRIEDNV
                                    VIHENGVENMTRDLKLA"
misc-feature      complement(220513..2213  /gene="STY3576"
                  37)
                                    /note="Pfam match to entry PF00557
                                    Peptidase-M24, metallopeptidase
                                    family M24, score 346.70, E-value
                                    2.6e-100"
misc-feature      complement(220774..2208  /gene="STY3576"
                  12)
                                    /note="PS00491 Aminopeptidase P
                                    and proline dipeptidase signature"
gene              222004..224193          /gene="STY3577"
                                    /note="synonym: fadB"
CDS               222004..224193          /gene="STY3577"
                                    /note="Fasta hit to YFCX-ECOLI
                                    (714 aa), 36% identity in 684 aa
                                    overlap Orthologue of E. coli fadB
                                    (FADB-ECOLI); Fasta hit to
                                    FADB-ECOLI (729 aa), 95% identity
                                    in 729 aa overlap"
                                    /codon-start=1
                                    /transl-table=11
                                    /product="large (alpha) subunit of
                                    the fatty acid-oxidizing
                                    multienzyme complex"
                                    /protein-id="CAD07910.1"
                                    /db-xref="GI:16504455"
                                    /db-xref="GOA:Q8Z3C6"
                                    /db-xref="SWISS-PROT:Q8Z3C6"
                                    /translation="MLYKGDTLYLDWLEDGIAEL
                                    VFDAPGSVNKLDTATVASLGQALE
                                    VLEKQHDLKGLLLRSNKAAFIVGADITEFLSLFL
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                                    VPTLAAVNGYALGGGCECVLATDYRLATPDLRIG
                                    LPETKLGIMPGFGGSVRLPRMLGA
                                    DSALEIIAAGKDVGAEHALKIGLVDGVVKQEKLI
                                    EGAIAVLRQAITGDLDWRAKRQPK
                                    LEPLKLSKIEAAMSFTIAKGMVAQTAGKHYPAPM
                                    TAVKTIEAAARFGREEALNLENKS
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                                    ETPKQAAVLGAGIMGGGIAYQSAW
                                    KGVPVIMKDINDKSLNLGMTEAAKLLNKQLERGK
                                    IDGLKLAGVISTIHPTLDYAGFDR
                                    VDVVVEAVVENPKVKKAVLAETEQKVRPETVLAS
                                    NTSTIPIGELASALERPENFCGMH
                                    FFNPVHRMPLVEIIRGEKSSDETIAKVVAWASKM
                                    GKTPIVVNNCPGFFVNRVLFPYFA
                                    GFSQLLRDGADFRKVDKVMEKQFGWPMGPAYLLD
                                    VVGIDTAHHAQAVMAAGFPQRMQK
                                    EYRDAIDALFDASRFGQKNGLGFWRYKEDSKGKP
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                                    DEIIARMMIPMINEVVRCLEEGIIASPAEADMAL
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```

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misc-feature     222055..222570          /gene="STY3577"
                                         /note="Pfam match to entry PF00378
                                         ECH, Enoyl-CoA hydratase/isomerase
                                         family, score 300.70, E-value
                                         1.7e-86"
misc-feature     222319..222381          /gene="STY3577"
                                         /note="PS00166 Enoyl-CoA
                                         hydratase/isomerase signature"
misc-feature     222325..222357          /gene="STY3577"
                                         /note="PS00013 Prokaryotic
                                         membrane lipoprotein lipid
                                         attachment site"
misc-feature     222949..223779          /gene="STY3577"
                                         /note="Pfam match to entry PF00725
                                         3HCDH, 3-hydroxyacyl-CoA
                                         dehydrogenase, score 579.90,
                                         E-value 1.6e-170"
misc-feature     223480..223554          /gene="STY3577"
                                         /note="PS00067 3-hydroxyacyl-CoA
                                         dehydrogenase signature"
gene             224203..225366          /gene="STY3578"
                                         /note="synonym: fadA"
CDS              224203..225366          /gene="STY3578"
                                         /note="Fasta hit to ATOB-ECOLI
                                         (394 aa), 44% identity in 401 aa
                                         overlap Fasta hit to YQEF-ECOLI
                                         (393 aa), 41% identity in 401 aa
                                         overlap Fasta hit to P77525 (401
                                         aa), 46% identity in 404 aa
                                         overlap Fasta hit to YFCY-ECOLI
                                         (436 aa), 35% identity in 428 aa
                                         overlap Orthologue of E. coli fadA
                                         (THIK-ECOLI); Fasta hit to
                                         THIK-ECOLI (387 aa), 95% identity
                                         in 387 aa overlap"
                                         /codon-start=1
                                         /transl-table=11
                                         /product="small (beta) subunit of
                                         the fatty acid-oxidizing
                                         multienzyme complex"
                                         /protein-id="CAD07911.1"
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                                         /db-xref="GOA:Q9L6L6"
                                         /db-xref="SWISS-PROT:Q9L6L6"
                                         /translation="MEQVVIVDAIRTPMGRSKGG
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                                         PHSVPAVTVNRLCGSSMQALHDAA
                                         RMIMTGDAQVCLVGGVEHMGHVPMSHGVDFHPGL
                                         SRNVAKAAGMMGLTAEMLSRLHGI
                                         SREMQDQFAARSHARAWAATQSGAFKTEIIPTGG
                                         HDADGVLKQFNYDEVIRPETTVEA
                                         LSTLRPAFDPVSGTVTAGTSSALSDGAAAMLVMS
                                         ESRARELGLKPRARIRSMAVVGCD
                                         PSIMGYGPVPASKLALKKAGLSASDIDVFEMNEA
                                         FAAQILPCIKDLGLMEQIDEKINL
                                         NGGAIALGHPLGCSGARISTTLINLMERKDAQFG
                                         LATMCIGLGQGIATVFERV"
misc-feature     224203..225363          /gene="STY3578"
                                         /note="Pfam match to entry PF00108
                                         thiolase, Thiolase, score 770.20,
                                         E-value 8.1e-228"
misc-feature     224461..224517          /gene="STY3578"
                                         /note="PS00098 Thiolases
                                         acyl-enzyme intermediate
                                         signature"
misc-feature     225199..225249          /gene="STY3578"
                                         /note="PS00737 Thiolases signature
                                         2"
misc-feature     225304..225345          /gene="STY3578"
                                         /note="PS00099 Thiolases active
                                         site"
gene             complement(225563..2273  /gene="STY3579"
                 86)
CDS              complement(225563..2273  /gene="STY3579"
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                                    /note="Similar to Campylobacter
                                    jejuni arylsulfatase atsA
                                    TR:Q46098 (EMBL:U38280) (620 aa)
                                    fasta scores: E(): 0, 59.4% id in
                                    613 aa"
                                    /codon-start=1
                                    /transl-table=11
                                    /product="possible transferase"
                                    /protein-id="CAD07912.1"
                                    /db-xref="GI:16504457"
                                    /db-xref="GOA:Q8Z3C5"
                                    /db-xref="SPTREMBL:Q8Z3C5"
                                    /translation="MKFKYALTSLALSVAILSSV
                                    PSTAFAIGGASGAKVDYQVQGKIG
                                    EVVMNPYDIAPLTAVIRNGGYQLRDVHVRIVPKE
                                    NGQEIAYKVNNKYLLTYGGIPVFG
                                    LYPDYVNTVEVEYTRIQGSKTENIKESYKMYAPP
                                    AYSESAGTKEEQSALFTIDVKKVS
                                    PEFKDRLYLLNNTKDKSGNGTRTVWNNPTGGALE
                                    WNFTTANAIIDTSGDIRWFMNPSS
                                    IYDLKSIYRAGVMMGFKQNQDGALSWGYGQRYVK
                                    YDIMGREIFNRRLPDNYNDFSHSM
                                    DNAPNGHYFLRVASSNYKRPDGKNVRTVRDVIAE
                                    VDQNGVVVDEWRLFDILDPYRDVI
                                    MKTLDQGAVCLNIDASQSGHTLSEEDLAALDSSD
                                    KFGDIVGSGAGRNWAHVNSVDYDS
                                    EDDSIIISFRHQSAIIKIGRDKKVKWILGTPAGW
                                    KAPFNAAILTPVDSKGQKISCQES
                                    GCEGDFDWTWTQHTAFKIDSKSKGDILYLSAFDN
                                    GDGRGLEQPAMQSMKYSRSVIYKI
                                    DQKNKTVQQIWQYGKERGNEWFSPVTSITEYQTD
                                    KNSVFVYSATAGGEFDLSVGAFTS
                                    LPNPYLEEFRWGEKEPAVEMQIHGARGYQAMPFS
                                    LTKALTE"
gene               complement(227640..2283  /gene="STY3580"
                   41)
                                    /note="synonym: ubiB"
CDS                complement(227640..2283  /gene="STY3580"
                   41)
                                    /note="Orthologue of E. coli ubiB
                                    (UBIB-ECOLI); Fasta hit to
                                    UBIB-ECOLI (232 aa), 91% identity
                                    in 232 aa overlap"
                                    /codon-start=1
                                    /transl-table=11
                                    /product="flavin reductase"
                                    /protein-id="CAD07913.1"
                                    /db-xref="GI:16504458"
                                    /db-xref="GOA:Q8Z3C4"
                                    /db-xref="SPTREMBL:Q8Z3C4"
                                    /translation="MTTLSCKVTSVEAITDTVYR
                                    VRLVPDAAFSFRAGQYLMVVMDER
                                    DKRPFSMASTPDEKGFIELHIGASELNLYAMAVM
                                    DRILKDREIVVDIPHGDAWLRDDE
                                    ERPLILIAGGTGFSYARSILLTALARNPARDVTI
                                    YWGGREEKHLYDLSELEALSVNHP
                                    NLRIEPVVEQPEEGWRGRTGTVLTAVLQDYGTLA
                                    GHDIYIAGRFEMAKIARDLFCHER
                                    NAREDRLFGDAFAFI"
misc-feature       complement(227703..2280  /gene="STY3580"
                   35)
                                    /note="Pfam match to entry PF00175
                                    oxidored-fad, Oxidoreductase
                                    FAD/NAD-binding domain, score
                                    130.20, E-value 3.9e-35"
gene               complement(228427..2299  /gene="STY3581"
                   05)
                                    /note="synonym: yigC"
CDS                complement(228427..2299  /gene="STY3581"
                   05)
                                    /note="Orthologue of E. coli yigC
                                    (YIGC-ECOLI); Fasta hit to
                                    YIGC-ECOLI (497 aa), 96% identity
                                    in 491 aa overlap"
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                       protein"
                       /protein-id="CAD07914.1"
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                       /db-xref="SPTREMBL:Q8Z3C3"
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                       AGGPALLFENPKGYAMPVLCNLFGTPKRVAMGMG
                       QDDVSALREVGKLLAFLKEPEPPK
                       GFRDLFDKLPQFKQVLNMPTKRLRGAPCQQKIAS
                       GDDVDLTRLPVMTCWPDDAAPLIT
                       WGLTVTRGPHKERQNLGIYRQQLIGKNKLIMRWL
                       SHRGGALDFQEWLAARPGERFPVS
                       VALGADPATILGAVTPVPDTLSEYAFAGLLRGTK
                       TEVVKCLSNDLEVPASAEIILEGY
                       IEPGEMAPEGPYGDHTGYYNEVDNFPVFTVTHIT
                       QREDAIYHSTYTGRPPDEPAVLGV
                       ALNEVFVPILQKQFPEIVDFYLPPEGCSYRLAVV
                       TMKKQYAGHAKRVMMGVWSFLRQF
                       MYTKFVIVCDDDVNARDWNDVIWAITTRMDPARD
                       TVLVENTPIDYLDFASPVSGLGSK
                       MGLDATNKWPGETQREWGRPIVKDPEVTARIDAI
                       WDELAIFK"
misc-feature     complement(228595..2298     /gene="STY3581"
                 69)
                                             /note="Pfam match to entry PF01977
                                             UPF0096, Protein of unknown
                                             function UPF0096, score 829.90,
                                             E-value 8.6e-246"
gene             230091..230579              /gene="STY3582"
                                             /note="synonym: rfaH"
CDS              230091..230579              /gene="STY3582"
                                             /note="Orthologue of E. coli rfaH
                                             (RFAH-ECOLI); Fasta hit to
                                             RFAH-ECOLI (162 aa), 88% identity
                                             in 162 aa overlap"
                                             /codon-start=1
                                             /transl-table=11
                                             /product="transcriptional
                                             activator"
                                             /protein-id="CAD07915.1"
                                             /db-xref="GI:16504460"
                                             /db-xref="SPTREMBL:Q8Z3C2"
                                             /translation="MQSWYLLYCKRGQLQRAQEH
                                             LERQAVSCLTPMITLEKMVRGKRT
                                             FVSEPLFPNYLFVEFDPEVIHTTTINATRGVSHF
                                             VRFGAHPAIVPSSVIHQLSIYKPE
                                             GVVDPETPYPGDSVIITEGAFEGLKAIFTEPDGE
                                             TRSMLLLNLLNKEVKQSVKNTGFR KI"
gene             complement(230587..2313     /gene="tatD"
                 69)
                                             /note="synonym: STY3583"
CDS              complement(230587..2313     /gene="tatD"
                 69)
                                             /note="Similar to Escherichia coli
                                             deoxyribonuclease TatD
                                             SW:TATD-ECOLI () (264 aa) fasta
                                             scores: E(): 0, 81.9% id in 260
                                             aa"
                                             /codon-start=1
                                             /transl-table=11
                                             /product="putative
                                             deoxyribonuclease"
                                             /protein-id="CAD07916.1"
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                                             /db-xref="SPTREMBL:Q8Z3C1"
                                             /translation="MFDIGVNLTSSQFAKDRDDV
                                             VARAFAAGVKGMLLTGTNIHESQQ
                                             ALKLARRYPHCWSTAGVHPHDSSQWSSASEDAII
                                             ALANQPEVVAIGECGLDFNRNFST
                                             PQEQERAFQAQLQIAAELQMPIFMHCRDAHERFL
                                             ALLDPWLDSLPGAILHCFTGSRQQ
                                             MQACVDRGLYIGITGWVCDERRGLELRELLPFIP
                                             AEKLLIETDAPYLLPRDLTPKPTS
                                             RRNEPAYLPHILERIALWRGEDPQWLAAMTDANA
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misc-feature	complement(230599..2313 54)	/gene="tatD"
		/note="Pfam match to entry PF01026 UPF0006, Metalloenzyme of unknown function UPF0006, score 375.20, E-value 6.5e-109"
misc-feature	complement(230755..2308 05)	/gene="tatD"
		/note="PS01091 Uncharacterized protein family UPF0006 signature 3"
misc-feature	complement(230971..2310 03)	/gene="tatD"
		/note="PS01090 Uncharacterized protein family UPF0006 signature 2"
gene	complement(231411..2321 90)	/gene="tatC"
		/note="synonym: STY3584"
CDS	complement(231411..2321 90)	/gene="tatC"
		/note="Similar to Escherichia coli sec-independent protein translocase protein TatC SW:TATC-ECOLI () (258 aa) fasta scores: E(): 0, 90.0% id in 259 aa" /codon-start=1 /transl-table=11 /product="sec-independent protein translocase protein" /protein-id="CAD07917.1" /db-xref="GI:16504462" /db-xref="SPTREMBL:Q9L6M3" /translation="MAVEDTQPLITHLIELRKRL LNCIVAVLLIFLALIYFANDIYHL VAAPLIKQMPQGATMIATDVASPFFTPIKLTFMV SLILSAPVILYQVWAFIAPALYKH ERRLVVPLLVSSSLLFYIGMAFAYFVVFPLAFGF LTHTAPEGVQVSTDIASYLSFVMA LFMAFGVAFEVPVAIVLLCWMGITTPEDLRKKRP YILVGAFIVGMLLTPPDVFSQTLL AIPMYCLFEIGVFCSRFYVGKRRTRDEDNEAETE KAEHTED"
misc-feature	complement(231528..2321 39)	/gene="tatC"
		/note="Pfam match to entry PF00902 UPF0032, MttB family UPF0032, score 351.60, E-value 8.6e-102"
misc-feature	complement(231672..2317 31)	/gene="tatC"
		/note="PS01218 Uncharacterized protein family UPF0032 signature"
gene	complement(232193..2327 41)	/gene="tatB"
		/note="synonym: STY3585"
CDS	complement(232193..2327 41)	/gene="tatB"
		/note="Similar to Escherichia coli sec-independent protein translocase protein TatB or MttA2 TR:O69415 (EMBL:AJ005830) (171 aa) fasta scores: E(): 0, 81.9% id in 182 aa Orthologue of E. coli O87926; Fasta hit to O87926 (145 aa), 80% identity in 156 aa overlap" /codon-start=1 /transl-table=11 /product="sec-independent protein translocase protein" /protein-id="CAD07918.1" /db-xref="GI:16504463" /db-xref="GOA:Q8Z3C0" /db-xref="SWISS-PROT:Q8Z3C0"

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                                              TVQNELTQELKLQEFQDSLKKVEKASLENLTPEL
                                              KASMDELRQAAESMKRTYSANDPE
                                              QASDEAHTIHNPVVKGNETQHEGVTPAAAETQAS
                                              APEQKPEPVKANVPESTETASVAA
                                              IDAEKKSAAPVVESSPSSSDKP"
gene            complement(232745..2329      /gene="tatA"
                99)

                                              /note="synonym: STY3586"
CDS             complement(232745..2329      /gene="tatA"
                99)

                                              /note="Similar to Escherichia coli
                                              sec-independent protein
                                              translocase TatA or MttA1
                                              TR:O65938 (EMBL:AJ005830) (103 aa)
                                              fasta scores: E(): 1.2e-23, 84.3%
                                              id in 89 aa Fasta hit to
                                              YBEC-ECOLI (67 aa), 60% identity
                                              in 68 aa overlap Orthologue of E.
                                              coli O65938; Fasta hit to O65938
                                              (103 aa), 84% identity in 89 aa
                                              overlap"
                                              /codon-start=1
                                              /transl-table=11
                                              /product="sec-independent protein
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                                              /db-xref="SWISS-PROT:P57045"
                                              /translation="MGGISIWQLLIVAVIVVLLF
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                                              QDKEQV"
gene            complement(233205..2348      /gene="aarF"
                45)

                                              /note="synonym: STY3587"
CDS             complement(233205..2348      /gene="aarF"
                45)

                                              /note="Similar to Escherichia coli
                                              ubiquinone biosynthesis protein
                                              AarF aarF SW:AARF-ECOLI (P27854;
                                              P27855; P76764; P27853) (546 aa)
                                              fasta scores: E(): 0, 94.3% id in
                                              546 aa"
                                              /codon-start=1
                                              /transl-table=11
                                              /product="ubiquinone biosynthesis
                                              protein"
                                              /protein-id="CAD07920.1"
                                              /db-xref="GI:16504465"
                                              /db-xref="GOA:Q9L6M4"
                                              /db-xref="SWISS-PROT:Q9L6M4"
                                              /translation="MTPGEVRRLYFIIRTFLSYG
                                              LDELIPRMRLTLPLRLWRYSLFWM
                                              PNRHKDKLLGERLRLALQELGPVWIKFGQMLSTR
                                              RDLFPPQIADQLALLQDKVAPFDG
                                              RLAKAQIEEAMGGLPVEAWFDDFDIQPLASASIA
                                              QVHTARLKSNGKEVVIKVIRPDIL
                                              PVIQADLKLIYRLARWVPRLLPDGRRLRPTEVVR
                                              EYEKTLIDELNLLRESANAIQLRR
                                              NFENSPMLYIPEVYSDYCSQNMMVMERIYGIPVS
                                              DVAALEKNGTNMKLLAERGVKVFF
                                              TQVFRDSFFHADMHPGNIFVSHEHPENPQYIGID
                                              CGIVGSLNKEDKRYLAENFIAFFN
                                              RDYRKVAELHVDSGWVPPDTNVEDFEFAIRTVCE
                                              PIFEKPLAEISFGHVLLNLFNTAR
                                              RFNMEVQPQLVLLQKTLLYVEGVGRQLYPQLDLW
                                              KTAKPFLESWIKDQVGIPALTRAL
                                              KEKAPFWVEKMPEIPELVYDSLRQGKYLQHSVDK
                                              IARELQVNHVRQSQSRYLLGIGAT
                                              LLLSGSFLLVNRPEWGLMPGWLMVGGVVVWLVGW
                                              RKTR"
gene            complement(234842..2354      /gene="STY3588"
                47)
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CDS	complement(234842..2354 47)	/gene="STY3588"
		/note="Orthologue of E. coli yigP (YIGP-ECOLI); Fasta hit to YIGP-ECOLI (201 aa), 87% identity in 201 aa overlap" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAD07921.1" /db-xref="GI:16504466" /db-xref="SPTREMBL:Q8Z3B9" /translation="MPFKPLVTAGIEGLLNTFLY RSPALKSARTRLQGKVLCVKLKGF STPLVLVFSERQVDVLGAWEGEADCTVITQASVL PKLRDRQQLAALIRSGELEVQGDI QVVQNFVALADLAEFDPAELLAPYTGDIAAESIG KVVRGGAKFLRHGFQRQQRYAAEA ITEEWRMAPGPLEVAWFAEETAAVERAVDSLTTR LEKLGAK"
gene	complement(235457..2362 12)	/gene="ubiE"
		/note="synonym: STY3589"
CDS	complement(235457..2362 12)	/gene="ubiE"
		/EC-number="2.1.1.-" /note="Similar to Escherichia coli ubiquinone/menaquinone biosynthesis methyltransferase UbiE ubiE SW:UBIE-ECOLI (P27851) (251 aa) fasta scores: E(): 0, 95.6% id in 251 aa" /codon-start=1 /transl-table=11 /product="ubiquinone/menaquinone biosynthesis methyltransferase UbiE" /protein-id="CAD07922.1" /db-xref="GI:16504467" /db-xref="GOA:Q9L6M6" /db-xref="SWISS-PROT:Q9L6M6" /translation="MVEDSQETTHFGFQTVAKEQ KADMVAHVFHSVASKYDVMNDLMS FGIHRLWKRFTIDCSGVRRGQTVLDLAGGTGDLT AKFSRMVGETGKVILADINDSMLK MGREKLRNIGVIGNVEYVQANAEALPFPDNTFDC ITISFGLRNVTEKEKALRSMFRVL KPGGRLLVLEFSKPIIEPLSKAYDAYSFHILPRI GSMVANDADSYRYLAESIRMHPDQ DTLKAMMQDAGFESVDYYNLTAGVVALHRGYKF"
misc-feature	complement(235463..2361 73)	/gene="ubiE"
		/note="Pfam match to entry PF01209 Ubie-methyltran, ubiE/COQ5 methyltransferase family, score 588.50, E-value 4.1e-173"
misc-feature	complement(236060..2361 07)	/gene="ubiE"
		/note="PS01183 ubiE/COQ5 methyltransferase family signature 1"
gene	complement(236308..2377 38)	/gene="STY3590"
		/note="synonym: yigN"
CDS	complement(236308..2377 38)	/gene="STY3590"
		/note="Orthologue of E. coli yigN (YIGN-ECOLI); Fasta hit to YIGN-ECOLI (475 aa), 87% identity in 475 aa overlap. Contains a possible N-terminal signal sequence and a possible coiled-coil region between residues 65..124"

```
                                        /transl-table=11
                                        /product="putative membrane
                                        protein"
                                        /protein-id="CAD07923.1"
                                        /db-xref="GI:16504468"
                                        /db-xref="GOA:Q9L6M7"
                                        /db-xref="SWISS-PROT:Q9L6M7"
                                        /translation="MDITLMISAVVALAAGAVIG
                                        WLATKAHADQIRADLIEERRELDI
                                        ELSAARQQLAQEAHWRSECELLNNELRSLHSINT
                                        SLEADLREVTTRLEATQQHAEDKI
                                        RQMINSEQRLSEQFENLANRIFEHSNRRVDEQNR
                                        QSLNSLLTPLREQLDGFRRQVQES
                                        FGKEAQERHTLAHEIRNLQQLNAQMAQEAINLTR
                                        ALKGDNKAQGNWGEVVLARVLEAS
                                        GLREGYEYETQVSIENDARSRMQPDVIVRLPQGK
                                        DVVIDAKMTLVAYERYFNAEDDYT
                                        REAALQEHIASVRNHIRLLGRKDYQQLPGLRSLD
                                        YVLMFIPVEPAFLLALDKQPELIT
                                        EALKNNIMLVSPTTLLVALRTIANLWRYEHQSRN
                                        AQHIADRASKLYDKMRLFVDDMSA
                                        IGQSLDKAQDNYRQAMKKLASGRGNVLAQAEAFR
                                        GLGVEIKREINPDLAEQAVTQDEE
                                        YRLRSIPEGRQDEHYPNDERVKQQLS"
gene               complement(237878..2386   /gene="udp"
                   39)
                                        /note="synonym: STY3591"
CDS                complement(237878..2386   /gene="udp"
                   39)
                                        /EC-number="2.4.2.3"
                                        /note="Similar to Escherichia coli
                                        uridine phosphorylase UDP
                                        SW:UDP-ECOLI (P12758) (252 aa)
                                        fasta scores: E(): 0, 97.2% id in
                                        252 aa and to Salmonella
                                        typhimurium uridine phosphorylase
                                        SW:UDP-SALTY () (252 aa) fasta
                                        scores: E(): 0, 99.2% id in 252
                                        aa"
                                        /codon-start=1
                                        /transl-table=11
                                        /product="uridine phosphorylase"
                                        /protein-id="CAD07924.1"
                                        /db-xref="GI:16504469"
                                        /db-xref="GOA:O33808"
                                        /db-xref="SWISS-PROT:O33808"
                                        /translation="MSKSDVFHLGLTKNDLQGAQ
                                        LAIVPGDPERVEKIAALMDKPVKL
                                        ASHREFTSWRAELDGKAVIVCSTGIGGPSTSIAV
                                        EELAQLGIRTFLRIGTTGAIQPHI
                                        NVGDVLVTTASVRLDGASLHFAPMEFPAVADFAC
                                        TTALVEAAKSIGATTHVGVTASSD
                                        TFYPGQERYDTYSGRVVRRFKGSMEEWQAMGVMN
                                        YEMESATLLTMCASQGLRAGMVAG
                                        VIVNRTQQEIPNAETMKQTESHAVKIVVEAARRL
                                        L"
misc-feature       complement(237893..2385   /gene="udp"
                   82)
                                        /note="Pfam match to entry PF01048
                                        PNP-UDP-1, Phosphorylase family,
                                        score 375.00, E-value 7.6e-109"
misc-feature       complement(238397..2384   /gene="udp"
                   44)
                                        /note="PS01232 Purine and other
                                        phosphorylases family 1 signature"
gene               238898..239710            /gene="STY3592"
                                        /note="synonym: ysgA"
CDS                238898..239710            /gene="STY3592"
                                        /note="Similar to Escherichia coli
                                        putative
                                        carboxymethylenebutenolidase YsgA
                                        SW:DLHH-ECOLI (P56262) (258 aa)
                                        fasta scores: E(): 0, 90.6% id in
                                        255 aa Orthologue of E. coli
                                        DLHH-ECOLI; Fasta hit to
```

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                                       in 255 aa overlap"
                                       /codon-start=1
                                       /transl-table=11
                                       /product="putative hydrolase"
                                       /protein-id="CAD07925.1"
                                       /db-xref="GI:16504470"
                                       /db-xref="GOA:Q8Z3B8"
                                       /db-xref="SWISS-PROT:Q8Z3B8"
                                       /translation="MTTTHPSGFAPAASPLAPTM
                                       IHTPDGAISAGITSIPSQGDDMPA
                                       YYARPKASDGALPVVIVVQEIFGVHEHIRDICRR
                                       LALEGYLAIAPELYFREGDPNDFA
                                       DIPTLLSGLVAKVPDSQVLADLDHVASWASRNGG
                                       DAHRLMITGFCWGGRITWLYAAHN
                                       PQLKAAVAWYGKLVGDTSLNSPKHPVDIATDLNA
                                       PVLGLYSGQDTSIPQESVETMRQA
                                       LRAANAKAEIVVYPDAGHAFNADYRPGYHEASAK
                                       DGWQRMLEWFAQYGGKKG"
misc-feature    239021..239695         /gene="STY3592"
                                       /note="Pfam match to entry PF01738
                                       DLH, Dienelactone hydrolase
                                       family, score 352.40, E-value
                                       4.7e-102"
gene            complement(239786..2411 /gene="STY3593"
                32)
CDS             complement(239786..2411 /gene="STY3593"
                32)

                                       /note="Fasta hit to YDEM-ECOLI
                                       (385 aa), 42% identity in 390 aa
                                       overlap Orthologue of E. coli aslB
                                       (ASLB-ECOLI); Fasta hit to
                                       ASLB-ECOLI (411 aa), 48% identity
                                       in 393 aa overlap"
                                       /codon-start=1
                                       /transl-table=11
                                       /product="putative regulatory
                                       protein"
                                       /protein-id="CAD07926.1"
                                       /db-xref="GI:16504471"
                                       /db-xref="SPTREMBL:Q8Z3B7"
                                       /translation="MSHGAGEPYFLTEMSDMAVA
                                       GCHVMAKPGGAICNIDCTYCFYLE
                                       KEALYPERNKNWRMSDETLEQFIRQHIAAQSGDR
                                       IDFAWQCGEPTMMGLPFFRRVVAL
                                       CEKYGDGRKITHALQTNGILVNDEWARFFAEQHF
                                       LIGLSIDGPASLHNHYRLNRAGKG
                                       THEQVVAAMARLKAHHVDFNTLTVVGKHNVGHAA
                                       DVYEFLLAAGSRFIQFIPLVERMS
                                       TDNSSVLNLVMPGESAAKLAPWTVPSWQYGEFLN
                                       QIFDIWVRRDVDRVYVQMFDVALA
                                       AWTAQQPVLCVHSETCGHAFALESNGDLYNCDHF
                                       VYPEHLLGNIHQHSIKTLNNSERA
                                       IAFGEAKRETLTADCRRCDYRFACHGGCPKHRFA
                                       VSPSGHPAHNYLCTGYKHFFQHVT
                                       PYMNVWRELLAQGYPMASIMRWLAQDARKDTGAV
                                       SRNHLCPCGSGKKYKNAVVKHS"
misc-feature    complement(240203..2408 /gene="STY3593"
                95)
                                       /note="Pfam match to entry PF01444
                                       MoaA-NifB-PqqE, moaA / nifB / pqqE
                                       family, score -26.10, E-value
                                       0.0081"
gene            complement(241467..2437 /gene="STY3594"
                31)
                                       /note="synonym: metE"
CDS             complement(241467..2437 /gene="STY3594"
                31)
                                       /note="Orthologue of E. coli metE
                                       (METE-ECOLI); Fasta hit to
                                       METE-ECOLI (752 aa), 94% identity
                                       in 751 aa overlap"
                                       /codon-start=1
                                       /transl-table=11
                                       /product="5-methyltetrahydropteroy
                                       ltriglutamate- homocysteine
```

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                                         /protein-id="CAD07927.1"
                                         /db-xref="GI:16504472"
                                         /db-xref="GOA:Q8Z3B6"
                                         /db-xref="SWISS-PROT:Q8Z3B6"
                                         /translation="MTILTHTLGFPRVGLRRELK
                                         KAQESYWAGNTTREALLAVGRELR
                                         ARHWEQQKQAGIDLLPVGDFAWYDHVLTTSLLLG
                                         NVPARHQNNDGSVDIDTLFRIGRG
                                         RAPTGEPAAAAEMTKWFNTNYHYIVPEFSKGQQF
                                         RLTWTQLLEEVDEALALGHKIKPV
                                         LLGPVTYLWLGKVKGEPFDRLTLLKDILPVYQHV
                                         LAELAKRGVEWVQIDEPALVLELP
                                         QAWLDAFKPAYDALAGQVKLLLTTYFEGVTPNLD
                                         TIIVLPVQGLHVDLIHGKDDVVEL
                                         HQRLPVDWLLSAGLINGRNVWRADLTEKYAQINA
                                         IVGKRALWVASSCSLLHSPIDLSV
                                         ETRLDTEVKSWFAFALQKCGELALLRDALNSGET
                                         AALEEWSVPIQARRHSHRVHNAAV
                                         EKRLAAITAQDSQRENPYEVRAEAQRARFKLPAW
                                         PTTTIGSFPQTTEIRGLRLDFKKG
                                         NLDANNYRTGIAEHIKQAIIEQERLGLDVLVHGE
                                         AERNDMVEYFGEHLDGFVFTQNGW
                                         VQSYGSRCVKPPVVIGDISRPAPITVEWAKYAQS
                                         LTDKPVKGMLTGPVTILCWSFPRE
                                         DVTRETIAKQIALALRDEVADLEAAGIGIIQIDE
                                         PALREGLPLRRSDWDAYLEWGVEA
                                         FRINAAVAKDETQIHTHMCYCEFNDIMDSIAALD
                                         ADVITIETSRSDMELLESFEAFDY
                                         PNEIGPGVYDIHSPNVPSVEWIEALLKKAAQRIP
                                         AQRLWVNPDCGLKTRGWPETRAAL
                                         ANMVKAAHNLRQAK"
misc-feature      complement(241485..2424   /gene="STY3594"
                  56)
                                         /note="Pfam match to entry PF01717
                                         Methionine-synt, Methionine
                                         synthase, vitamin-B12 independent,
                                         score 775.00, E-value 3.1e-229"
gene              243980..244933             /gene="STY3595"
                                         /note="synonym: metR"
CDS               243980..244933             /gene="STY3595"
                                         /note="Orthologue of E. coli metR
                                         (METR-ECOLI); Fasta hit to
                                         METR-ECOLI (317 aa), 92% identity
                                         in 317 aa overlap"
                                         /codon-start=1
                                         /transl-table=11
                                         /product="trans-activator of metE
                                         and metH"
                                         /protein-id="CAD07928.1"
                                         /db-xref="GI:16504473"
                                         /db-xref="GOA:P05984"
                                         /db-xref="SWISS-PROT:P05984"
                                         /translation="MIEIKHLKTLQALRNSGSLA
                                         AAAAVLHQTQSALSHQFSDLEQRL
                                         GFRLFVRKSQPLRFTPQGEVLLQLANQVLPQISR
                                         ALQACNEPQQTRLRIAIECHSCIQ
                                         WLTPALENFRASWPQVEMDFTSGVTFDPQPALQQ
                                         GELDLVMTSDILPRSGLHYSPMFD
                                         FEVRLVLAPDHPLASKTQITPEDLASETLLIYPV
                                         QRSRLDVWRHFLQPAGISPLLKSV
                                         DNTLLLIQMVAARMGIAALPHWVVESVERQGLVV
                                         TKTLGDGLWSRLYAAVRDGDQRQA
                                         VTEAFIRSTRDHACDHLPFVRSAERPIFDAPTAK
                                         PGSQPRL"
misc-feature      243989..244408             /gene="STY3595"
                                         /note="Pfam match to entry PF00126
                                         HTH-1, Bacterial regulatory
                                         helix-turn-helix protein, lysR
                                         family, score 156.20, E-value
                                         5.7e-43"
misc-feature      244031..244123             /gene="STY3595"
                                         /note="PS00044 Bacterial
                                         regulatory proteins, lysR family
                                         signature"
gene              complement(244821..2457   /gene="STY3596"
```

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                                              /note="synonym: yigM"
CDS                 complement(244821..2457  /gene="STY3596"
                    20)
                                              /note="Orthologue of E. coli yigM
                                              (YIGM-ECOLI); Fasta hit to
                                              YIGM-ECOLI (288 aa), 89% identity
                                              in 291 aa overlap. Contains
                                              multiple possible membrane
                                              spanning hydrophobic domains. Note
                                              the large overlap with the
                                              downstream CDS."
                                              /codon-start=1
                                              /transl-table=11
                                              /product="putative membrane
                                              protein"
                                              /protein-id="CAD07929.1"
                                              /db-xref="GI:16504474"
                                              /db-xref="GOA:Q9L6N3"
                                              /db-xref="SWISS-PROT:Q9L6N3"
                                              /translation="MALLIITTILWAFSFSLFGE
                                              YLAGHVDSYFAVLIRVGLAALVFL
                                              PFLRTRGHNLKTISLYMLVGAMQLGIMYMLSFHA
                                              YLYLTVSELLLFTVLTPLYITLIY
                                              DVMSQRRLRWGYAFSALLAVIGAGIIRYDRVTDH
                                              FWVGLLLVQLSNISFAIGMVGYKR
                                              LMETRPMPQHNAFAWFYLGAFLVAAVAWSLLGNA
                                              QKLPETTLQWSILVFLGVVASGIG
                                              YFMWNYGATQVDAGTLGIMNNMHVPAGLLVNLAI
                                              WHQQPHWPSFITGAAVILASLWVH
misc-feature        complement(244890..2452  RKWVAPRSAQTADDRRRDPASSE"
                    76)                       /gene="STY3596"

                                              /note="Pfam match to entry PF00892
                                              DUF6, Integral membrane protein
                                              DUF6, score 37.10, E-value 4e-07"
gene                complement(245801..2466  /gene="yigL"
                    01)
                                              /note="synonym: STY3597"
CDS                 complement(245801..2466  /gene="yigL"
                    01)
                                              /note="Similar to Salmonella
                                              typhimurium LT2 YigL protein yigL
                                              TR:AAF33430 (EMBL:UNNKOWN
                                              ACCESSION) (266 aa) fasta scores:
                                              E(): 0, 100.0% id in 266 aa, and
                                              to Escherichia coli hypothetical
                                              29.8 kDa protein in pldb-metr
                                              intergenic region. hypothetical
                                              29.8 kda protein in pldb-metr
                                              intergenic region SW:YIGL-ECOLI
                                              (P27848) (265 aa) fasta scores:
                                              E(): 0, 84.5% id in 265 aa Fasta
                                              hit to COF-ECOLI (272 aa), 39%
                                              identity in 260 aa overlap
                                              Orthologue of E. coli yigL
                                              (YIGL-ECOLI); Fasta hit to
                                              YIGL-ECOLI (265 aa), 85% identity
                                              in 265 aa overlap"
                                              /codon-start=1
                                              /transl-table=11
                                              /product="conserved hypothetical
                                              protein"
                                              /protein-id="CAD07930.1"
                                              /db-xref="GI:16504475"
                                              /db-xref="GOA:Q9L6N4"
                                              /db-xref="SPTREMBL:Q9L6N4"
                                              /translation="MYQVVASDLDGTLLSPDHTL
                                              SPYAKETLKLLTARGIHFVFATGR
                                              HHVDVGQIRDNLEIKSYMITSNGARVHDTDGNLV
                                              FTHNLDSDIASDLFGVVNANPDIV
                                              TNVYRDDEWFMNRHRPDEMRFFKEAVFNYSLFEP
                                              ALLEPEGVSKVFFTSDTHEKLLPL
                                              EQAINARWGDRVNVSFSTLTCLEVMAGGVSKGHA
                                              LEAVAQAMGYSLKECIAFGDGMND
                                              AEMLTMAGKGCIMGNAHQRLKDLYPELEVIGINA
```

misc-feature	complement(245849..2465 92)	/gene="yigL"
		/note="Pfam match to entry PF00592 DUF3, Cof family DUF3, score 373.60, E-value 2e-108"
misc-feature	complement(245900..2459 68)	/gene="yigL"
		/note="PS01229 Hypothetical cof family signature 2"
misc-feature	complement(246557..2465 92)	/gene="yigL"
		/note="PS01228 Hypothetical cof family signature 1"
gene	complement(246617..2476 33)	/gene="STY3598"
		/note="synonym: pldB"
CDS	complement(246617..2476 33)	/gene="STY3598"
		/note="Orthologue of E. coli pldB (PLDB-ECOLI); Fasta hit to PLDB-ECOLI (340 aa), 82% identity in 336 aa overlap" /codon-start=1 /transl-table=11 /product="lysophospholipase L2" /protein-id="CAD07931.1" /db-xref="GI:16504476" /db-xref="GOA:Q8Z3B5" /db-xref="SPTREMBL:Q8Z3B5" /translation="MFQQQNDWETRENAFAAFAM GPLTDFWRQREEAEFIGVDNIPVR FVRFRNDSNDRTIVICPGRIESYVKYAELAYDLF HLGFDIFIIDHRGQGRSGRMLSDP HRGHVDHFNDYVEDLAAFWQQEIEPGSWRKRYIL AHSMGGAIATLFLQRHRVRCDAIA LTAPMFGIVIRLPSFMVRHILDWAEGHQRIREDY AIGTGQWRALPFGMNALTHSRQRY QRNLRFYADEPQLRVGGPTWHWVREGILAGEQVL AGASDDTTPTLLIQAEEERVVDNR THDRFCEIRAAAGYPCEGGKPLVIKGAYHEILFE KDAMRSVALNAIVEFFNKPNLSSG NRFA"
misc-feature	complement(246665..2473 90)	/gene="STY3598"
		/note="Pfam match to entry PF00561 abhydrolase, alpha/beta hydrolase fold, score 111.50, E-value 1.6e-29"
gene	247744..248364	/gene="rhtB" /note="synonym: STY3599"
CDS	247744..248364	/gene="rhtB" /note="Similar to Escherichia coli homoserine/homoserine lactone efflux protein RhtB SW:RHTB-ECOLI (P27847) (206 aa) fasta scores: E(): 0, 89.3% id in 206 aa" /codon-start=1 /transl-table=11 /product="homoserine/homoserine lactone efflux protein" /protein-id="CAD07932.1" /db-xref="GI:16504477" /db-xref="GOA:Q8Z3B4" /db-xref="SWISS-PROT:Q8Z3B4" /translation="MTFEWWFAYLLTSTLLSLSP GSGAINTMTTSINHGYRGAAASIA GLQTGLGIHIVLVGVGLGTLFSRSLIAFEILKWA GAAYLIWLGIQQWRAAGAIDLHTL AQTQSRGRLFKRAIFVNLTNPKSIVFLAALFPQF IMPQQPQLAQYLILGVTTIVVDMI VMTGYATLAQRIAAWIKGPKQMKALNKAFGSLFM LVGALLASARHA"
misc-feature	247948..248262	/gene="rhtB" /note="Pfam match to entry PF01810 LysE, LysE type translocator, score 127.60, E-value 2.2e-34"

```
                                          /note="synonym: STY3600"
CDS              complement(248404..2490  /gene="rhtC"
                 24)
                                          /note="Similar to Escherichia coli
                                          threonine efflux protein rhtC
                                          SW:RHTC-ECOLI (P27846) (206 aa)
                                          fasta scores: E(): 0, 91.3% id in
                                          206 aa"
                                          /codon-start=1
                                          /transl-table=11
                                          /product="threonine efflux
                                          protein"
                                          /protein-id="CAD07933.1"
                                          /db-xref="GI:16504478"
                                          /db-xref="GOA:Q8Z3B3"
                                          /db-xref="SWISS-PROT:Q8Z3B3"
                                          /translation="MLMLFFTVAMVHIVALMSPG
                                          PDFFFVSQTAVSRSRKEAMMGVLG
                                          ITCGVMVWAGVALLGLHLIIEKMAWLHTIIMVGG
                                          GLYLCWMGYQMLRGALKKQDAAAS
                                          SPHIELAQSGRSFLKGLLTNLSNPKAIIYFGSVF
                                          SLFVGDNVGAAARWGIFALITLET
                                          LAWFTVVASLFALPKMRRGYQRLAKWIDGFAGAL
                                          FAGFGIHLIISR"
misc-feature     complement(248497..2488  /gene="rhtC"
                 23)
                                          /note="Pfam match to entry PF01810
                                          LysE, LysE type translocator,
                                          score 145.70, E-value 8e-40"
gene             complement(249088..2509  /gene="recQ"
                 17)
                                          /note="synonym: STY3601"
CDS              complement(249088..2509  /gene="recQ"
                 17)
                                          /EC-number="3.6.1.-"
                                          /note="Similar to Escherichia coli
                                          ATP-dependent DNA helicase RecQ
                                          SW:RECQ-ECOLI (P15043; P76762)
                                          (607 aa) fasta scores: E(): 0,
                                          94.6% id in 608 aa"
                                          /codon-start=1
                                          /transl-table=11
                                          /product="ATP-dependent DNA
                                          helicase"
                                          /protein-id="CAD07934.1"
                                          /db-xref="GI:16504479"
                                          /db-xref="GOA:Q8Z3B2"
                                          /db-xref="SPTREMBL:Q8Z3B2"
                                          /translation="MAQAEVLNLESGAKQVLQET
                                          FGYQQFRPGQEAIIDTALSGRDCL
                                          VVMPTGGGKSLCYQIPALLLDGLTVVVSPLISLM
                                          KDQVDQLLANGVAAACLNSTQSRE
                                          QQLEVMAGCRTGQIRLLYIAPERLMLDNFLDHLA
                                          HWNPVLLAVDEAHCISQWGHDFRP
                                          EYAALGQLRQRFPALPFMALTATADDTTRQDIIR
                                          LLGLNDPLIQISSFDRPNIRYMLM
                                          EKFKPLDQLMRYVQEQRGKSGIIYCNSRAKVEDT
                                          AARLQSRGISAAAYHAGLENAIRA
                                          DVQEKFQRDDLQIVVATVAFGMGINKPNVRFVVH
                                          FDIPRNIESYYQETGRAGRDGLPA
                                          EAMLFYDPADMAWLRRCLEEKPAGQLQDIERHKL
                                          NAMGAFAEAQTCRRLVLLNYFGEG
                                          RQEPCGNCDICLDPPKQYDGLNDAQIALSTIGRV
                                          NQRFGMGYVVEVIRGANNQRIRDF
                                          GHDKLKVYGMGREKSHEHWVSVIRQLIHLGLVMQ
                                          NIAQHSALQLTDAARPVLRGDVPL
                                          KLAVPRIVALKPRVMQKSFGGNYDRKLFAKLRKL
                                          RKAIADEENIPPYVVFNDATLIEM
                                          AEQMPVSASEMLSVNGVGMRKLERFGKEFMALIR
                                          AHVDGDDEE"
misc-feature     complement(249091..2493  /gene="recQ"
                 33)
                                          /note="Pfam match to entry PF00570
                                          HRDC, HRDC domain, score 130.40,
```

misc-feature	complement(249925..2501 70)	/gene="recQ"

/note="Pfam match to entry PF00271
helicase-C, Helicases conserved
C-terminal domain, score 98.50,
E-value 1.3e-25"

misc-feature	complement(250303..2508 72)	/gene="recQ"

/note="Pfam match to entry PF00270
DEAD, DEAD/DEAH box helicase,
score 121.60, E-value 1.5e-37"

gene	complement(251001..2518 70)	/gene="STY3602"

/note="synonym: pldA"

CDS	complement(251001..2518 70)	/gene="STY3602"

/note="Orthologue of E. coli pldA
(PA1-ECOLI); Fasta hit to
PA1-ECOLI (289 aa), 92% identity
in 289 aa overlap"
/codon-start=1
/transl-table=11
/product="detergent-resistant
phospholipase A"
/protein-id="CAD07935.1"
/db-xref="GI:16504480"
/db-xref="GOA:P37442"
/db-xref="SWISS-PROT:P37442"
/translation="MRAILRGLLPATLLPLAAYA
QEATIKEVHDAPAVRGSIIANMLQ
EHDNPFTLYPYDTNYLIYTNTSDLNKEAISTYNW
SENARKDEVKFQLSLAFPLWRGIL
GPNSVLGASYTQKSWWQLSNSKESSPFRETNYEP
QLFLGFATDYRFAGWTLRDVEMGY
NHDSNGRSDPTSRSWNRLYTRLMAENGNWLVEVK
PWYVIGSTDDNPDITKYMGYYQLK
IGYHLGEAVLSAKGQYNWNTGYGGAEVGLSYPVT
KHVRLYTQVYSGYGESLIDYNFNQ
TRVGVGVMLNDIF"

misc-feature	complement(251013..2518 07)	/gene="STY3602"

/note="Pfam match to entry PF02253
PLA1, Phospholipase A1, score
584.10, E-value 9e-172"

gene	252035..252502	/gene="STY3603"

/note="synonym: yigI"

CDS	252035..252502	/gene="STY3603"

/note="Orthologue of E. coli yigI
(YIGI-ECOLI); Fasta hit to
YIGI-ECOLI (155 aa), 97% identity
in 155 aa overlap"
/codon-start=1
/transl-table=11
/product="conserved hypothetical
protein"
/protein-id="CAD07936.1"
/db-xref="GI:16504481"
/db-xref="GOA:P40725"
/db-xref="SWISS-PROT:P40725"
/translation="MSAVLTAEQALKLVGEMFVY
HMPFNRALGLELERYEKAFAQLAF
NNQPMMVGNWAQSILHGGVIASALDVAAGLVCVG
STLTRHETISEDELRQRLSRMGTI
DLRVDYLRPGRGNRFTATSSLLRAGNKVAVARVE
LHNEDQLYIASATATYMVG"

gene	252546..253430	/gene="STY3604"
CDS	252546..253430	/gene="STY3604"

/note="Similar to Escherichia coli
chloramphenicol-sensitive protein
RarD SW:RARD-ECOLI (P27844) (296
aa) fasta scores: E(): 0, 90.4% id
in 293 aa and to Pseudomonas
aeruginosa
chloramphenicol-sensitive protein
RarD SW:RARD-PSEAE (O68827) (299

CDS   complement(254368..2553   /gene="STY3607"
                            18)

                                                      /note="Similar to Salmonella
                                                      typhimurium magnesium and cobalt
                                                      transport protein cora. magnesium
                                                      and cobalt transport protein cora
                                                      SW:CORA-SALTY (P31138) (316 aa)
                                                      fasta scores: E(): 0, 100.0% id in
                                                      316 aa, and to Escherichia coli
                                                      magnesium and cobalt transport
                                                      protein CorA corA SW:CORA-ECOLI
                                                      (P27841) (316 aa) fasta scores:
                                                      E(): 0, 97.5% id in 316 aa
                                                      Orthologue of E. coli corA
                                                      (CORA-ECOLI); Fasta hit to
                                                      CORA-ECOLI (316 aa), 98% identity
                                                      in 316 aa overlap"
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gene   complement(255790..2579   /gene="STY3608"
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                                                      /note="synonym: uvrD"
CDS   complement(255790..2579   /gene="STY3608"
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    AUTHOR (AU):           Kraev,A.; Quednau,B.D.; Leach,S.; Li,X.F.; Dong,H.;
                           Winkfein,R.; Perizzolo,M.; Cai,X.; Yang,R.;
                           Philipson,K.D.; Lytton,J.
    TITLE (TI):            Molecular cloning of a third member of the
                           potassium-dependent  ***sodium***  -  ***calcium***
                             ***exchanger***   gene family, NCKX3
    JOURNAL (SO):          J. Biol. Chem., 276 (25), 23161-23172 (  ***2001***  )
    OTHER SOURCE (OS):     CA 136:145918
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    AUTHOR (AU):           Quednau,B.D.; Philipson,K.D.
    TITLE (TI):            Direct Submission
    JOURNAL (SO):          Submitted (17-JUL-2000) Physiology, UCLA School of
                           Medicine, 675 Charles Young Drive, MRL Bldg., Rm.
                           3-645, Los Angeles, CA 90095, USA


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L4   ANSWER 236 OF 473   GENBANK.RTM.   COPYRIGHT 2004 on STN

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DIVISION CODE (CI):        Primates
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   AUTHOR (AU):            Kraev,A.; Quednau,B.D.; Leach,S.; Li,X.F.; Dong,H.;
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                           Philipson,K.D.; Lytton,J.
   TITLE (TI):             Molecular cloning of a third member of the
                           potassium-dependent   ***sodium***  -  ***calcium***
                           ***exchanger***   gene family, NCKX3
   JOURNAL (SO):           J. Biol. Chem., 276 (25), 23161-23172 (  ***2001***  )
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   AUTHOR (AU):            Kraev,A.S.
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   JOURNAL (SO):           Submitted (15-JUL-1999) Banting and Best Department of
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DIVISION CODE (CI):     Other vertebrates
DATE (DATE):            11 Feb 2000
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                        (NCKX) mRNA, complete cds.
SOURCE:                 chicken.
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REFERENCE:              1  (bases 1 to 2182)
   AUTHOR (AU):         Prinsen,C.F.; Szerencsei,R.T.; Schnetkamp,P.P.
   TITLE (TI):          Molecular cloning and functional expression of the
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                        retinal cone photoreceptors
   JOURNAL (SO):        J. Neurosci., 20 (4), 1424-1434 (  ***2000***  )
   OTHER SOURCE (OS):   CA 132:332359
REFERENCE:              2  (bases 1 to 2182)
   AUTHOR (AU):         Prinsen,C.F.M.; Schnetkamp,P.P.M.
   TITLE (TI):          Direct Submission
   JOURNAL (SO):        Submitted (17-AUG-1999) Physiology and Biophysics,
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DIVISION CODE (CI):   Other vertebrates
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                         (NCKX) mRNA, complete cds.
SOURCE: chicken.
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  TITLE (TI):   Molecular cloning and functional expression of the
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                         retinal cone photoreceptors
  JOURNAL (SO):   J. Neurosci., 20 (4), 1424-1434 (***2000***)
  OTHER SOURCE (OS):   CA 132:332359
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  AUTHOR (AU):   Prinsen,C.F.M.; Schnetkamp,P.P.M.
  TITLE (TI):   Direct Submission
  JOURNAL (SO):   Submitted (17-AUG-1999) Physiology and Biophysics,
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DIVISION CODE (CI):          Primates
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   AUTHOR (AU):              Prinsen,C.F.; Szerencsei,R.T.; Schnetkamp,P.P.
   TITLE (TI):               Molecular cloning and functional expression of the
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   JOURNAL (SO):             J. Neurosci., 20 (4), 1424-1434 (  ***2000***  )
   OTHER SOURCE (OS):        CA 132:332359
REFERENCE:                   2  (bases 1 to 2221)
   AUTHOR (AU):              Prinsen,C.F.M.; Szerencsei,R.T.; Schnetkamp,P.P.M.
   TITLE (TI):               Direct Submission
   JOURNAL (SO):             Submitted (05-OCT-1998) Physiology and Biophysics,
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DIVISION CODE (CI):         Primates
DATE (DATE):                13 Mar 2001
DEFINITION (DEF):           Homo sapiens    ***sodium***   /   ***calcium***
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                            cds.
                               ***human***   .
SOURCE:
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NUCLEIC ACID COUNT (NA):    754 a    579 c    718 g    763 t
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  AUTHOR (AU):              Van Eylen,F.; Bollen,A.; Herchuelz,A.
  TITLE (TI):               NCX1 Na/Ca exchanger splice variants in pancreatic
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  JOURNAL (SO):             J. Endocrinol., 168 (3), 517-526 (  ***2001***  )
  OTHER SOURCE (OS):        CA 134:351070
REFERENCE:                  2  (bases 1 to 2814)
  AUTHOR (AU):              Van Eylen,F.; Bollen,A.; Herchuelz,A.
  TITLE (TI):               Direct Submission
  JOURNAL (SO):             Submitted (23-NOV-1998) Pharmacodynamie, Brussels Free
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L4   ANSWER 244 OF 473   GENBANK.RTM.   COPYRIGHT 2004 on STN

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DIVISION CODE (CI):          Primates
DATE (DATE):                 27 Oct 2000
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    AUTHOR (AU):             Scheller,T.; Kraev,A.; Skinner,S.; Carafoli,E.
    TITLE (TI):              Cloning of the multipartite promoter of the
                               ***sodium*** - ***calcium***     ***exchanger***
                             gene NCX1 and characterization of its activity in
                             vascular smooth muscle cells
    JOURNAL (SO):            J. Biol. Chem., 273 (13), 7643-7649 (  ***1998***  )
    OTHER SOURCE (OS):       CA 129:1331
REFERENCE:                   2  (bases 1 to 830)
    AUTHOR (AU):             Kraev,A.S.
    TITLE (TI):              Direct Submission
    JOURNAL (SO):            Submitted (06-MAY-1997) A.S. Kraev, Swiss Federal
                             Institute of Technology, Laboratory of Biochemistry
                             III, Universitaetstr. 16, Zurich, CH-8092, SWITZERLAND

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DIVISION CODE (CI):             Primates
DATE (DATE):                    27 Oct 2000
DEFINITION (DEF):               Homo sapiens ncx1 gene, exon 1a, 1b and 1c.
SOURCE:                           ***human***  .
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REFERENCE:                      1   (bases 1 to 5282)
   AUTHOR (AU):                 Scheller,T.; Kraev,A.; Skinner,S.; Carafoli,E.
   TITLE (TI):                  Cloning of the multipartite promoter of the
                                 ***sodium*** - ***calcium***    ***exchanger***
                                gene NCX1 and characterization of its activity in
                                vascular smooth muscle cells
   JOURNAL (SO):                J. Biol. Chem., 273 (13), 7643-7649 (  ***1998***  )
   OTHER SOURCE (OS):           CA 129:1331
REFERENCE:                      2   (bases 1 to 5282)
   AUTHOR (AU):                 Kraev,A.S.
   TITLE (TI):                  Direct Submission
   JOURNAL (SO):                Submitted (06-MAY-1997) A.S. Kraev, Swiss Federal
                                Institute of Technology, Laboratory of Biochemistry
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                                 ***sodium***   -   ***calcium***    ***exchanger***
                              gene NCX1 and characterization of its activity in
                              vascular smooth muscle cells
    JOURNAL (SO):             J. Biol. Chem., 273 (13), 7643-7649 (  ***1998***  )
    OTHER SOURCE (OS):        CA 129:1331
REFERENCE:                    2  (bases 1 to 563)
    AUTHOR (AU):              Kraev,A.S.
    TITLE (TI):               Direct Submission
    JOURNAL (SO):             Submitted (06-MAY-1997) A.S. Kraev, Swiss Federal
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GenBank ACC. NO. (GBN):   Y13032
GenBank VERSION (VER):    Y13032.1  GI:2463212
CAS REGISTRY NO. (RN):    197682-63-6
SEQUENCE LENGTH (SQL):    583
MOLECULE TYPE (CI):       mRNA; linear
DIVISION CODE (CI):       Primates
DATE (DATE):              27 Oct 2000
DEFINITION (DEF):         Homo sapiens NCX1 mRNA alternative 5'end, exon 1a, 1e
                          and 2.
  SOURCE:                     ***human***    .
    ORGANISM (ORGN):      Homo sapiens
                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                          Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                          Hominidae; Homo
NUCLEIC ACID COUNT (NA): 178 a     107 c    151 g    147 t
COMMENT:
      Related sequences: M91368, X91213.
REFERENCE:                1  (bases 1 to 583)
    AUTHOR (AU):          Scheller,T.; Kraev,A.; Skinner,S.; Carafoli,E.
    TITLE (TI):           Cloning of the multipartite promoter of the
                            ***sodium***  -  ***calcium***    ***exchanger***
                          gene NCX1 and characterization of its activity in
                          vascular smooth muscle cells
    JOURNAL (SO):         J. Biol. Chem., 273 (13), 7643-7649 (  ***1998***  )
    OTHER SOURCE (OS):    CA 129:1331
REFERENCE:                2  (bases 1 to 583)
    AUTHOR (AU):          Kraev,A.S.
    TITLE (TI):           Direct Submission
    JOURNAL (SO):         Submitted (06-MAY-1997) A.S. Kraev, Swiss Federal
                          Institute of Technology, Laboratory of Biochemistry
                          III, Universitaetstr. 16, Zurich, CH-8092, SWITZERLAND

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LOCUS (LOC):              HSY12885     GenBank (R)
GenBank ACC. NO. (GBN):   Y12885
GenBank VERSION (VER):    Y12885.1  GI:2463210
CAS REGISTRY NO. (RN):    197682-62-5
SEQUENCE LENGTH (SQL):    328
MOLECULE TYPE (CI):       mRNA; linear
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DATE (DATE):                27 Oct 2000
DEFINITION (DEF):           Homo sapiens NCX1 mRNA alternative 5'end, exon 1d and
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SOURCE:                          ***human***   .
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                            Hominidae; Homo
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COMMENT:
      Related sequences: M91368, X91213.
REFERENCE:                  1   (bases 1 to 328)
    AUTHOR (AU):            Scheller,T.; Kraev,A.; Skinner,S.; Carafoli,E.
    TITLE (TI):             Cloning of the multipartite promoter of the
                              ***sodium***   -   ***calcium***   ***exchanger***
                            gene NCX1 and characterization of its activity in
                            vascular smooth muscle cells
    JOURNAL (SO):           J. Biol. Chem., 273 (13), 7643-7649 (  ***1998***  )
    OTHER SOURCE (OS):      CA 129:1331
REFERENCE:                  2   (bases 1 to 328)
    AUTHOR (AU):            Kraev,A.S.
    TITLE (TI):             Direct Submission
    JOURNAL (SO):           Submitted (01-MAY-1997) A.S. Kraev, Swiss Federal
                            Institute of Technology, Laboratory of Biochemistry
                            III, Universitaetstr. 16, Zurich, CH-8092, SWITZERLAND


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DIVISION CODE (CI):         Primates
DATE (DATE):                27 Oct 2000
DEFINITION (DEF):           Homo sapiens NCX1 mRNA alternative 5'end, exon 1d, 1c
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SOURCE:                          ***human***   .
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REFERENCE:                  1   (bases 1 to 558)
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      TITLE (TI):            Cloning of the multipartite promoter of the
                               ***sodium***  -  ***calcium***      ***exchanger***
                             gene NCX1 and characterization of its activity in
                             vascular smooth muscle cells
      JOURNAL (SO):          J. Biol. Chem., 273 (13), 7643-7649 (  ***1998***  )
      OTHER SOURCE (OS):     CA 129:1331
   REFERENCE:                2  (bases 1 to 558)
      AUTHOR (AU):           Kraev,A.S.
      TITLE (TI):            Direct Submission
      JOURNAL (SO):          Submitted (01-MAY-1997) A.S. Kraev, Swiss Federal
                             Institute of Technology, Laboratory of Biochemistry
                             III, Universitaetstr. 16, Zurich, CH-8092, SWITZERLAND

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exon            1..84                   /note="number 1d"
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LOCUS (LOC):              RNU53420      GenBank (R)
GenBank ACC. NO. (GBN):   U53420
GenBank VERSION (VER):    U53420.1  GI:1552525
CAS REGISTRY NO. (RN):    181290-29-9
SEQUENCE LENGTH (SQL):    4854
MOLECULE TYPE (CI):       mRNA; linear
DIVISION CODE (CI):       Rodents
DATE (DATE):              4 Oct 1996
DEFINITION (DEF):         Rattus norvegicus   ***sodium***  -  ***calcium***
                            ***exchanger***   form 3 (NCX3) mRNA, complete cds.
SOURCE:                   Norway rat.
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   AUTHOR (AU):           Nicoll,D.A.; Quednau,B.D.; Qui,Z.; Xia,Y.R.;
                          Lusis,A.J.; Philipson,K.D.
   TITLE (TI):            Cloning of a third mammalian Na+-Ca2+ exchanger, NCX3
   JOURNAL (SO):          J. Biol. Chem., 271 (40), 24914-24921 (  ***1996***  )
   OTHER SOURCE (OS):     CA 125:267098
REFERENCE:                2  (bases 1 to 4854)
   AUTHOR (AU):           Nicoll,D.A.; Philipson,K.D.
   TITLE (TI):            Direct Submission
   JOURNAL (SO):          Submitted (02-APR-1996) Physiology, University of
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4441 ctccaatgtt tgtgtctgag gtgggggaga agaaggtatt ctactgagga tgtctctaag
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4681 agcatgttca taagatagga actggaatcc ttcatcttcc ccaacacccc ccttgttcct
4741 gcctgttttt aaacctcata aagctctctg ttcccagact gtggggtatt tcttataccc
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LOCUS (LOC):   OSTA136   GenBank (R)
GenBank ACC. NO. (GBN): X91807
GenBank VERSION (VER):   X91807.1 GI:1136121
CAS REGISTRY NO. (RN): 172012-10-1
SEQUENCE LENGTH (SQL):   1677
MOLECULE TYPE (CI):   mRNA; linear
DIVISION CODE (CI):   Plants, fungi, algae
DATE (DATE):   3 Nov 2000
DEFINITION (DEF):   O.sativa mRNA for alpha-tubulin (clone OSTA-136).
SOURCE: Oryza sativa (japonica cultivar-group).
 ORGANISM (ORGN):   Oryza sativa (japonica cultivar-group)

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                          Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida;
                          Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza
NUCLEIC ACID COUNT (NA): 310 a    507 c    471 g    389 t
COMMENT:
     Overlaps with Z11931.
REFERENCE:              1   (bases 1 to 1677)
     AUTHOR (AU):       Kraev,A.; Chumakov,I.; Carafoli,E.
     TITLE (TI):        The organization of the   ***human***    gene NCX1
                        encoding the   ***sodium***  -  ***calcium***
                        ***exchanger***
     JOURNAL (SO):      Genomics, 37 (1), 105-112 (  ***1996***   )
     OTHER SOURCE (OS): CA 125:267114
REFERENCE:              2   (bases 1 to 1677)
     AUTHOR (AU):       Maestroni,A.; Giani,S.; Breviario,D.
     TITLE (TI):        Rice alpha-tubulin cDNAs
     JOURNAL (SO):      Unpublished
REFERENCE:              3   (bases 1 to 1677)
     AUTHOR (AU):       Breviaro,D.
     TITLE (TI):        Direct Submission
     JOURNAL (SO):      Submitted (25-SEP-1995) D. Breviaro, Instituto
                        Biosintesi Vegetali CNR, Via Bassini n 15, I-20133
                        Milano, ITALY

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                                                VFNAVGGGTGSGLGSLLLERLSVD
                                                YGKKSKLGFTVYPSPQVSTSVVEPYNSVLSTHSL
                                                LEHTDVAVLLDNEAIYDICRRSLD
                                                IERPTYTNRNRLVSQVISSLTASLRFDGALNVDV
                                                NEFQTNLVPYPRIHFMLSSYAPAI
                                                SAEKAYHEQLSVAEITNSAFEPSSMMAKCDPRHG
                                                KYMACCLMYRGDVVPKDVNAAVAT
                                                IKTKRTIQFVDWCPTGFKCGINYQPPSVVPGGDL
                                                AKVQRAVCMISNSTSVVEVFSRID
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                                                ALEKDYEEVGSEFDDGDEGDEGDE Y"

SEQUENCE (SEQ):
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     121 atccaggtcg ggaacgcgtg ctgggagctc tattgcctcg agcatggcat ccagcctgat
     181 ggacagatgc ccggtgacaa gaccgttggg ggaggtgatg atgcttttaa caccttcttc
     241 agtgagactg gtgctgggaa gcatgtcccc cgtgctgtct cgtcgatct tgagcctacc
     301 atgattgatg aggtgaggac tggtgactac cgccagctct ccaccctga gcaggtcatc
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     421 attgttgatc tgtgccttga ccgcatcagg aagcttgccg acaactgcac tggtctccag
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     601 tcccctcagg tctccacctc tgtggttgag ccatacaaca gtgtcctctc cacccactcc
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1021 gcgtgctgcc tgatgtaccg cggcgacgtg gtccccaagg acgtgaacgc cgcggtggcc
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LOCUS (LOC):   HSNCX22   GenBank (R)
GenBank ACC. NO. (GBN):   X93017
GenBank VERSION (VER):   X93017.1 GI:1067133
CAS REGISTRY NO. (RN):   170817-51-3
SEQUENCE LENGTH (SQL):   2534
MOLECULE TYPE (CI):   DNA; linear
DIVISION CODE (CI):   Primates
DATE (DATE):   12 Nov 2000
DEFINITION (DEF):   Homo sapiens partial SCL8A3 gene for solute carrier
                            family 8 (***sodium***   /   ***calcium***
                            exchanger   ), member 3 (SCL8A3), exon 2.
SOURCE: ***human***   .
 ORGANISM (ORGN):   Homo sapiens
                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                            Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                            Hominidae; Homo
NUCLEIC ACID COUNT (NA):   602 a   595 c   644 g   693 t
COMMENT:
     Similar to X91213.
REFERENCE: 1 (bases 1 to 2534)
  AUTHOR (AU):   Kraev,A.; Chumakov,I.; Carafoli,E.
  TITLE (TI):   The organization of the   ***human***   gene NCX1
                            encoding the   ***sodium***   -   ***calcium***
                            exchanger
  JOURNAL (SO):   Genomics, 37 (1), 105-112 (***1996***   )
  OTHER SOURCE (OS):   CA 125:267114
REFERENCE: 2 (bases 1 to 2534)
  AUTHOR (AU):   Kraev,A.S.
  TITLE (TI):   Direct Submission
  JOURNAL (SO):   Submitted (14-NOV-1995) A.S. Kraev, Swiss Federal
                            Institute of Technology, Laboratory of Biochemistry
                            III, Universitaetstr. 16, Zurich, CH-8092, SWITZERLAND

FEATURES (FEAT):
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                                             /clone-lib="Stratagene genomic
                                             #946204"
gene   281..2126   /gene="SLC8A3"
exon   281..2126   /gene="SLC8A3"
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                                             /product="solute carrier family 8
                                             (sodium/calcium exchanger), member
                                             3"

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  301 acaactggtg ctgcaataga agccagtggc taagtctcgt gtatggcgtg gttaaggttg
  361 cagcctctca cctctgcctt cctccatttt gggctggtta cctttgtgct cttcctgaat
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2521 atctatgagc tttg
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LOCUS (LOC):                 HSNCX19      GenBank (R)
GenBank ACC. NO. (GBN):      X91216
GenBank VERSION (VER):       X91216.1  GI:1061138
CAS REGISTRY NO. (RN):       170612-18-7
SEQUENCE LENGTH (SQL):       431
MOLECULE TYPE (CI):          DNA; linear
DIVISION CODE (CI):          Primates
DATE (DATE):                 24 Nov 2000
DEFINITION (DEF):            H.sapiens ncx1 gene (exon 9).
SOURCE:                        ***human***   .
 ORGANISM (ORGN):            Homo sapiens
                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                             Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                             Hominidae; Homo
NUCLEIC ACID COUNT (NA): 127 a    95 c    108 g    101 t
REFERENCE:                   1
  AUTHOR (AU):               Kraev,A.; Chumakov,I.; Carafoli,E.
  TITLE (TI):                The organization of the    ***human***    gene NCX1
                             encoding the    ***sodium***  -  ***calcium***
                             ***exchanger***
  JOURNAL (SO):              Genomics, 37 (1), 105-112 (   ***1996***   )
  OTHER SOURCE (OS):         CA 125:267114
REFERENCE:                   2   (bases 1 to 431)
  AUTHOR (AU):               Kraev,A.S.
  TITLE (TI):                Direct Submission
  JOURNAL (SO):              Submitted (07-SEP-1995) A.S. Kraev, Swiss Federal
                             Institute of Technology, Laboratory of Biochemistry
                             III, Universitaetstr. 16, Zurich, CH-8092, SWITZERLAND


FEATURES (FEAT):
  Feature Key      Location                     Qualifier
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   121 atgacaagca gccactgacc agcaaagagg aagaggagag gcgcattgca gaaatggggc
   181 gccccatcct gggagagcca accaagttgg aagtgatcat tgaagaatcc tatgaattca
   241 aggtatgctc accaacactg cccaccagga gccagtctca ccttgggaca gaaactgttc
   301 ataggggttgg ccaaagctta agatccacct ggaaagagta gtagatgtaa tttcaggaac
   361 tggcttgtga attgagagcc tttggggcca aattggaatt atagagttaa tcaggaacca
   421 aggagtcctg t
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LOCUS (LOC):              HSNCX11      GenBank (R)
GenBank ACC. NO. (GBN):   X92368
GenBank VERSION (VER):    X92368.1  GI:1061130
CAS REGISTRY NO. (RN):    170612-17-6
SEQUENCE LENGTH (SQL):    390
MOLECULE TYPE (CI):       DNA; linear
DIVISION CODE (CI):       Primates
DATE (DATE):              24 Nov 2000
DEFINITION (DEF):         H.sapiens ncx1 gene (exon 1).
SOURCE:                      ***human***   .
  ORGANISM (ORGN):        Homo sapiens
                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                          Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                          Hominidae; Homo
NUCLEIC ACID COUNT (NA):  73 a    85 c    121 g    111 t
REFERENCE:                1
  AUTHOR (AU):            Kraev,A.; Chumakov,I.; Carafoli,E.
  TITLE (TI):             Molecular biological studies of the cardiac
                             ***sodium***  -  ***calcium***     ***exchanger***
  JOURNAL (SO):           Ann. N. Y. Acad. Sci., 779, 103-109 (  ***1996***  )
  OTHER SOURCE (OS):      CA 125:134211
REFERENCE:                2  (bases 1 to 390)
  AUTHOR (AU):            Kraev,A.; Chumakov,I.; Carafoli,E.
  TITLE (TI):             The organization of the   ***human***   gene NCX1
                          encoding the   ***sodium***  -  ***calcium***
                          ***exchanger***
  JOURNAL (SO):           Genomics, 37 (1), 105-112 (  ***1996***  )
  OTHER SOURCE (OS):      CA 125:267114
REFERENCE:                3  (bases 1 to 390)
  AUTHOR (AU):            Kraev,A.S.
  TITLE (TI):             Direct Submission
  JOURNAL (SO):           Submitted (13-OCT-1995) A.S. Kraev, Swiss Federal
                          Institute of Technology, Laboratory of Biochemistry
                          III, Universitaetstr. 16, Zurich, CH-8092, Switzerland
  OTHER SOURCE (OS):      CA 125:267114
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	X91614.1:205..311,	
	X91614.1:839..942,	
	X91214.1:38..58,	
	X91214.1:478..495,	
	X91214.1:600..614,	
	X91215.1:201..270,	
	X91216.1:112..242,	
	X91217.1:154..253,	
	X91963.1:115..390,	

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                        X91217.1:154..253,
                        X91963.1:115..390,
                        X91647.1:58..3536)
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  181 ccatttgctg ctcataaggc tacacttccc tctgctttgg caaacgagcg gcttctaaat
  241 ttgtgtgtgt gtgtgtgtgt gtgtgtgtgt gtgtgtgtgt gtgatgtggt gtgtgcgcgc
  301 ctgcacattt ttctgggtgt ccgcgcttcc cagagtgaaa ttgctcgggc tggtgcgtct
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LOCUS (LOC):                  HSNCX18        GenBank (R)
GenBank ACC. NO. (GBN):       X91215
GenBank VERSION (VER):        X91215.1  GI:1061137
CAS REGISTRY NO. (RN):        170612-16-5
SEQUENCE LENGTH (SQL):        381
MOLECULE TYPE (CI):           DNA; linear
DIVISION CODE (CI):           Primates
DATE (DATE):                  24 Nov 2000
DEFINITION (DEF):             H.sapiens ncx1 gene (exon 8).
SOURCE:                          ***human***   .
  ORGANISM (ORGN):            Homo sapiens
                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                              Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                              Hominidae; Homo
NUCLEIC ACID COUNT (NA):      94 a    98 c    66 g    123 t
REFERENCE:                    1
    AUTHOR (AU):              Kraev,A.; Chumakov,I.; Carafoli,E.
    TITLE (TI):               The organization of the    ***human***    gene NCX1
                              encoding the    ***sodium***   -   ***calcium***
                              ***exchanger***
    JOURNAL (SO):             Genomics, 37 (1), 105-112 (   ***1996***   )
    OTHER SOURCE (OS):        CA 125:267114
REFERENCE:                    2   (bases 1 to 381)
    AUTHOR (AU):              Kraev,A.S.
    TITLE (TI):               Direct Submission
    JOURNAL (SO):             Submitted (07-SEP-1995) A.S. Kraev, Swiss Federal
                              Institute of Technology, Laboratory of Biochemistry
                              III, Universitaetstr. 16, Zurich, CH-8092, SWITZERLAND


FEATURES (FEAT):
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  gene                  201..270                    /gene="ncx1"
  exon                  201..270                    /gene="ncx1"
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   121 ttagcttact aattccacaa agctctgata gcaaatcatg caatccattc tgctgatttt
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   361 tgtaaacatt gctaatatgc t
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LOCUS (LOC):	HSNCX1567 GenBank (R)
GenBank ACC. NO. (GBN):	X91214
GenBank VERSION (VER):	X91214.1 GI:1061136
CAS REGISTRY NO. (RN):	170612-15-4
SEQUENCE LENGTH (SQL):	800
MOLECULE TYPE (CI):	DNA; linear
DIVISION CODE (CI):	Primates
DATE (DATE):	24 Nov 2000
DEFINITION (DEF):	H.sapiens ncx1 gene (exons 5, 6 and 7).
SOURCE:	***human*** .
ORGANISM (ORGN):	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
	Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
	Hominidae; Homo
NUCLEIC ACID COUNT (NA):	206 a 125 c 126 g 343 t
REFERENCE:	1
AUTHOR (AU):	Kraev,A.; Chumakov,I.; Carafoli,E.
TITLE (TI):	The organization of the ***human*** gene NCX1
	encoding the ***sodium*** - ***calcium***
	exchanger
JOURNAL (SO):	Genomics, 37 (1), 105-112 (***1996***)
OTHER SOURCE (OS):	CA 125:267114
REFERENCE:	2 (bases 1 to 800)
AUTHOR (AU):	Kraev,A.S.
TITLE (TI):	Direct Submission
JOURNAL (SO):	Submitted (07-SEP-1995) A.S. Kraev, Swiss Federal
	Institute of Technology, Laboratory of Biochemistry
	III, Universitaetstr. 16, Zurich, CH-8092, SWITZERLAND

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..800	/organism="Homo sapiens"
		/db-xref="taxon:9606"
		/chromosome="2"
		/map="p21-23"
		/cell-line="WI38"
		/cell-type="fibroblast"
		/tissue-type="lung"
		/clone-lib="Statagene #946204"
gene	38..614	/gene="ncx1"
exon	38..58	/gene="ncx1"
		/number=5
		/usedin=X92368:RNA
		/label=ex5
exon	478..495	/gene="ncx1"
		/number=6
		/usedin=X92368:RNA
		/label=ex6
exon	600..614	/gene="ncx1"
		/number=7
		/usedin=X92368:RNA
		/label=ex7

SEQUENCE (SEQ):
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     1 ttaattctgt gtttgtcttt gtctgtttcc ttcacagccc tgttattgaa tgagcttggt
    61 aagcatttca tttcttgcat ttcctttcca tttttctaga ttattttcca tttccgtcag
   121 gtgatacagt agctctgtga cttttatttc tcttgacttg ctagcaagat tgttgtttag
   181 ggctattgac ctcattttgt caaggtcaaa tagtttatat tgcatttta atttagtaca
   241 accttttgaa aaatcggtga tttcttaggt atgcacaaga attaaatttg tgcattaaat
   301 ctcataatct taaaagaacg attagtgatt cagtcatgaa cattttccta gtcttcttaa
   361 ttgtaaatat aatttggcaa gtaccttggg tgggttgtca ggcagtctga tgtcactggt
   421 atttgttatg tagagtgtca aattataaca tttgttgttg ttttttttc ttttttaggtg
   481 gcttcacaat aacaggtatg aattttttcaa gtctaatgct atctaacttt tactgtctgt
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  601 aaaatacctg tttggtaaga cttatttttt taatgttcct tattttttccc caaataccct
  661 taaccatcaa tccaaaccta catcttatgt aacttgcatt aatatttaac tgtggcacat
  721 ggtgtcgtct tgctggtttt acacatttaa cgttttacaa attaataatg tgtgtgtgtt
  781 gtgtttataa gctgttcata
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LOCUS (LOC):                  HSNCX134      GenBank (R)
GenBank ACC. NO. (GBN):       X91614
GenBank VERSION (VER):        X91614.1  GI:1061135
CAS REGISTRY NO. (RN):        170612-14-3
SEQUENCE LENGTH (SQL):        1468
MOLECULE TYPE (CI):           DNA; linear
DIVISION CODE (CI):           Primates
DATE (DATE):                  24 Nov 2000
DEFINITION (DEF):             H.sapiens ncx1 gene (exons 3 & 4).
SOURCE:                         ***human***  .
  ORGANISM (ORGN):            Homo sapiens
                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                              Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                              Hominidae; Homo
NUCLEIC ACID COUNT (NA):      440 a    335 c    279 g    414 t
REFERENCE:                    1  (bases 1 to 1468)
    AUTHOR (AU):              Kraev,A.; Chumakov,I.; Carafoli,E.
    TITLE (TI):               The organization of the    ***human***    gene NCX1
                              encoding the    ***sodium***  -   ***calcium***
                                ***exchanger***
    JOURNAL (SO):             Genomics, 37 (1), 105-112 (  ***1996***   )
    OTHER SOURCE (OS):        CA 125:267114
REFERENCE:                    2  (bases 1 to 1468)
    AUTHOR (AU):              Kraev,A.S.
    TITLE (TI):               Direct Submission
    JOURNAL (SO):             Submitted (17-SEP-1995) A.S. Kraev, Swiss Federal
                              Institute of Technology, Laboratory of Biochemistry
                              III, Universitaetsstr. 16, Zurich, CH-8092, SWITZERLAND
    OTHER SOURCE (OS):        CA 125:267114
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FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..1468	/organism="Homo sapiens"
		/db-xref="taxon:9606"
		/chromosome="2"
		/map="p21-23"
		/cell-line="WI38"
		/cell-type="fibroblast"
		/tissue-type="lung"
		/clone-lib="Stratagene #946204"
gene	205..942	/gene="ncx1"
exon	205..311	/gene="ncx1"
		/number=3
		/usedin=X92368:RNA
		/label=ex3
exon	839..942	/gene="ncx1"
		/number=4
		/usedin=X92368:RNA
		/label=ex4

SEQUENCE (SEQ):
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    1 caggggagct atgcattggg tgaaatctct gatctttcat acctatctga tacccattct
   61 tgaagaaaaa actcacagta cagaagtttc tcgattactg tttgtctgaa agtgcagctg
  121 gttaaccttg ctttcctctt ctctatgttc cttctcttct ctttcctctt ccccttgttc
  181 gtcaatttct attctctgtt tcagcaaaac aatatcagtc aaggtaattg atgatgagga
  241 gtatgagaaa aacaagacct tcttccttga gattggagag ccccgcctgg tggagatgag
  301 tgagaagaaa ggtgggggag ctgctccagg gctgagccaa cagcttctgc tggcctgtgc
  361 cacccctgga tgcctgcact cttcagaaca tgacttacaa tgcacacatc cctccaccta
  421 tgtaacaggg cacagatctc atgctgagcc acagtaggca ggcctgtagc tacatcagcc
  481 agcgttaggt gcgctgcatt aacgtctgag agattaattt tcagggcagt caatcaagca
  541 tccatttctg ggaaagttgc tgcagatgcc atgcaatgcc atgccaaaat accccaaaat
  601 gggtacctac tgactgctaa ctgaagcggg aataattcgt gaaagtgata aattagcaaa
  661 gaaaacttaa tggggggccag ccaagagtac ccaagatgcc cttttacata cttcaggagg
  721 cccatgtgct gccagttctc cctccataac atcacagtaa cattcagctt ggtggacacc
  781 aagagcatga gcgtgtgact ccaaccattt gttttgcctt tgtcttgtgt cccacagga
  841 agatcattac cattagaata tttgaccgtg aggaatatga gaaagagtgc agtttctccc
  901 ttgtgcttga ggaaccaaaa tggataagaa gaggaatgaa aggtgtgaga gtaaacaaag
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1021 ctctcctctt cctcggcttc caagtactat acttcattgc cttttgaagct ttagcaattt
1081 catttccctt ccctaattca caagtgcaac aggcaacgcc cactttcttc aggaaatgcc
1141 aactaacctt gattgcaacc agatttaata acactgaaag ggatttctgt aattcagaaa
1201 tgattacata aaagaatgtg tttagttttt cactactcac ggtttattct aaaatgtcac
1261 tccaattatt aaatcttccc taaaatttta gtgataaaga cgacttaata cctcatcaat
1321 catacctcaa taaagctgga aaaaagaaac tgcttaatac ctattagtat tagtagatga
1381 ccctaatggc aactaacagg aaacttcaga attcaaataa ttaggcttct ttggagaaca
1441 cagtttaaaa atatttaata agaacaaa
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LOCUS (LOC):                    HSNCX12       GenBank (R)
GenBank ACC. NO. (GBN):         X91213
GenBank VERSION (VER):          X91213.1  GI:1061134
CAS REGISTRY NO. (RN):          170612-13-2
SEQUENCE LENGTH (SQL):          2129
MOLECULE TYPE (CI):             DNA; linear
DIVISION CODE (CI):             Primates
DATE (DATE):                    24 Nov 2000
DEFINITION (DEF):               H.sapiens ncx1 gene (exon 2).
SOURCE:                           ***human***   .
  ORGANISM (ORGN):              Homo sapiens
                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                                Hominidae; Homo
NUCLEIC ACID COUNT (NA):        590 a    381 c    523 g    635 t
REFERENCE:                      1
  AUTHOR (AU):                  Kraev,A.; Chumakov,I.; Carafoli,E.
  TITLE (TI):                   The organization of the   ***human***   gene NCX1
                                encoding the   ***sodium***  -  ***calcium***
                                ***exchanger***
  JOURNAL (SO):                 Genomics, 37 (1), 105-112 (  ***1996***  )
  OTHER SOURCE (OS):            CA 125:267114
REFERENCE:                      2  (bases 1 to 2129)
  AUTHOR (AU):                  Kraev,A.S.
  TITLE (TI):                   Direct Submission
  JOURNAL (SO):                 Submitted (07-SEP-1995) A.S. Kraev, Swiss Federal
                                Institute of Technology, Laboratory of Biochemistry
                                III, Universitaetstr. 16, Zurich, CH-8092, SWITZERLAND
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FEATURES (FEAT):
  Feature Key       Location                    Qualifier
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source            1..2129                 /organism="Homo sapiens"
                                          /db-xref="taxon:9606"
                                          /chromosome="2"
                                          /map="p21-23"
                                          /cell-line="WI38"
                                          /cell-type="fibroblast"
                                          /tissue-type="lung"
                                          /clone-lib="Stratagene #946204"
gene              108..1936               /gene="ncx1"
exon              108..1936               /gene="ncx1"
                                          /number=2
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SEQUENCE (SEQ):
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  121 gaagtgtcat gtacaacatg cggcgattaa gtctttcacc caccttttca atgggatttc
  181 atctgttagt tactgtgagt ctcttatttt cccatgtgga ccatgtaatt gctgagacag
  241 aaatggaagg agaaggaaat gaaactggtg aatgtactgg atcatattac tgtaagaaag
  301 gggtgatttt gcccatttgg gaaccccaag acccttcttt tggggacaaa attgctagag
  361 ctactgtgta ttttgtggcc atggtctaca tgtttcttgg agtctctatc atagctgatc
  421 ggttcatgtc ctctatagaa gtcatcacat ctcaagaaaa agaaataacc ataaagaaac
  481 ccaatggaga gaccaccaag acaactgtga ggatctggaa tgaaacagtt ctaacctga
  541 ccttgatggc cctgggatct tctgctcctg agattctcct ttcagtaatt gaagtgtgtg
  601 gccataactt cactgcagga gacctcggtc ctagcaccat cgtgggaagt gctgcattca
  661 atatgttcat cattattgca ctctgtgttt atgtggtgcc tgacggagag acaaggaaga
  721 ttaagcattt gcgtgtcttc tttgtgacag cagcctggag catctttgcc tacacctggc
  781 tttacattat tttgtctgtc atatctcctg gtgttgtgga ggtctggaa ggtttgctta
  841 ctttcttctt ctttcccatc tgtgttgtgt tcgcttgggt agcggatagg agacttctgt
  901 tttacaagta tgtctacaag aggtatcgag ctggcaagca gagggggatg attattgaac
  961 atgaaggaga caggccatct tctaagactg aaattgaaat ggacgggaaa gtggtcaatt
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1081 atgatgaaga agctaggcga gaaatggcta ggattctgaa ggaacttaag cagaagcatc
1141 cagataaaga aatagagcaa ttaatagaat tagctaacta ccaagtccta agtcagcagc
1201 aaaaaagtag agcatttttat cgcattcaag ctactcgcct catgactgga gctggcaaca
1261 ttttaaagag gcatgcagct gaccaagcaa ggaaggctgt cagcatgcac gaggtcaaca
1321 ctgaagtgac tgaaaatgac cctgttagta agatcttctt tgaacaaggg acatatcagt
1381 gtctggagaa ctgtggtact gtggcccttta ccattatccg cagaggtggt gatttgacta
1441 acactgtgtt tgttgacttc agaacagagg atggcacagc aaatgctggg tctgattatg
1501 aatttactga aggaactgtg gtgtttaagc ctggtgatac ccagaaggaa atcagagtgg
1561 gtatcataga tgatgatatc tttgaggagg atgaaaattt ccttgtgcat ctcagcaatg
1621 tcaaagtatc ttctgaagct tcagaagatg gcatactgga agccaatcat gtttctacac
1681 ttgcttgcct cggatctccc tccactgcca ctgtaactat ttttgatgat gaccacgcag
1741 gcatttttac ttttgaggaa cctgtgactc atgtgagtga gagcattggc atcatggagg
1801 tgaaagtatt gagaacatct ggagctcgag gaaatgttat cgttccatat aaaaccatcg
1861 aagggactgc cagaggtgga ggggaggatt ttgtaggacac ttgtggagag ctcgaattcc
1921 agaatgatga aattgtgtaa gttctatatt atatatgtgt gtgtgtgtgt gtgtgtgtgt
1981 ggttcagtgt gtttatgaat gtgagtctgt gcatcatttt ttaaattaaa tagcatgcaa
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LOCUS (LOC):                  HSNCX112      GenBank (R)
GenBank ACC. NO. (GBN):       X91647
GenBank VERSION (VER):        X91647.1  GI:1061133
CAS REGISTRY NO. (RN):        170612-12-1
SEQUENCE LENGTH (SQL):        3777
MOLECULE TYPE (CI):           DNA; linear
DIVISION CODE (CI):           Primates
DATE (DATE):                  24 Nov 2000
DEFINITION (DEF):             H.sapiens ncx1 gene (exon 12).
SOURCE:                       ***human***  .
  ORGANISM (ORGN):            Homo sapiens
                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                              Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                              Hominidae; Homo
NUCLEIC ACID COUNT (NA):      1078 a    753 c    726 g    1220 t
REFERENCE:                    1
    AUTHOR (AU):              Kraev,A.; Chumakov,I.; Carafoli,E.
    TITLE (TI):               The organization of the    ***human***    gene NCX1
                              encoding the    ***sodium***  -  ***calcium***
                              ***exchanger***
    JOURNAL (SO):             Genomics, 37 (1), 105-112 (  ***1996***  )
    OTHER SOURCE (OS):        CA 125:267114
REFERENCE:                    2  (bases 1 to 3777)
    AUTHOR (AU):              Kraev,A.S.
    TITLE (TI):               Direct Submission
    JOURNAL (SO):             Submitted (19-SEP-1995) A.S. Kraev, Swiss Federal
                              Institute of Technology, Laboratory of Biochemistry
                              III, Universitaetsstr. 16, Zurich, CH-8092, SWITZERLAND
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FEATURES (FEAT):
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                                           /map="p21-23"
                                           /cell-line="WI38"
                                           /cell-type="fibroblast"
                                           /tissue-type="lung"
                                           /clone-lib="Stratagene #946204"
gene               58..3536                /gene="ncx1"
exon               58..3536                /gene="ncx1"
                                           /number=12
                                           /usedin=X92368:RNA
                                           /label=ex12
variation          2718                    /gene="ncx1"
                                           /replace="c"
variation          3012..3013              /gene="ncx1"
                                           /replace="t"
variation          3129                    /gene="ncx1"
                                           /replace="t"
polyA-signal       3519..3524              /gene="ncx1"
polyA-site         3537
variation          3589..3591              /replace="ta"
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SEQUENCE (SEQ):
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    61 catttgccag caaagtggca gccacccagg accagtatgc agacgcctcc ataggtaacg
   121 tcacgggcag caacgcggtg aatgtcttcc tgggaatcgg tgtggcctgg tccatcgctg
   181 ccatctacca cgcagccaat ggggaacagt tcaaagtgtc ccctggcaca ctagctttct
   241 ctgtcactct cttcaccatt tttgctttca tcaatgtggg ggtgctgctg tatcggcgga
   301 ggccagaaat cggaggtgag ctgggtgggc cccggactgc caagctcctc acatcctgcc
   361 tctttgtgct cctatggctc ttgtacattt tcttctcctc cctggaggcc tactgccaca
   421 taaaaggctt ctaaaggaac tatcagatat agtaaattta tatatataca tatatataca
   481 taaaaattat gtataatgga cagaggaaac tgacatttgt catgttcact tacctgctga
   541 tggaatccag cttcaagagc atactctgta ctagggccga agtaaaaaac catcacctcc
   601 cattcccagg ggcatcatca tgttcaacaa ggcatggagg cagggcatct ttgcagctca
   661 gtctagaagg gctgcactct ctccaggttg ataaatcctt aaggctttga tttgttttgt
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   781 ttttgttttg ttttgttttt tgggagagt cagggttgtt gctttctctt gtggaaagtg
   841 aaaccatcca aatgtaaatg ggttttggta aaaatttaaa tcattagtat tcccctcac
   901 ctcccccaat cacttaaaaa tattttggat taagaaaaat ctgggcatgg aagaagaaag
   961 aagcatgtct tcatcgtatt accaaagttc atgcttatct ccggaatgtg agtggaggtg
  1021 aagctgcctc caagaagaag cataaaagtg gaatggagcc aggaaatccg atggttctag
  1081 aaatagtctg atatttaaac atgtgatacc tggcagtctc gtttaacagg tacaaggaaa
  1141 acgtgcctag attcccagga acatgcaaaa tcctttcttt cttatctctt tagctctgga
  1201 ctgtgattgg caaggtcctt cttccagcat tcagcccagc taagccccca ggtgccccat
  1261 cccaaccctg ttcctcctgt ccacctgcca tcccctatgc aaacagtaag aataaccccca
  1321 ttcaaaaagc acatcatcgt tttccatttg cattaacatg tgtctcagtc ccatgttgcc
  1381 gttgcttggg attgtctgtc agttttattt tcaaaggcat ccatggcttg cacaatcctg
  1441 ttccagtcat gactgaacat ttgctccttc ttcatgtgcc gttcggaaat gttgttgtga
  1501 tacctgttac acagtgcatg gtgaaaaaca aataaaacaa aacaaagagt atctgtatat
  1561 agtagagtat agtacatact gttctcccat ttggcaatgt tgattggaca ttgaagacat
  1621 aagtgagttt tcttttcacc tgagttgtta cttttgtgct gttattgagt ttgattaatt
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  1741 agcaataact gtcatgtggg gagaagttaa agctattgag aggatagcag gcaaactaca
  1801 aagatcttca tggaaaaatta gccatgtgga acacatcaga ggcctctaaa aatcacccat
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  2041 ggctattttg agccctgttt ctttcactgt ccagtctagt cctctttgat tatatcagta
  2101 gttgctgagt aagaaagaag ccaggtgac caacgggcct ttaaaagtgt tgtctcctct
  2161 acttatgctg aaagagaagg caattaaata agactagtac ctcccaggag gattggactg
  2221 ggatatttt aacccttttaa aaagaatagc tgtttctatg ttaaaatacc aaagaacatg
  2281 gataaaccca acattccaaa gtagtgagtc cactaatgag aaaaataata gaatgacttt
  2341 ggtcaacctc tcggagactt ctgtgtctat aaggaatccc aggctggaga cattcctagc
  2401 cctctgtatt gattcaaaaa tacttaataa attaaagctg ttgagactta ttttttcttc
  2461 tgtcactcag taaccatgat ccttcctcat ttaataaaca tttggtgact gaatgagtaa
  2521 ttaaatgctg gttacccact taatgtgcca ggtagtatga tactttctgg ggactaagcc
  2581 atgaacaaaa cagtctagat ccctgccctc agaagggtta cagtttatgt gattactatt
  2641 ttcatgagta aaagtgaaga aagccatatg gaaagatttt tatcttgcaa gaaaaaacaa
  2701 ttatgaaact ctttttaagat aaacacactg aaactgtatc aaagcaattg tccaaattgt
  2761 atttataccc aagaatttct ttaactaaga gagcataagg catatgtttg gaaaaccacc
  2821 ctctttatct ttgaccggct tgcagataaa tatatctctc cattttaaac caagaagggc
  2881 aatcatgttg gtgatccaga tcactgagaa agcccagtgt atcccatctt ttatctttgt
  2941 tgggcaatgga acttttctat ggcccacact ttacaattct ttgtcattct aacccatcct
  3001 tcccatccctt atttttttt ttttgagaa ttgctaaatg gaaagctagc ctagaagcac
  3061 caagtaaata tattcaagga atataagttg tttaaacatt agaaaaattt ttgcactcat
  3121 tttttagcag tattaggaat gtcaataatc ctgtagcaaa ttttcacaga gaacttaag
  3181 aaattcttgc attggtcgat ttcaatttga aagctttttg gtttgtttgc ttttttaaatt
  3241 ttcatgttct aggaaactat gattctggtt gttcaggatt gttattatta tagttgtgta
  3301 aaattatttt attttgtgtg tattgtgcac agcttggggg ggggcgggaa atgcactaat
  3361 tgtgctcttc cttataaatg gtacatatta ctgacacaga caaataaagt ttctaattgt
  3421 ttctgattta atcactagtg atacagcata ttctgtatga aatgttttct cctttctcat
  3481 tgtcatctac ttcatttttt gttttcatgt tttgaagaaa taaaaccaa aatggtatta
  3541 ttgtgcaact ggtatcatca tccaaagaaa aaaacagaca ccaagtattc aaactcttgc
  3601 aaacgtcaac ccttcggtca tgcaatgttc tcttttaat gtcccaggag aacacagtgt
  3661 cagaatattt gtctgtccta cagtgctgag atatatgttg gacattcctc catttcactg
  3721 attttttta cgttgcttag tatgactcta tctacatcct ttcctgcatc caggatc
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LOCUS (LOC):   HSNCX111   GenBank (R)
GenBank ACC. NO. (GBN): X91963
GenBank VERSION (VER):   X91963.1 GI:1061132
CAS REGISTRY NO. (RN):   170612-11-0
SEQUENCE LENGTH (SQL):   399
MOLECULE TYPE (CI):   DNA; linear
DIVISION CODE (CI):   Primates
DATE (DATE):   24 Nov 2000

SOURCE: ***human***   .
  ORGANISM (ORGN):   Homo sapiens
                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                               Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                               Hominidae; Homo
NUCLEIC ACID COUNT (NA): 87 a   93 c   109 g   110 t
REFERENCE: 1 (bases 1 to 399)
  AUTHOR (AU):   Kraev,A.; Chumakov,I.; Carafoli,E.
  TITLE (TI):   The organization of the   ***human***   gene NCX1
                               encoding the   ***sodium***   - ***calcium***
                               exchanger
  JOURNAL (SO):   Genomics, 37 (1), 105-112 (***1996***   )
  OTHER SOURCE (OS):   CA 125:267114
REFERENCE: 2 (bases 1 to 399)
  AUTHOR (AU):   Kraev,A.S.
  TITLE (TI):   Direct Submission
  JOURNAL (SO):   Submitted (04-OCT-1995) A.S. Kraev, Swiss Federal
                               Institute of Technology, Laboratory of Biochemistry
                               III, Universitaetsstr. 16, Zurich, CH-8092, SWITZERLAND
  OTHER SOURCE (OS):   CA 125:267114

FEATURES (FEAT):
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source   1..399   /organism="Homo sapiens"
                                                 /db-xref="taxon:9606"
                                                 /chromosome="2"
                                                 /map="p21-23"
                                                 /clone="809 b 6"
                                                 /clone-lib="CEPH megaYAC"
gene   115..390   /gene="ncx1"
exon   115..390   /gene="ncx1"
                                                 /number=11
                                                 /usedin=X92368:RNA
                                                 /label=ex11

SEQUENCE (SEQ):
      1 atggcctcct gtcacagagt ggagggatga ccgacctaga taggagagat tgagagagag
     61 gaagacccgg caacacaggt tgtgatgaaa tgtgcttcct tccattctct ctaggggaag
    121 atgatgacga cgatgaatgt ggggaagaga agctgccctc ctgtttcgat tacgtgatgc
    181 actttctgac tgtgttctgg aaggtcctgt ttgccttcgt cccccctact gaatactgga
    241 atggctgggc gtgtttcatt gtctccatcc tcatgattgg cctactgaca gctttcattg
    301 gagacctggc ttcccacttt ggctgcacca ttggcctgaa agattctgtg actgcagtcg
    361 tgttcgtcgc acttggaaca tcagtgccag gtacaaatt

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LOCUS (LOC):   HSNCX110   GenBank (R)
GenBank ACC. NO. (GBN):   X91217
GenBank VERSION (VER):   X91217.1 GI:1061131
CAS REGISTRY NO. (RN):   170612-10-9
SEQUENCE LENGTH (SQL):   602
MOLECULE TYPE (CI):   DNA; linear
DIVISION CODE (CI):   Primates
DATE (DATE):   24 Nov 2000
DEFINITION (DEF):   H.sapiens ncx1 gene (exon 10).
SOURCE: ***human***   .
  ORGANISM (ORGN):   Homo sapiens
                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                               Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                               Hominidae; Homo
NUCLEIC ACID COUNT (NA): 184 a   115 c   112 g   191 t
REFERENCE: 1
  AUTHOR (AU):   Kraev,A.; Chumakov,I.; Carafoli,E.
  TITLE (TI):   The organization of the   ***human***   gene NCX1
                               encoding the   ***sodium***   - ***calcium***
                               exchanger
  JOURNAL (SO):   Genomics, 37 (1), 105-112 (***1996***   )
  OTHER SOURCE (OS):   CA 125:267114
REFERENCE: 2 (bases 1 to 602)
  AUTHOR (AU):   Kraev,A.S.
  TITLE (TI):   Direct Submission
  JOURNAL (SO):   Submitted (07-SEP-1995) A.S. Kraev, Swiss Federal
                               Institute of Technology, Laboratory of Biochemistry
                               III, Universitaetsstr. 16, Zurich, CH-8092, SWITZERLAND

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FEATURES (FEAT):
  Feature Key          Location                    Qualifier
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source               1..602                      /organism="Homo sapiens"
                                                  /db-xref="taxon:9606"
                                                  /chromosome="2"
                                                  /map="p21-23"
                                                  /cell-line="WI38"
                                                  /cell-type="fibroblast"
                                                  /tissue-type="lung"
                                                  /clone-lib="Statagene #946204"
gene                 154..253                    /gene="ncx1"
exon                 154..253                    /gene="ncx1"
                                                  /number=10
                                                  /usedin=X92368:RNA
                                                  /label=ex10


SEQUENCE (SEQ):
     1 ataatcataa cagtgtttga tgtcaatact attattttga gcctaacatc tgctaccttt
    61 atataactct ggagtttcaa aatcaacaag gtcttggatt tcctgaggcc ttagcgaacc
   121 cagcatttat attttttcttt tcaacatttc tagagtactg tggacaaact cattaagaag
   181 acaaacctgg cccttgtggt tgggactaac agctggagag aacagttcat tgaagctatc
   241 actgtcagtg ctggtgagtg cctttctctg catattataa attaaaattg cccaatctga
   301 gctgagtttt cctactgtgg ctacttggtc tatggcaaag caccaaaggg cttccatggc
   361 aaaattaagg gagaaataag tttatttgtt aatgtatgca cattttaaag actaaattga
   421 ctatctagat gaagcaaatg tcttcacaca tgacatttttc ctccatctat attgcatctt
   481 tctggaaata gacaagataa atttaaagcg ttttgtgtct ctaattcacg aatagccaat
   541 cactaggctt tgtctggaaa attccctgta agcagcacaa aggtggccaa gtcaaggtca
   601 ag


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LOCUS (LOC):              CENACAEX        GenBank (R)
GenBank ACC. NO. (GBN):   X91803
GenBank VERSION (VER):    X91803.1  GI:2826758
CAS REGISTRY NO. (RN):    169791-31-5
SEQUENCE LENGTH (SQL):    2844
MOLECULE TYPE (CI):       mRNA; linear
DIVISION CODE (CI):       Invertebrates
DATE (DATE):              3 Nov 2000
DEFINITION (DEF):         C.elegans mRNA for protein similar to vertebrate Na/Ca
                          exchanger (CE-NCX1).
SOURCE:                   Caenorhabditis elegans.
 ORGANISM (ORGN):         Caenorhabditis elegans
                          Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
                          Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
NUCLEIC ACID COUNT (NA): 777 a    606 c    675 g    786 t
COMMENT:
     On Jan 31, 1998 this sequence version replaced gi:1009383.
REFERENCE:                1   (bases 1 to 2439)
   AUTHOR (AU):           Kraev,A.; Chumakov,I.; Carafoli,E.
   TITLE (TI):            Molecular biological studies of the cardiac
                              ***sodium***  -  ***calcium***     ***exchanger***
   JOURNAL (SO):          Ann. N. Y. Acad. Sci., 779, 103-109 (  ***1996***   )
   OTHER SOURCE (OS):     CA 125:134211
REFERENCE:                2   (bases 406 to 2844)
   AUTHOR (AU):           Kraev,A.; Chumakov,I.; Carafoli,E.
   TITLE (TI):            The organization of the   ***human***   gene NCX1
                          encoding the    ***sodium***  -  ***calcium***
                              ***exchanger***
   JOURNAL (SO):          Genomics, 37 (1), 105-112 (  ***1996***   )
   OTHER SOURCE (OS):     CA 125:134211
REFERENCE:                3   (bases 1 to 2844)
   AUTHOR (AU):           Kraev,A.S.
   TITLE (TI):            Direct Submission
   JOURNAL (SO):          Submitted (25-SEP-1995) A.S. Kraev, Swiss Federal
                          Institute of Technology, Laboratory of Biochemistry
                          III, Universitaetstr. 16, Zurich, CH-8092, SWITZERLAND


FEATURES (FEAT):
  Feature Key          Location                    Qualifier
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source               1..2844                     /organism="Caenorhabditis elegans"
                                                  /strain="Bristol N2"
                                                  /db-xref="taxon:6239"
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CDS   40..2682

SEQUENCE (SEQ):
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     61 ttgttccttg ttgtctcgtt gactacactt gggcaatacg cagctgagcc gcaaaatgga
    121 gaaataattc acgtatcttc ccaacgtata cccgggcctg agccggcttg tgctccggct
    181 aagccatgtt cccccggagt tatcgtacca gtttggcagc catcggaaaa cctgtcagaa
    241 tgcaaaatat ggttccgtgc aattgtctat ttaatcgcat tggcctattt attctttggt
    301 gtctcaattg tggcggatcg attcatggcg tctattgaag tgatcacttc tcagcagaaa
    361 tctgtgaaaa tgaagaagat aaccggtgaa catttcacaa taatggtacg tgtctggaat
    421 gaaacagtca gtaacctgac gctaatggct ctcggatcct cagccccca gattttgctc
    481 tcggtcattg aaatttgcgg aaataatttc gaagctggag agctgggacc atcgacaatt
    541 gttggatcag ctgctttaa cctattcatt attattgcag tctgtattat ggctattcca
    601 aacggcgaga cccgtcgagt acaacataat ggtgtgttct gggttactgt agtttggtct
    661 acatttgcat acgtctggct ttacctaatc ctgagtgtgt tcagtccggg agaagttgaa
    721 gtatgggagg gtgtgctcac ttttgtgttt ttcccgctaa ctgtgggcag tgcctacttt
    781 gccgatgcac atgctgggca attcggtcag agactaatct ccggacccct ctcctcgttc
    841 gtaaggaggt caccacgccg ttctccgtcc aaaaaaaccc gggaaaacgt ggaaaatgga
    901 gccggactcc caggggatgc aactcaaaat ttgataggag gagacgccga cgccctggca
    961 tttgaaattc acagacgtca ctacctggat attttcaaac aattgagatc ggagcatcca
   1021 gatgctccag tcgttgaact tgagaagcat gccatggaga aagttgtcgg agagcagaag
   1081 aaatcaagag ctttttatag aattcagaca actaggaaaa tgatcggtag tggagatatt
   1141 cagaaaaaat tgaagaaaag taataaactg gagccaatgg ttgttcaaaa aaccatggcc
   1201 accgtggagt tcgaccctcc tcactataca tgtctggaga atgttggtga cgtgtaccta
   1261 accgtcaaat gtgaccgagg atccgtacca gaggatacca cagttacggt acattataga
   1321 actattgctg ataccgctca agctgaatcc gactttgtgc acaccgaagg aacaatcact
   1381 tttgagccag acagactgaa caaaaaatc aaagtcggaa ttgtggacaa cgacatctac
   1441 gaggacgacg agcagttcat ggtccggctc tcacaagtcc gagccttccg ttcagagcac
   1501 ttttccagtg tgccggctcg gctgggtctc gcagcgacag ctaccgtaat cattgtggac
   1561 gatgatcatg ctggaagctt tggcttcttg tcagaaaaat tcaaatgcac agagtcatgt
   1621 ggctcatttg tggcagaagt tatacggtca cgtggagccc gtggtaaggt gtcaattcct
   1681 tataagactg ttgatggagc cgccaaatcg ccacaggact atgagcatca ggagggtgtg
   1741 ctgaagtttg ccgatgagca gtctaaagcc gaaatctaca ttccgattgt caacgatgat
   1801 gaatatgaaa aacacgaaga tttctatatt gagctcggtg agcccatttg gcacagggaa
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1921 gtagtgatca cagaagaccg agaattcaag aattttatgg atagagcatt ggtaacagcg
1981 aatacctcga ttatggtcgg aacttcgagt tggaagcaac aattcactga agcctggact
2041 ttggagccgg aggaggagga cggagaagtc acgactatgg aaaagttat gcattatatt
2101 gcattaccat ggaagctact gtttgccctg attccaccga ctgactattt taatggttgg
2161 ctatgttttg tggttgcaat tgcgatgatt ggactattaa ccgcatttat tggtgatatc
2221 gctgcagctt ttgggtgtac agttgggcta aaggactctg tgaccgccct caccttggtc
2281 gcaatgggaa cttctcttcc agacacattt gcgtcccgca ccgccgcagt tggagatcaa
2341 tgggctgacg gatcgattgg taatgtgact ggaagtaatg ctgttaatgt attcttgggt
2401 attggaattg cctggatgat tgctgcctgt gtacatgcct accggggtac caagttttta
2461 gtcgccacag gctccttggc cttctcggta acaatgttcc taattggctc agtcgtatgt
2521 gtcgccttac tccaatatcg tcgtttcaat cgaaaagtca acggagagtt aggcggtcca
2581 atgggctggc ggatcatttc cgccggaatt ttcgtctccg tttggctttt gtatatcgtc
2641 ctcacgcacac tagaggccta ttgtgattatt aaggggattct aatttttaatt ttttctttaa
2701 tttttcaaaa atttctaaat tttctcaaaa gccataattt cccaattttt cacctaaaaa
2761 tcaaagaatc aatactacaa actacattcc cgtgtctttt acttttatac atcaatcaat
2821 caatcaataa ataataaaac attt
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LOCUS (LOC):                  HSNCX1       GenBank (R)
GenBank ACC. NO. (GBN):       X91221
GenBank VERSION (VER):        X91221.1  GI:987078
CAS REGISTRY NO. (RN):        168878-73-7
SEQUENCE LENGTH (SQL):        591
MOLECULE TYPE (CI):           mRNA; linear
DIVISION CODE (CI):           Primates
DATE (DATE):                  24 Nov 2000
DEFINITION (DEF):             H.sapiens mRNA for NCX1 protein 3'UTR.
SOURCE:                          ***human***   .
  ORGANISM (ORGN):            Homo sapiens
                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                              Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                              Hominidae; Homo
NUCLEIC ACID COUNT (NA):      168 a    86 c    96 g    241 t
REFERENCE:                    1  (bases 1 to 591)
    AUTHOR (AU):              Kraev,A.; Chumakov,I.; Carafoli,E.
    TITLE (TI):               The organization of the    ***human***    gene NCX1
                              encoding the    ***sodium***  -  ***calcium***
                              ***exchanger***
    JOURNAL (SO):             Genomics, 37 (1), 105-112 (   ***1996***   )
    OTHER SOURCE (OS):        CA 125:267114
REFERENCE:                    2  (bases 1 to 591)
    AUTHOR (AU):              Kraev,A.S.
    TITLE (TI):               Direct Submission
    JOURNAL (SO):             Submitted (31-AUG-1995) A.S. Kraev, Swiss Federal
                              Institute of Technology, Laboratory of Biochemistry
                              III, Universitaetstr. 16, Zurich, CH-8092, SWITZERLAND
    OTHER SOURCE (OS):        CA 125:267114
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   Feature Key        Location                    Qualifier
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source            1..591                     /organism="Homo sapiens"
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                                             /clone="141435"
                                             /tissue-type="placenta"
                                             /clone-lib="Soares Placenta Nb2HP"
gene              1..591                     /gene="NCX1"
3'UTR             1..591                     /gene="NCX1"
polyA-signal      574..579                   /gene="NCX1"
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SEQUENCE (SEQ):
     1 tggaactttt ctatggccca cactttacaa ttctttgtca ttctaaccca tccttcccat
    61 ccttattttt ttttttttg agaattgcta aatggaaagc tagcctagaa gcaccaagta
   121 aatatattca aggaatataa gttgtttaaa cattagaaaa attttgcac tcattttta
   181 gctgtattag gaatgtcaat aatcctgtag caaattttca cagagaactt aagaaattc
   241 ttgcattggt cgatttcaat ttgaaagctt tttggtttgt ttgcttttta aattttcatg
   301 ttctaggaaa ctatgattct ggttgttcag gattgttatt attatagttg tgtaaaatta
   361 ttttattttg tgtgtattgt gcacagcttg gggggggggc gggaaatgca ctaattgtgc
   421 tcttccttat aaatggtaca tattactgac acagacaaat aaagtttcta attgtttctg
   481 atttaatcac tagtgataca gcatattctg tatgaaatgt tttctccttt ctcattgtca
   541 tctacttcat ttttgtttt catgtttga agaaataaaa accaaaatgg t
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LOCUS (LOC):                T19755        GenBank (R)
GenBank ACC. NO. (GBN):     T19755
GenBank VERSION (VER):      T19755.1  GI:597500
CAS REGISTRY NO. (RN):      160365-54-8
SEQUENCE LENGTH (SQL):      211
MOLECULE TYPE (CI):         mRNA; linear
DIVISION CODE (CI):         Expressed sequence tag
DATE (DATE):                28 Nov 1994
DEFINITION (DEF):           957R Heart Homo sapiens cDNA clone 957 similar to
                               ***Sodium***  /  ***calcium***     ***exchanger***   ,
                            mRNA sequence.
SOURCE:                        ***human***   .
  ORGANISM (ORGN):          Homo sapiens
                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                            Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                            Hominidae; Homo
NUCLEIC ACID COUNT (NA):    41 a    54 c    66 g    49 t    1 others
COMMENT:
       Other_ESTs: 957F
       Contact: Liew CC
       Brigham and Women's Hospital
       Harvard Medical School
       75 Francis St. Boston, MA 02115, USA
       Tel: 6177328915
       Fax: 6179750995
       Email: cliew@rics.bwh.harvard.edu
       Seq primer: GACACCAGACCAACTGGTAATG.
REFERENCE:                  1  (bases 1 to 211)
   AUTHOR (AU):             Liew,C.C.; Hwang,D.M.; Fung,Y.W.; Laurenssen,C.;
                            Cukerman,E.; Tsui,S.y; Lee,C.Y.
   TITLE (TI):              A catalogue of genes in the cardiovascular system as
                            identified by expressed sequence tags
   JOURNAL (SO):            Proc. Natl. Acad. Sci. U.S.A., 91, 10645-10649 (
                               ***1994***   )
   OTHER SOURCE (OS):       CA 122:2521

FEATURES (FEAT):
   Feature Key          Location                   Qualifier
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source               1..211                    /organism="Homo sapiens"
                                               /db-xref="taxon:9606"
                                               /clone="957"
                                               /clone-lib="Heart"
                                               /lab-host="E.coli Y1090"
                                               /note="Vector: Lambda gt11;
                                               Site-1: EcoRI; Site-2: EcoRI"


SEQUENCE (SEQ):
     1 cgagagaaag ctagtgtgcc aggggacact ttgaastgtt ccccattggc tgcgtggtag
    61 atggcagcga tgggccaggc cacaccgatt cccaggaaga cattcaccgc gttgctgccc
   121 gtgacgttac ctatggaggc gtctgcatac tggtcctggg tggctgccac tttgctggca
   181 aatgtgtctg gcactgatgt tccaagtgcg a
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LOCUS (LOC):                T19754        GenBank (R)
GenBank ACC. NO. (GBN):     T19754
GenBank VERSION (VER):      T19754.1  GI:597499
CAS REGISTRY NO. (RN):      160365-53-7
SEQUENCE LENGTH (SQL):      261
MOLECULE TYPE (CI):         mRNA; linear
DIVISION CODE (CI):         Expressed sequence tag
DATE (DATE):                28 Nov 1994
DEFINITION (DEF):           957F Heart Homo sapiens cDNA clone 957 similar to
                               ***Sodium***  /  ***calcium***     ***exchanger***   ,
                            mRNA sequence.
SOURCE:                        ***human***   .
  ORGANISM (ORGN):          Homo sapiens
                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                            Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                            Hominidae; Homo
NUCLEIC ACID COUNT (NA):    68 a    53 c    68 g    71 t    1 others
COMMENT:
       Other_ESTs: 957R
       Contact: Liew CC
```

Harvard Medical School
75 Francis St. Boston, MA 02115, USA
Tel: 6177328915
Fax: 6179750995
Email: cliew@rics.bwh.harvard.edu
Seq primer: GGTGGCGACGACTCCTGGAGCC.
REFERENCE: 1   (bases 1 to 261)
    AUTHOR (AU):   Liew,C.C.; Hwang,D.M.; Fung,Y.W.; Laurenssen,C.;
                         Cukerman,E.; Tsui,S.y; Lee,C.Y.
    TITLE (TI):   A catalogue of genes in the cardiovascular system as
                         identified by expressed sequence tags
    JOURNAL (SO):   Proc. Natl. Acad. Sci. U.S.A., 91, 10645-10649 (
                         1994   )
    OTHER SOURCE (OS):   CA 122:2521

FEATURES (FEAT):
    Feature Key   Location   Qualifier
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source   1..261   /organism="Homo sapiens"
                                                 /db-xref="taxon:9606"
                                                 /clone="957"
                                                 /clone-lib="Heart"
                                                 /lab-host="E.coli Y1090"
                                                 /note="Vector: Lambda gt11;
                                                 Site-1: EcoRI; Site-2: EcoRI"

SEQUENCE (SEQ):
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     61 ctggcccttg tggttgggac taacagctgg agagaacagt tcattgaagc tatcactgtc
    121 agtvctgggg aagatgatga cgacgatgaa tgtggggaag agaagctgcc ctcctgtttc
    181 gattacgtga tgcactttct gactgtgttc tggaaggtcc tgtttgcctt cgtcccccct
    241 acttaatact ggaatggctg g

L4   ANSWER 266 OF 473   MEDLINE on STN
AN   2002303597   MEDLINE
DN   PubMed ID: 12045895
TI   Extracellular ATP effects on calcium signaling in cultured   ***human***
     non-pigmented ciliary body epithelium.
AU   Cullinane A B; Coca-Prados M; Harvey B J
CS   Wellcome Trust Cellular Physiology Research Unit, Department of
     Physiology, National University of Ireland, Cork, Ireland..
     abcullinane@hotmail.com
NC   EY-04873 (NEI)
SO   Current eye research,   ***(2001 Dec)***   23 (6) 448-54.
     Journal code: 8104312. ISSN: 0271-3683.
CY   England: United Kingdom
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   200207
ED   Entered STN: 20020605
     Last Updated on STN: 20020709
     Entered Medline: 20020708

L4   ANSWER 267 OF 473   MEDLINE on STN
AN   2002161303   MEDLINE
DN   PubMed ID: 11892938
TI   KB-R7943. Kanebo.
AU   Billman G E
CS   Ohio State University, Columbus 43210, USA.. billman.1@pop.service.ohio-
     state.edu
SO   Current opinion in investigational drugs (London, England : 2000),
     (2001 Dec)   2 (12) 1740-5. Ref: 40
     Journal code: 100965718. ISSN: 1472-4472.
CY   England: United Kingdom
DT   Journal; Article; (JOURNAL ARTICLE)
     General Review; (REVIEW)
     (REVIEW, TUTORIAL)
LA   English
FS   Priority Journals
EM   200208
ED   Entered STN: 20020315
     Last Updated on STN: 20020830
     Entered Medline: 20020829

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AN    2002066545    MEDLINE
DN    PubMed ID: 11793976
TI    Sodium-calcium exchange in platelets of diabetics.
AU    Bose R; Li Y; Woo V
CS    Dept. of Pharmacology, Dept. of Internal Medicine, University of Manitoba,
      Winnipeg, Manitoba R3W OW3, Canada.
SO    Proceedings of the Western Pharmacology Society,    ***(2001)***    44
      183-4.
      Journal code: 7505899. ISSN: 0083-8969.
CY    United States
DT    Journal; Article; (JOURNAL ARTICLE)
LA    English
FS    Priority Journals
EM    200207
ED    Entered STN: 20020125
      Last Updated on STN: 20020703
      Entered Medline: 20020702


L4    ANSWER 269 OF 473        MEDLINE on STN
AN    2002005301    MEDLINE
DN    PubMed ID: 11121788
TI    How can overexpression of Na(+),Ca(2+)-exchanger compensate the negative
      inotropic effects of downregulated SERCA?.
CM    Comment on: Cardiovasc Res. 2001 Jan;49(1):38-47. PubMed ID: 11121794
      Comment in: Cardiovasc Res. 2001 Apr;50(1):167-9. PubMed ID: 11345943
AU    Isenberg G
SO    Cardiovascular research,    ***(2001 Jan)***    49 (1) 1-6.   Ref: 14
      Journal code: 0077427. ISSN: 0008-6363.
CY    Netherlands
DT    Commentary
      Editorial
      General Review; (REVIEW)
      (REVIEW, TUTORIAL)
LA    English
FS    Priority Journals
EM    200203
ED    Entered STN: 20020121
      Last Updated on STN: 20020313
      Entered Medline: 20020312


L4    ANSWER 270 OF 473        MEDLINE on STN
AN    2001697034    MEDLINE
DN    PubMed ID: 11746521
TI    Hypoxia-induced increase in intracellular calcium concentration in
      endothelial cells: role of the Na(+)-glucose cotransporter.
AU    Berna N; Arnould T; Remacle J; Michiels C
CS    Laboratoire de Biochimie et Biologie Cellulaire, Facultes Universitaires
      Notre-Dame de la Paix, 61, rue de Bruxelles, B-5000 Namur, Belgium.
SO    Journal of cellular biochemistry,    ***(2001)***    84 (1) 115-31.
      Journal code: 8205768. ISSN: 0730-2312.
CY    United States
DT    Journal; Article; (JOURNAL ARTICLE)
LA    English
FS    Priority Journals
EM    200203
ED    Entered STN: 20011218
      Last Updated on STN: 20020314
      Entered Medline: 20020313


L4    ANSWER 271 OF 473        MEDLINE on STN
AN    2001692115    MEDLINE
DN    PubMed ID: 11735253
TI    Reperfusion arrhythmias: new insights into the role of the Na(+)/Ca(2+)
      exchanger.
CM    Comment on: J Mol Cell Cardiol. 2001 Oct;33(10):1861-9. PubMed ID:
      11603927
AU    Van Wagoner D R; Bond M
SO    Journal of molecular and cellular cardiology,    ***(2001 Dec)***    33 (12)
      2071-4.
      Journal code: 0262322. ISSN: 0022-2828.
CY    England: United Kingdom
DT    Commentary
      Editorial
LA    English
FS    Priority Journals
```

L4   ANSWER 272 OF 473   MEDLINE on STN
AN   2001680091   MEDLINE
DN   PubMed ID: 11723027
TI   Ionic mechanism of delayed afterdepolarizations in ventricular cells
       isolated from   ***human***   end-stage failing hearts.
AU   Verkerk A O; Veldkamp M W; Baartscheer A; Schumacher C A; Klopping C; van
       Ginneken A C; Ravesloot J H
CS   Department of Physiology, Experimental and Molecular Cardiology Group,
       Academic Medical Center, University of Amsterdam, The Netherlands..
       a.o.verkerk@amc.uva.nl
SO   Circulation,   ***(2001 Nov 27)***   104 (22) 2728-33.
       Journal code: 0147763. ISSN: 1524-4539.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Abridged Index Medicus Journals; Priority Journals
EM   200201
ED   Entered STN: 20011203
       Last Updated on STN: 20020201
       Entered Medline: 20020131

L4   ANSWER 273 OF 473   MEDLINE on STN
AN   2001652037   MEDLINE
DN   PubMed ID: 11704553
TI   Localization of thiazide-sensitive Na(+)-Cl(-) cotransport and associated
       gene products in mouse DCT.
CM   Comment in: Am J Physiol Renal Physiol. 2001 Dec;281(6):F1019-20. PubMed
       ID: 11704551
AU   Campean V; Kricke J; Ellison D; Luft F C; Bachmann S
CS   Department of Anatomy, Medical Faculty of the Charite, Humboldt
       University, 13353 Berlin, Germany.
SO   American journal of physiology. Renal physiology,   ***(2001 Dec)***   281
       (6) F1028-35.
       Journal code: 100901990. ISSN: 0363-6127.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   200112
ED   Entered STN: 20011114
       Last Updated on STN: 20020123
       Entered Medline: 20011227

L4   ANSWER 274 OF 473   MEDLINE on STN
AN   2001652036   MEDLINE
DN   PubMed ID: 11704552
TI   Distribution of transcellular calcium and sodium transport pathways along
       mouse distal nephron.
CM   Comment in: Am J Physiol Renal Physiol. 2001 Dec;281(6):F1019-20. PubMed
       ID: 11704551
AU   Loffing J; Loffing-Cueni D; Valderrabano V; Klausli L; Hebert S C; Rossier
       B C; Hoenderop J G; Bindels R J; Kaissling B
CS   Institute of Anatomy, University of Zurich, CH-8057 Zurich..
       jloffing@anatom.unizh.ch
SO   American journal of physiology. Renal physiology,   ***(2001 Dec)***   281
       (6) F1021-7.
       Journal code: 100901990. ISSN: 0363-6127.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   200112
ED   Entered STN: 20011114
       Last Updated on STN: 20020123
       Entered Medline: 20011227

L4   ANSWER 275 OF 473   MEDLINE on STN
AN   2001528012   MEDLINE
DN   PubMed ID: 11573936
TI   A disulfide bond is required for functional assembly of NCX1 from
       complementary fragments.

CS   Department of Physiology, UCLA School of Medicine, Los Angeles, CA
      90095-1760, USA.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   200112
ED   Entered STN: 20011001
      Last Updated on STN: 20020122
      Entered Medline: 20011204

AN   2001518213   MEDLINE
DN   PubMed ID: 11565424
TI   [Calcium-transporting systems and calcium regulation in cardiomyocytes].
      Kal'tsiitransportiruiushchie sistemy i reguliatsiia kontsentratsii
      kal'tsiia v kardiomiotsitakh.
AU   Aleksandrova E A
CS   Volgograd State Pedagogical University.
CY   Russia: Russian Federation
DT   Journal; Article; (JOURNAL ARTICLE)
      General Review; (REVIEW)
      (REVIEW, TUTORIAL)
LA   Russian
FS   Priority Journals
EM   200112
ED   Entered STN: 20010924
      Last Updated on STN: 20020122
      Entered Medline: 20011204

AN   2001511177   MEDLINE
DN   PubMed ID: 11558150
TI   Delayed apoptosis and its regulation in astrocytes.
AU   Takuma K
CS   Department of Analytical Chemistry, Faculty of Pharmaceutical Sciences,
      Kobe Gakuin University, 518 Arise, Ikawadani-cho, Nishi-ku, Kobe 651-2180,
      Japan.
CY   Japan
DT   Journal; Article; (JOURNAL ARTICLE)
      General Review; (REVIEW)
      (REVIEW, TUTORIAL)
LA   Japanese
FS   Priority Journals
EM   200112
ED   Entered STN: 20010918
      Last Updated on STN: 20020122
      Entered Medline: 20011204

AN   2001492633   MEDLINE
DN   PubMed ID: 11534550
TI   Abstracts of the American Physiological Society Conferences. Cellular and
      Molecular Physiology of Sodium-Calcium Exchange, Banff, Alberta, Canada,
      October 10-14, 2001. Genome and Hormones: An Integrative Approach to
      Gender Differences in Physiology, Pittsburgh, Pennsylvania, USA, October
      17-20, 2001.
AU   Anonymous
CY   United States
DT   Conference; Conference Article; (CONGRESSES)
      (OVERALL)
LA   English
FS   Priority Journals

AN   2001480930   MEDLINE
DN   PubMed ID: 11524394
TI   Patients with end-stage congestive heart failure treated with
      beta-adrenergic receptor antagonists have improved ventricular myocyte
      calcium regulatory protein abundance.
AU   Kubo H; Margulies K B; Piacentino V 3rd; Gaughan J P; Houser S R
CS   Cardiovascular Research Group, Department of Physiology and Section of
      Cardiology, Temple University School of Medicine, Philadelphia, PA 19140,
      USA.
NC   AG-17022 (NIA)
      HL-03560 (NHLBI)
      HL-33921 (NHLBI)
      HL-61495 (NHLBI)
SO   Circulation,   ***(2001 Aug 28)***   104 (9) 1012-8.
      Journal code: 0147763. ISSN: 1524-4539.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Abridged Index Medicus Journals; Priority Journals
EM   200109
ED   Entered STN: 20010830
      Last Updated on STN: 20010917
      Entered Medline: 20010913

AN   2001444431   MEDLINE
DN   PubMed ID: 11054465
TI   Acquired delayed rectifier channelopathies: how heart disease and
      antiarrhythmic drugs mimic potentially-lethal congenital cardiac
      disorders.
CM   Comment on: Cardiovasc Res. 2000 Nov;48(2):300-9. PubMed ID: 11054476
AU   Nattel S
SO   Cardiovascular research,   ***(2000 Nov)***   48 (2) 188-90.
      Journal code: 0077427. ISSN: 0008-6363.
CY   Netherlands
DT   Commentary
      Editorial
LA   English
FS   Priority Journals
EM   200109
ED   Entered STN: 20010813
      Last Updated on STN: 20011001
      Entered Medline: 20010927

AN   2001420888   MEDLINE
DN   PubMed ID: 11470457
TI   Cardiac   ***sodium*** - ***calcium***   ***exchanger*** : a
      double-edged sword.
CM   Comment on: Cardiovasc Res. 2001 Aug 1;51(2):241-50. PubMed ID: 11470463
AU   Conway S J; Koushik S V
SO   Cardiovascular research,   ***(2001 Aug 1)***   51 (2) 194-7. Ref: 44
      Journal code: 0077427. ISSN: 0008-6363.
CY   Netherlands
DT   Commentary
      Editorial
      General Review; (REVIEW)
      (REVIEW, TUTORIAL)
LA   English
FS   Priority Journals
EM   200109
ED   Entered STN: 20011001
      Last Updated on STN: 20011001
      Entered Medline: 20010927

AN   2001419684   MEDLINE
DN   PubMed ID: 11467418
TI   Evidence for mechanistic alterations of Ca2+ homeostasis in Type 2
      diabetes mellitus.

AN   2001405677   MEDLINE
DN   PubMed ID: 11456400
TI   Hypoxia delays the intracellular Ca2+ clearance by Na+-Ca2+ exchanger in
      human   adult cardiac myocytes.
AU   Park S I; Park E J; Kim N H; Baek W K; Lee Y T; Lee C J; Suh C K
CS   Department of Physiology and Biophysics, Inha University College of
      Medicine, Inchon, Korea.
SO   Yonsei medical journal,   ***(2001 Jun)***   42 (3) 333-7.
      Journal code: 0414003. ISSN: 0513-5796.
CY   Korea (South)
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   200108
ED   Entered STN: 20010820
      Last Updated on STN: 20010820
      Entered Medline: 20010816

AN   2001387548   MEDLINE
DN   PubMed ID: 11443225
TI   Intracellular Ca2+ release sparks atrial pacemaker activity.
AU   Lipsius S L; Huser J; Blatter L A
CS   Department of Physiology, Stritch School of Medicine, Loyola University
      Chicago, Maywood, Illinois 60153, USA.
SO   News in physiological sciences : an international journal of physiology
      produced jointly by the International Union of Physiological Sciences and
      the American Physiological Society,   ***(2001 Jun)***   16 101-6. Ref:
      20
      Journal code: 8609378. ISSN: 0886-1714.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
      General Review; (REVIEW)
      (REVIEW, TUTORIAL)
LA   English
FS   Priority Journals
EM   200107
ED   Entered STN: 20010730
      Last Updated on STN: 20010730
      Entered Medline: 20010726

AN   2001366257   MEDLINE
DN   PubMed ID: 11426897
TI   Leucocyte intracellular pH and Na+/H+ exchanger isoform-1 activity in
      postpartum women with pre-eclampsia.
AU   Lee V M; Halligan A W; Ng L L
CS   Department of Medicine and Therapeutics, Leicester Royal Infirmary, UK.
SO   BJOG : an international journal of obstetrics and gynaecology,   ***(2001*
      ***   Jun)***   108 (6) 615-22.
      Journal code: 100935741. ISSN: 1470-0328.
CY   England: United Kingdom
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Abridged Index Medicus Journals; Priority Journals
EM   200107
ED   Entered STN: 20010730
      Last Updated on STN: 20030304
      Entered Medline: 20010726

TI   Potent and selective inhibition of the   ***human***   Na+/H+ exchanger
      isoform NHE1 by a novel aminoguanidine derivative T-162559.
AU   Kawamoto T; Kimura H; Kusumoto K; Fukumoto S; Shiraishi M; Watanabe T;
      Sawada H
CS   Discovery Research Laboratories IV, Pharmaceutical Discovery Research
      Division, Takeda Chemical Industries, Ltd., 17-85, Jusohonmachi 2-chome,
      Yodogawa-ku, 532-8686, Osaka, Japan.. Kawamoto_Tomohiro@takeda.co.jp
SO   European journal of pharmacology,   ***(2001 May 18)***   420 (1) 1-8.
      Journal code: 1254354. ISSN: 0014-2999.
CY   Netherlands
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   200108
ED   Entered STN: 20010903
      Last Updated on STN: 20010903
      Entered Medline: 20010830

AN   2001338297   MEDLINE
DN   PubMed ID: 11164999
TI   The physiology of brain histamine.
AU   Brown R E; Stevens D R; Haas H L
CS   Institut fur Neurophysiologie, Heinrich-Heine-Universitat, D-40001,
      Dusseldorf, Germany.. brown@uni-duesseldorf.de
SO   Progress in neurobiology,   ***(2001 Apr)***   63 (6) 637-72.   Ref: 340
      Journal code: 0370121. ISSN: 0301-0082.
CY   England: United Kingdom
DT   Journal; Article; (JOURNAL ARTICLE)
      General Review; (REVIEW)
      (REVIEW, ACADEMIC)
LA   English
FS   Priority Journals
EM   200106
ED   Entered STN: 20010618
      Last Updated on STN: 20010618
      Entered Medline: 20010614

AN   2001329720   MEDLINE
DN   PubMed ID: 11397782
TI   Arrhythmogenesis and contractile dysfunction in heart failure: Roles of
      sodium-calcium exchange, inward rectifier potassium current, and residual
      beta-adrenergic responsiveness.
CM   Comment in: Circ Res. 2001 Jun 8;88(11):1095-6. PubMed ID: 11397771
AU   Pogwizd S M; Schlotthauer K; Li L; Yuan W; Bers D M
CS   Department of Medicine, University of Illinois, Chicago, IL, USA.
NC   HL-30077 (NHLBI)
      HL-46929 (NHLBI)
      HL-64724 (NHLBI)
SO   Circulation research,   ***(2001 Jun 8)***   88 (11) 1159-67.
      Journal code: 0047103. ISSN: 1524-4571.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   200107
ED   Entered STN: 20010716
      Last Updated on STN: 20010716
      Entered Medline: 20010712

AN   2001329709   MEDLINE
DN   PubMed ID: 11397771
TI   New era for translational research in cardiac arrhythmias.
CM   Comment on: Circ Res. 2001 Jun 8;88(11):1159-67. PubMed ID: 11397782
AU   Adachi-Akahane S; Kurachi Y
SO   Circulation research,   ***(2001 Jun 8)***   88 (11) 1095-6.
      Journal code: 0047103. ISSN: 1524-4571.
CY   United States
DT   Commentary
      Editorial
LA   English
FS   Priority Journals

ED   Entered STN: 20010716
     Last Updated on STN: 20010730
     Entered Medline: 20010712

L4   ANSWER 290 OF 473   MEDLINE on STN
AN   2001296967   MEDLINE
DN   PubMed ID: 11377809
TI   Mitochondria as target for antiischemic drugs.
AU   Morin D; Hauet T; Spedding M; Tillement J
CS   Laboratoire de Pharmacologie and Centre National de La Recherche
     Scientifique, Faculte de Medecine de Paris XII, 8 rue du General Sarrail,
     F-94010 Creteil, France.. morin@univ-paris12.fr
SO   Advanced drug delivery reviews,   ***(2001 Jul 2)***   49 (1-2) 151-74.
     Ref: 229
     Journal code: 8710523. ISSN: 0169-409X.
CY   Netherlands
DT   Journal; Article; (JOURNAL ARTICLE)
     General Review; (REVIEW)
     (REVIEW LITERATURE)
LA   English
FS   Priority Journals
EM   200108
ED   Entered STN: 20010806
     Last Updated on STN: 20010806
     Entered Medline: 20010802

L4   ANSWER 291 OF 473   MEDLINE on STN
AN   2001290066   MEDLINE
DN   PubMed ID: 11348995
TI   Cardiac Na(+)-Ca(2+) exchange: molecular and pharmacological aspects.
AU   Shigekawa M; Iwamoto T
CS   Department of Molecular Physiology, National Cardiovascular Center
     Research Institute, Suita, Osaka, Japan.. shigekaw@ri.ncvc.go.jp
SO   Circulation research,   ***(2001 May 11)***   88 (9) 864-76. Ref: 139
     Journal code: 0047103. ISSN: 1524-4571.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
     General Review; (REVIEW)
     (REVIEW, TUTORIAL)
LA   English
FS   Priority Journals
EM   200106
ED   Entered STN: 20010702
     Last Updated on STN: 20010702
     Entered Medline: 20010628

L4   ANSWER 292 OF 473   MEDLINE on STN
AN   2001285835   MEDLINE
DN   PubMed ID: 11243417
TI   KB-R7943, a selective Na+/Ca2+ exchange inhibitor, protects against
     ischemic acute renal failure in mice by inhibiting renal endothelin-1
     overproduction.
AU   Yamashita J; Ogata M; Takaoka M; Matsumura Y
CS   Department of Pharmacology, Osaka University, of Pharmaceutical Sciences,
     Takatsuki, Japan.
SO   Journal of cardiovascular pharmacology,   ***(2001 Mar)***   37 (3) 271-9.
     Journal code: 7902492. ISSN: 0160-2446.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   200105
ED   Entered STN: 20010529
     Last Updated on STN: 20010529
     Entered Medline: 20010524

L4   ANSWER 293 OF 473   MEDLINE on STN
AN   2001239912   MEDLINE
DN   PubMed ID: 11334878
TI   Effect of 2',4'-dichlorobenzamil hydrochloride, a Na(+)-Ca(2+) exchange
     inhibitor, on   ***human***   spermatozoa.
AU   Reddy P R; Patni A; Sharma A; Gupta S; Tiwary A K
CS   Department of Pharmaceutical Sciences and Drug Research, Punjabi
     University, 147 002, Patiala, India.
NC   N01MH30003 (NIMH)

CY   Netherlands
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   200109
ED   Entered STN: 20011001
     Last Updated on STN: 20011001
     Entered Medline: 20010927

L4   ANSWER 294 OF 473   MEDLINE on STN
AN   2001239739   MEDLINE
DN   PubMed ID: 11334793
TI   The effects of the Na(+)/Ca(++) exchange blocker on osmotic blood-brain
     barrier disruption.
AU   Bhattacharjee A K; Nagashima T; Kondoh T; Tamaki N
CS   Department of Neurosurgery, Kobe University School of Medicine, 7-5-1
     Kusunoki Cho, Chuo-Ku, 650-0017, Kobe, Japan.
SO   Brain research,   ***(2001 May 11)***   900 (2) 157-62.
     Journal code: 0045503. ISSN: 0006-8993.
CY   Netherlands
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   200109
ED   Entered STN: 20010910
     Last Updated on STN: 20010910
     Entered Medline: 20010906

L4   ANSWER 295 OF 473   MEDLINE on STN
AN   2001236342   MEDLINE
DN   PubMed ID: 11264230
TI   Inhibition of aggregation of rabbit and   ***human***   platelets induced
     by adrenaline and 5-hydroxytryptamine by KB-R7943, a Na(+)/Ca(2+) exchange
     inhibitor.
AU   Takano S; Kimura J; Ono T
CS   Department of Pharmacology, School of Medicine, Fukushima Medical
     University, Hikari-ga-oka 1, Fukushima 960-1295, Japan..
     s-takano@cc.fmu.ac.jp
SO   British journal of pharmacology,   ***(2001 Apr)***   132 (7) 1383-8.
     Journal code: 7502536. ISSN: 0007-1188.
CY   England: United Kingdom
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   200105
ED   Entered STN: 20010521
     Last Updated on STN: 20010521
     Entered Medline: 20010517

L4   ANSWER 296 OF 473   MEDLINE on STN
AN   2001236215   MEDLINE
DN   PubMed ID: 11134012
TI   The transport activity of the Na+-Ca2+ exchanger NCX1 expressed in HEK 293
     cells is sensitive to covalent modification of intracellular cysteine
     residues by sulfhydryl reagents.
AU   Ren X; Kasir J; Rahamimoff H
CS   Department of Biochemistry, Hebrew University-Hadassah Medical School,
     Jerusalem 91120, Israel.
SO   Journal of biological chemistry,   ***(2001 Mar 23)***   276 (12) 9572-9.
     Journal code: 2985121R. ISSN: 0021-9258.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   200105
ED   Entered STN: 20010517
     Last Updated on STN: 20030105
     Entered Medline: 20010503

L4   ANSWER 297 OF 473   MEDLINE on STN
AN   2001216796   MEDLINE
DN   PubMed ID: 11247757
TI   Platelet hyperactivity and abnormal Ca(2+) homeostasis in diabetes
     mellitus.

AN 2001112639   MEDLINE
DN PubMed ID: 11035002
TI Helix packing of functionally important regions of the cardiac
    Na(+)-Ca(2+) exchanger.
AU Qiu Z; Nicoll D A; Philipson K D
CS Department of Physiology, UCLA School of Medicine, Los Angeles, California
    90095-1760, USA.
NC HL49101 (NHLBI)
SO Journal of biological chemistry,   ***(2001 Jan 5)***   276 (1) 194-9.
    Journal code: 2985121R. ISSN: 0021-9258.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200102
ED Entered STN: 20010322
    Last Updated on STN: 20010322
    Entered Medline: 20010208

AN 2001034525   MEDLINE
DN PubMed ID: 10949914
TI Interaction between the actions of taurine and angiotensin II.
AU Schaffer S W; Lombardini J B; Azuma J
CS Department of Pharmacology, School of Medicine, University of South
    Alabama, Mobile 36688, USA.
SO Amino acids,   ***(2000)***   18 (4) 305-18. Ref: 81
    Journal code: 9200312. ISSN: 0939-4451.
CY Austria
DT Journal; Article; (JOURNAL ARTICLE)
    General Review; (REVIEW)
    (REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 200011
ED Entered STN: 20010322
    Last Updated on STN: 20010322
    Entered Medline: 20001130

AN 2001025369   MEDLINE
DN PubMed ID: 11029397
TI Increased Na(+)-Ca(2+) exchanger in the failing heart.
CM Comment on: Circ Res. 2000 Oct 13;87(8):690-8. PubMed ID: 11029405
AU Pogwizd S M
SO Circulation research,   ***(2000 Oct 13)***   87 (8) 641-3.
    Journal code: 0047103. ISSN: 1524-4571.
CY United States
DT Commentary
    Editorial
LA English
FS Priority Journals
EM 200011
ED Entered STN: 20010322
    Last Updated on STN: 20010521
    Entered Medline: 20001113

AN 2001012611   MEDLINE
DN PubMed ID: 11009553

L4   ANSWER 302 OF 473   MEDLINE on STN
AN   2001010239   MEDLINE
DN   PubMed ID: 10953508
TI   [Na+/Ca+ exchange: structure, mechanism, regulation and function].
     Na+/Ca2+ vymena: struktura, mechanismus, regulace a funkce.
AU   Stengl M; Pucelik P
CS   Fyziologicky ustav LF UK, Plzen.. stengl@lfp.cuni.cz
SO   Ceskoslovenska fysiologie / Ustredni ustav biologicky,   ***(2000 May)***
     49 (2) 73-90. Ref: 166
     Journal code: 2984710R. ISSN: 1210-6313.
CY   Czech Republic
DT   Journal; Article; (JOURNAL ARTICLE)
     General Review; (REVIEW)
     (REVIEW, ACADEMIC)
LA   Czech
FS   Priority Journals
EM   200010
ED   Entered STN: 20010322
     Last Updated on STN: 20010322
     Entered Medline: 20001026

L4   ANSWER 303 OF 473   MEDLINE on STN
AN   2000479346   MEDLINE
DN   PubMed ID: 11023899
TI   Na(+)-Ca(2+)-K(+) currents measured in insect cells transfected with the
     retinal cone or rod Na(+)-Ca(2+)-K(+) exchanger cDNA.
AU   Sheng J Z; Prinsen C F; Clark R B; Giles W R; Schnetkamp P P
CS   Department of Physiology and Biophysics and the MRC Group on Ion
     Channels/Transporters, Faculty of Medicine, University of Calgary,
     Calgary, Alberta T2N 4N1, Canada.
SO   Biophysical journal,   ***(2000 Oct)***   79 (4) 1945-53.
     Journal code: 0370626. ISSN: 0006-3495.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   200011
ED   Entered STN: 20010322
     Last Updated on STN: 20010322
     Entered Medline: 20001113

L4   ANSWER 304 OF 473   MEDLINE on STN
AN   2000441615   MEDLINE
DN   PubMed ID: 10845086
TI   Sodium-calcium exchange: a molecular perspective.
AU   Philipson K D; Nicoll D A
CS   Department of Physiology, UCLA School of Medicine 90095-1760, USA..
     kphilipson@mednet.ucla.edu
SO   Annual review of physiology,   ***(2000)***   62 111-33. Ref: 11
     Journal code: 0370600. ISSN: 0066-4278.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
     General Review; (REVIEW)
     (REVIEW, TUTORIAL)
LA   English
FS   Priority Journals
EM   200009
ED   Entered STN: 20000928
     Last Updated on STN: 20000928
     Entered Medline: 20000918

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AN      2000439723      MEDLINE
DN      PubMed ID: 10905082
TI      [Neuroprotective effect of sodium channel blockers in ischemia: the
        pathomechanism of early ischemic dysfunction].
        A Na(+)-csatorna-gatlok neuroprotektiv hatasa ischaemiaban: az ischaemia
        patomechanizmusanak elmeleti alapjai.
AU      Adam-Vizi V
CS      Semmelweis Egyetem, Altalanos Orvostudomanyi Kar, Orvosi Biokemia Intezet,
        Budapest.
SO      Orvosi hetilap,    ***(2000 Jun 4)***    141 (23) 1279-86.  Ref: 95
        Journal code: 0376412. ISSN: 0030-6002.
CY      Hungary
DT      Journal; Article; (JOURNAL ARTICLE)
        General Review; (REVIEW)
        (REVIEW, TUTORIAL)
LA      Hungarian
FS      Priority Journals
EM      200009
ED      Entered STN: 20000928
        Last Updated on STN: 20000928
        Entered Medline: 20000919


L4      ANSWER 306 OF 473       MEDLINE on STN
AN      2000424106      MEDLINE
DN      PubMed ID: 10900141
TI      Calcitriol upregulates expression and activity of the 1b isoform of the
        plasma membrane calcium pump in immortalized distal kidney tubular cells.
AU      Glendenning P; Ratajczak T; Dick I M; Prince R L
CS      Department of Medicine, University of Western Australia, Nedlands, Western
        Australia, 6009, Australia.. paulglen@cyllene.uwa.edu.au
SO      Archives of biochemistry and biophysics,    ***(2000 Aug 1)***    380 (1)
        126-32.
        Journal code: 0372430. ISSN: 0003-9861.
CY      United States
DT      Journal; Article; (JOURNAL ARTICLE)
LA      English
FS      Priority Journals
EM      200009
ED      Entered STN: 20000915
        Last Updated on STN: 20000915
        Entered Medline: 20000907


L4      ANSWER 307 OF 473       MEDLINE on STN
AN      2000407127      MEDLINE
DN      PubMed ID: 10935554
TI      Left ventricular assist device-induced reverse ventricular remodeling.
AU      Burkhoff D; Holmes J W; Madigan J; Barbone A; Oz M C
CS      Department of Medicine, Columbia University, New York, NY 10032, USA..
        db59@columbia.edu
SO      Progress in cardiovascular diseases,    ***(2000 Jul-Aug)***    43 (1)
        19-26.  Ref: 22
        Journal code: 0376442. ISSN: 0033-0620.
CY      United States
DT      Journal; Article; (JOURNAL ARTICLE)
        General Review; (REVIEW)
        (REVIEW, TUTORIAL)
LA      English
FS      Abridged Index Medicus Journals; Priority Journals
EM      200008
ED      Entered STN: 20000901
        Last Updated on STN: 20000901
        Entered Medline: 20000822


L4      ANSWER 308 OF 473       MEDLINE on STN
AN      2000400859      MEDLINE
DN      PubMed ID: 10822169
TI      D609-phosphatidylcholine-specific phospholipase C inhibitor attenuates
        thapsigargin-induced sodium influx in   ***human***   lymphocytes.
AU      Nofer J R; Junker R; Seedorf U; Assmann G; Zidek W; Tepel M
CS      Institut fur Klinische Chemie und Laboratoriumsmedizin,
        Zentrallaboratorium, Westfalische Wilhelms-Universitat, A. Schweitzer Str
        33, 48-149, Munster, Germany.. nofer@uni-muenster.de
SO      Cellular signalling,    ***(2000 May)***    12 (5) 289-96.
        Journal code: 8904683. ISSN: 0898-6568.
CY      ENGLAND: United Kingdom
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L4   ANSWER 309 OF 473   MEDLINE on STN
AN   2000247144   MEDLINE
DN   PubMed ID: 10785365
TI   The N-terminal portion of the main cytosolic loop mediates K+ sensitivity
         in the retinal rod Na+/Ca2+-K+-exchanger.
AU   Seiler E P; Guerini D; Guidi F; Carafoli E
CS   Department of Biochemistry III, Swiss Federal Institute of Technology
         (ETH), Zurich, Switzerland.
SO   European journal of biochemistry / FEBS,   ***(2000 May)***   267 (9)
         2461-72.
         Journal code: 0107600. ISSN: 0014-2956.
CY   GERMANY: Germany, Federal Republic of
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   200006
ED   Entered STN: 20000622
         Last Updated on STN: 20000622
         Entered Medline: 20000615

L4   ANSWER 310 OF 473   MEDLINE on STN
AN   2000217335   MEDLINE
DN   PubMed ID: 10751314
TI   Alternatively spliced isoforms of the rat eye sodium/calcium+potassium
         exchanger NCKX1.
AU   Poon S; Leach S; Li X F; Tucker J E; Schnetkamp P P; Lytton J
CS   Department of Biochemistry and Molecular Biology and Department of
         Physiology and Biophysics, University of Calgary, Calgary, Alberta, Canada
         T2N 4N1.
SO   American journal of physiology. Cell physiology,   ***(2000 Apr)***   278
         (4) C651-60.
         Journal code: 100901225. ISSN: 0363-6143.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   200004
ED   Entered STN: 20000505
         Last Updated on STN: 20000505
         Entered Medline: 20000427

L4   ANSWER 311 OF 473   MEDLINE on STN
AN   2000155916   MEDLINE
DN   PubMed ID: 10691802
TI   Renal sodium/calcium exchange; a vasodilator that is defective in
         salt-sensitive hypertension.
AU   Bell P D; Mashburn N; Unlap M T
CS   Nephrology Research and Training Center, Departments of Medicine and
         Physiology, Division of Nephrology, University of Alabama at Birmingham,
         Birmingham, AL 35294, USA.
NC   3R01DK32032 (NIDDK)
         HL50163 (NHLBI)
SO   Acta physiologica Scandinavica,   ***(2000 Jan)***   168 (1) 209-14.   Ref:
         35
         Journal code: 0370362. ISSN: 0001-6772.
CY   ENGLAND: United Kingdom
DT   Journal; Article; (JOURNAL ARTICLE)
         General Review; (REVIEW)
         (REVIEW, TUTORIAL)
LA   English
FS   Priority Journals
EM   200003
ED   Entered STN: 20000407
         Last Updated on STN: 20000407
         Entered Medline: 20000327

L4   ANSWER 312 OF 473   MEDLINE on STN
AN   2000076496   MEDLINE

TI   The retinal rod Na(+)/Ca(2+),K(+) exchanger contains a noncleaved signal
      sequence required for translocation of the N terminus.
AU   McKiernan C J; Friedlander M
CS   Department of Cell Biology, The Scripps Research Institute, La Jolla,
      California 92037, USA.
NC   5F32 EY06820 (NEI)
SO   Journal of biological chemistry,   ***(1999 Dec 31)***   274 (53)
      38177-82.
      Journal code: 2985121R. ISSN: 0021-9258.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   200002
ED   Entered STN: 20000218
      Last Updated on STN: 20000218
      Entered Medline: 20000208

L4   ANSWER 313 OF 473   MEDLINE on STN
AN   2000071617   MEDLINE
DN   PubMed ID: 10603950
TI   Sarcoplasmic reticulum proteins in heart failure.
AU   Lehnart S E; Schillinger W; Pieske B; Prestle J; Just H; Hasenfuss G
CS   Medizinische Klinik III, Universitat Freiburg, Germany.
SO   Annals of the New York Academy of Sciences,   ***(1998 Sep 16)***   853
      220-30. Ref: 52
      Journal code: 7506858. ISSN: 0077-8923.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
      General Review; (REVIEW)
      (REVIEW, TUTORIAL)
LA   English
FS   Priority Journals
EM   200001
ED   Entered STN: 20000124
      Last Updated on STN: 20000124
      Entered Medline: 20000107

L4   ANSWER 314 OF 473   MEDLINE on STN
AN   2000040157   MEDLINE
DN   PubMed ID: 10571527
TI   Sodium-calcium exchange: the phantom menace.
CM   Comment on: Circ Res. 1999 Nov 26;85(11):1009-19. PubMed ID: 10571531
AU   Goldhaber J I
SO   Circulation research,   ***(1999 Nov 26)***   85 (11) 982-4.
      Journal code: 0047103. ISSN: 0009-7330.
CY   United States
DT   Commentary
      Editorial
LA   English
FS   Priority Journals
EM   200001
ED   Entered STN: 20000114
      Last Updated on STN: 20000114
      Entered Medline: 20000105

L4   ANSWER 315 OF 473   MEDLINE on STN
AN   2000006744   MEDLINE
DN   PubMed ID: 10536662
TI   Heterogeneous transmural gene expression of calcium-handling proteins and
      natriuretic peptides in the failing   ***human***   heart.
CM   Comment in: Cardiovasc Res. 1999 Aug 1;43(2):279-81. PubMed ID: 10536655
AU   Prestle J; Dieterich S; Preuss M; Bieligk U; Hasenfuss G
CS   Abteilung Kardiologie und Pneumologie, Georg-August-Universitat Gottingen,
      Germany.. jprestle@mdv.gwdg.de
SO   Cardiovascular research,   ***(1999 Aug 1)***   43 (2) 323-31.
      Journal code: 0077427. ISSN: 0008-6363.
CY   Netherlands
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   199911
ED   Entered STN: 20000111
      Last Updated on STN: 20000229
      Entered Medline: 19991108

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L4    ANSWER 316 OF 473      MEDLINE on STN
AN    1999440255     MEDLINE
DN    PubMed ID: 10510560
TI    [Structure and function of selected Ca(2+) transport systems in cardiac
      cells].
      Struktura a funkcia vybranych Ca(2+)-transportnych systemov v srdcovych
      bunkach.
AU    Zacikova L; Krizanova O
CS    Ustav molekularnej fyziologie a genetiky Slovenskej akademie vied,
      Bratislava.
SO    Ceskoslovenska fysiologie / Ustredni ustav biologicky,    ***(1999 May)***
      48 (2) 62-76.  Ref: 148
      Journal code: 2984710R. ISSN: 1210-6313.
CY    Czech Republic
DT    Journal; Article; (JOURNAL ARTICLE)
      General Review; (REVIEW)
      (REVIEW, ACADEMIC)
LA    Slovak
FS    Priority Journals
EM    199910
ED    Entered STN: 19991101
      Last Updated on STN: 19991101
      Entered Medline: 19991021


L4    ANSWER 317 OF 473      MEDLINE on STN
AN    1999367311     MEDLINE
DN    PubMed ID: 10436268
TI    Na(+)/Ca(2+) exchange inhibitors modulate thapsigargin-induced Ca(2+) and
      Na(+) influx in   ***human***   lymphocytes.
AU    Nofer J R; Pulawski E; Junker R; Seedorf U; Assmann G; Zidek W; Tepel M
CS    Institut fur Klinische Chemie und Laboratoriumsmedizin,
      Zentrallaboratorium, Westfalische Wilhelms-Universitat, Albert Schweizer
      Strasse 33, D-48149 Munster, Germany.
SO    International journal of clinical & laboratory research,    ***(1999)***
      29 (2) 89-92.
      Journal code: 9206491. ISSN: 0940-5437.
CY    GERMANY: Germany, Federal Republic of
DT    Journal; Article; (JOURNAL ARTICLE)
LA    English
FS    Priority Journals
EM    199910
ED    Entered STN: 19991026
      Last Updated on STN: 20021210
      Entered Medline: 19991012


L4    ANSWER 318 OF 473      MEDLINE on STN
AN    1999339017     MEDLINE
DN    PubMed ID: 10410828
TI    Mechanism underlying the strong positive inotropic effects of LND-623:
      specific inhibition of Na, K-ATPase isoforms and exclusion of cellular
      sites of contractile control.
AU    Maixent J M; Lelievre L; Berrebi-Bertrand I
CS    Laboratoire de Recherche Cardiologique, Faculte de Medecine, Universite de
      la Mediterranee, Marseille, France.
SO    Cardiovascular drugs and therapy / sponsored by the International Society
      of Cardiovascular Pharmacotherapy,    ***(1998 Dec)***    12 (6) 585-94.
      Journal code: 8712220. ISSN: 0920-3206.
CY    United States
DT    Journal; Article; (JOURNAL ARTICLE)
LA    English
FS    Priority Journals
EM    199909
ED    Entered STN: 19990925
      Last Updated on STN: 19990925
      Entered Medline: 19990914


L4    ANSWER 319 OF 473      MEDLINE on STN
AN    1999322472     MEDLINE
DN    PubMed ID: 10390518
TI    Sodium/calcium exchange: its physiological implications.
AU    Blaustein M P; Lederer W J
CS    Departments of Physiology, University of Maryland School of Medicine,
      Baltimore, USA.
NC    HL-25675 (NHLBI)
      HL-45215 (NHLBI)
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CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
        General Review; (REVIEW)
        (REVIEW, TUTORIAL)
LA   English
FS   Priority Journals
EM   199907
ED   Entered STN: 19990806
        Last Updated on STN: 19990806
        Entered Medline: 19990723

L4   ANSWER 320 OF 473   MEDLINE on STN
AN   1999255385   MEDLINE
DN   PubMed ID: 10320357
TI   cDNA cloning and functional expression of the dolphin retinal rod Na-Ca+K
        exchanger NCKX1: comparison with the functionally silent bovine NCKX1.
AU   Cooper C B; Winkfein R J; Szerencsei R T; Schnetkamp P P
CS   Departments of Physiology & Biophysics and of Biochemistry & Molecular
        Biology, and MRC Group on Ion Channels and Transporters, The University of
        Calgary, 3330 Hospital Drive, N.W., Calgary, Alberta, T2N 4N1 Canada.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   199906
ED   Entered STN: 19990618
        Last Updated on STN: 19990618
        Entered Medline: 19990607

L4   ANSWER 321 OF 473   MEDLINE on STN
AN   1999233987   MEDLINE
DN   PubMed ID: 10217649
TI   Reduced sodium pump alpha1, alpha3, and beta1-isoform protein levels and
        Na+,K+-ATPase activity but unchanged Na+-Ca2+ exchanger protein levels in
            human   heart failure.
AU   Schwinger R H; Wang J; Frank K; Muller-Ehmsen J; Brixius K; McDonough A A;
        Erdmann E
CS   Klinik III fur Innere Medizin der Universitat zu Koln (Germany)..
        Robert.Schwinger@medizin.uni-koeln.de
NC   DK34316 (NIDDK)
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Abridged Index Medicus Journals; Priority Journals
EM   199905
ED   Entered STN: 19990601
        Last Updated on STN: 20010521
        Entered Medline: 19990517

L4   ANSWER 322 OF 473   MEDLINE on STN
AN   1999216483   MEDLINE
DN   PubMed ID: 10198283
TI   Reactive oxygen metabolites increase mitochondrial calcium in endothelial
        cells: implication of the Ca2+/Na+ exchanger.
AU   Jornot L; Maechler P; Wollheim C B; Junod A F
CS   Respiratory Division and Division of Clinical Biochemistry, Department of
        Internal Medicine, University Hospital, Switzerland..
        lan.h.jornot@hcuge.ch
CY   ENGLAND: United Kingdom
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   199907
ED   Entered STN: 19990727
        Last Updated on STN: 19990727
        Entered Medline: 19990709

AN   1999207220   MEDLINE
DN   PubMed ID: 10191496
TI   The Ca2+ pumps and the Na+/Ca2+ exchangers.
AU   Guerini D
CS   Institute of Biochemistry, Swiss Federal Institute of Technology (ETH),
        Zurich, Switzerland.. guerini@bc.biol.ethz.ch
SO   Biometals : an international journal on the role of metal ions in biology,
        biochemistry, and medicine,   ***(1998 Dec)***   11 (4) 319-30. Ref: 116
        Journal code: 9208478. ISSN: 0966-0844.
CY   Netherlands
DT   Journal; Article; (JOURNAL ARTICLE)
        General Review; (REVIEW)
        (REVIEW, ACADEMIC)
LA   English
FS   Priority Journals
EM   199904
ED   Entered STN: 19990511
        Last Updated on STN: 20000303
        Entered Medline: 19990426

L4   ANSWER 324 OF 473   MEDLINE on STN
AN   1999190721   MEDLINE
DN   PubMed ID: 10089232
TI   Regulatory function of Na-Ca exchange in the heart: milestones and
        outlook.
AU   Egger M; Niggli E
CS   Department of Physiology, University of Bern, Buhlplatz 5, CH-3012 Bern,
        Switzerland.
SO   Journal of membrane biology,   ***(1999 Mar 15)***   168 (2) 107-30. Ref:
        208
        Journal code: 0211301. ISSN: 0022-2631.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
        General Review; (REVIEW)
        (REVIEW, ACADEMIC)
LA   English
FS   Priority Journals
EM   199905
ED   Entered STN: 19990607
        Last Updated on STN: 19990607
        Entered Medline: 19990527

L4   ANSWER 325 OF 473   MEDLINE on STN
AN   1999189802   MEDLINE
DN   PubMed ID: 10089932
TI   Na+/Ca++ exchanger and myocardial ischemia/reperfusion.
AU   Mochizuki S; Jiang C
CS   Department of Medicine, Jikei University, School of Medicine, Tokyo,
        Japan.
SO   Japanese heart journal,   ***(1998 Nov)***   39 (6) 707-14.
        Journal code: 0401175. ISSN: 0021-4868.
CY   Japan
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   199904
ED   Entered STN: 19990420
        Last Updated on STN: 19990420
        Entered Medline: 19990407

L4   ANSWER 326 OF 473   MEDLINE on STN
AN   1999184735   MEDLINE
DN   PubMed ID: 10082981
TI   Metabolic pathways in the regulation of invertebrate and vertebrate
        Na+/Ca2+ exchange.
AU   DiPolo R; Beauge L
CS   Laboratorio de Permeabilidad Ionica, Centro de Biofisica y Bioquimica,
        IVIC, Apartado 21827, Caracas 1020-A, Venezuela.. ridipolo@cbb.ivic.ve
SO   Biochimica et biophysica acta,   ***(1999 Feb 25)***   1422 (1) 57-71.
        Ref: 82
        Journal code: 0217513. ISSN: 0006-3002.
CY   Netherlands
DT   Journal; Article; (JOURNAL ARTICLE)
        General Review; (REVIEW)
        (REVIEW, TUTORIAL)

L4   ANSWER 327 OF 473   MEDLINE on STN
AN   1999170405   MEDLINE
DN   PubMed ID: 10072189
TI   Mechanisms involved in the cellular calcium homeostasis in vascular smooth
      muscle: calcium pumps.
AU   Marin J; Encabo A; Briones A; Garcia-Cohen E C; Alonso M J
CS   Departamento de Farmacologia y Terapeutica, Facultad de Medicina,
      Universidad Autonoma de Madrid, Spain.. Jesus.Marin@uam.es
SO   Life sciences,   ***(1999)***   64 (5) 279-303. Ref: 253
      Journal code: 0375521. ISSN: 0024-3205.
CY   ENGLAND: United Kingdom
DT   Journal; Article; (JOURNAL ARTICLE)
      General Review; (REVIEW)
      (REVIEW, ACADEMIC)
LA   English
FS   Priority Journals
EM   199903
ED   Entered STN: 19990402
      Last Updated on STN: 19990402
      Entered Medline: 19990323

L4   ANSWER 328 OF 473   MEDLINE on STN
AN   1999081222   MEDLINE
DN   PubMed ID: 9865624
TI   Immunohistochemical localization of Na+/Ca2+ exchanger in   ***human***
      retina and retinal pigment epithelium.
AU   Loeffler K U; Mangini N J
CS   Universitats-Augenklinik, Bonn, Germany.. karinloeffler@compuserve.com
NC   EY01792 (NEI)
      EY11308 (NEI)
SO   Graefe's archive for clinical and experimental ophthalmology = Albrecht
      von Graefes Archiv fur klinische und experimentelle Ophthalmologie,
       (1998 Dec)   236 (12) 929-33.
      Journal code: 8205248. ISSN: 0721-832X.
CY   GERMANY: Germany, Federal Republic of
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   199903
ED   Entered STN: 19990326
      Last Updated on STN: 19990326
      Entered Medline: 19990316

L4   ANSWER 329 OF 473   MEDLINE on STN
AN   1999072302   MEDLINE
DN   PubMed ID: 9856482
TI   Chromosomal localization and genomic organization of the   ***human***
      retinal rod Na-Ca+K exchanger.
AU   Tucker J E; Winkfein R J; Murthy S K; Friedman J S; Walter M A; Demetrick
      D J; Schnetkamp P P
CS   Department of Biochemistry & Molecular Biology, and the MRC Group on Ion
      Channels/Transporters, Faculty of Medicine, University of Calgary, Canada.
SO   Human genetics,   ***(1998 Oct)***   103 (4) 411-4.
      Journal code: 7613873. ISSN: 0340-6717.
CY   GERMANY: Germany, Federal Republic of
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
OS   GENBANK-AF062922; GENBANK-AF062923; GENBANK-AF076932; GENBANK-AF076933;
      GENBANK-AF076934; GENBANK-AF076935; GENBANK-AF076936; GENBANK-AF076937;
      GENBANK-AF076938; GENBANK-AF076939; GENBANK-AF076940; GENBANK-AF076941;
      GENBANK-AF076942; GENBANK-AF076943; GENBANK-AF076944; GENBANK-AF076945;
      GENBANK-AF076946; GENBANK-AF076947; GENBANK-AF076948; GENBANK-AF076949
EM   199812
ED   Entered STN: 19990115
      Last Updated on STN: 20000303
      Entered Medline: 19981223

L4   ANSWER 330 OF 473   MEDLINE on STN

TI   A Glanzmann thrombasthenia-like phenotype caused by a defect in inside-out
      signaling through the integrin alpha(IIb)beta3.
AU   Tomiyama Y; Shiraga M; Kinoshita S; Ambo H; Kurata Y; Matsuzawa Y; Kunicki
      T J
CS   Second Department of Internal Medicine, Osaka University Medical School,
      Suita, Japan.

TI   Involvement of Na+/Ca2+ exchanger in inside-out signaling through the
      platelet integrin IIbbeta3.
AU   Shiraga M; Tomiyama Y; Honda S; Suzuki H; Kosugi S; Tadokoro S; Kanakura
      Y; Tanoue K; Kurata Y; Matsuzawa Y
CS   Second Department of Internal Medicine, Osaka University Medical School
      and Department of Blood Transfusion, Osaka University Hospital, Osaka,
      Japan, USA.

TI   Is ouabain produced by the adrenal gland?.
AU   Foster R H; Prat H; Rothman I
CS   Department of Physiology and Biophysics, Faculty of Medicine, University
      of Chile, Santiago.

TI   Ca2+ mobilization and pumping out mechanism.
AU   Mikoshiba K
CS   Department of Molecular Neurobiology, University of Tokyo, Japan.

L4   ANSWER 334 OF 473   MEDLINE on STN
AN   1999004449   MEDLINE
DN   PubMed ID: 9788152
TI   Na(+)-Ca2+ exchange.
AU   Matsuoka S; Noma A
CS   Department of Physiology, Faculty of Medicine, Kyoto University, Japan.
SO   Tanpakushitsu kakusan koso. Protein, nucleic acid, enzyme,   ***(1998***
   ***   Sep)***   43 (12 Suppl) 1555-60. Ref: 49
       Journal code: 0413762. ISSN: 0039-9450.
CY   Japan
DT   Journal; Article; (JOURNAL ARTICLE)
       General Review; (REVIEW)
       (REVIEW, TUTORIAL)
LA   Japanese
FS   Priority Journals
EM   199902
ED   Entered STN: 19990216
       Last Updated on STN: 19990216
       Entered Medline: 19990203

L4   ANSWER 335 OF 473   MEDLINE on STN
AN   1999002133   MEDLINE
DN   PubMed ID: 9785953
TI   Modeling the cellular basis of altered excitation-contraction coupling in
       heart failure.
AU   Winslow R L; Rice J; Jafri S
CS   Department of Biomedical Engineering, Johns Hopkins University School of
       Medicine, Baltimore, MD 21205, USA.. rwinslow@bme.jhu.edu
NC   HL60133 (NHLBI)
SO   Progress in biophysics and molecular biology,   ***(1998)***   69 (2-3)
       497-514. Ref: 45
       Journal code: 0401233. ISSN: 0079-6107.
CY   ENGLAND: United Kingdom
DT   Journal; Article; (JOURNAL ARTICLE)
       General Review; (REVIEW)
       (REVIEW, TUTORIAL)
LA   English
FS   Priority Journals
EM   199811
ED   Entered STN: 19990106
       Last Updated on STN: 19990106
       Entered Medline: 19981116

L4   ANSWER 336 OF 473   MEDLINE on STN
AN   1998428557   MEDLINE
DN   PubMed ID: 9755808
TI   Mode-actions of the Na(+)-Ca2+ exchanger: from genes to mechanisms to a
       new strategy in brain disorders.
AU   Fang Y; Rong M; He L; Zhou C
CS   Department of Anesthesiology, Zhong Shan Hospital, Shanghai Medical
       University, China.
SO   Biomedicine & pharmacotherapy = Biomedecine & pharmacotherapie,
       (1998)   52 (4) 145-56.
       Journal code: 8213295. ISSN: 0753-3322.
CY   France
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   199810
ED   Entered STN: 19981029
       Last Updated on STN: 20000303
       Entered Medline: 19981021

L4   ANSWER 337 OF 473   MEDLINE on STN
AN   1998365285   MEDLINE
DN   PubMed ID: 9688596
TI   Differential inhibition of Na+/Ca2+ exchanger isoforms by divalent cations
       and isothiourea derivative.
AU   Iwamoto T; Shigekawa M
CS   Department of Molecular Physiology, National Cardiovascular Center

L4   ANSWER 338 OF 473   MEDLINE on STN
AN   1998318765   MEDLINE
DN   PubMed ID: 9654696
TI   [New aspects of the pathophysiology of heart failure].
     Neue Aspekte zur Pathophysiologie der Herzinsuffizienz.
AU   Pieske B
CS   Abteilung fur Kardiologie und Pneumologie, Zentrums Innere Medizin,
     Georg-August-Universitat Gottingen, Deutschand.
SO   Wiener medizinische Wochenschrift (1946),   ***(1998)***   148 (5) 108-20.
     Ref: 168
     Journal code: 8708475. ISSN: 0043-5341.
CY   Austria
DT   Journal; Article; (JOURNAL ARTICLE)
     General Review; (REVIEW)
     (REVIEW, TUTORIAL)
LA   German
FS   Priority Journals
EM   199808
ED   Entered STN: 19980910
     Last Updated on STN: 19980910
     Entered Medline: 19980828

L4   ANSWER 339 OF 473   MEDLINE on STN
AN   1998295677   MEDLINE
DN   PubMed ID: 9633920
TI   Simulation study of cellular electric properties in heart failure.
AU   Priebe L; Beuckelmann D J
CS   Department of Medicine III, University of Cologne, Germany.
SO   Circulation research,   ***(1998 Jun 15)***   82 (11) 1206-23.
     Journal code: 0047103. ISSN: 0009-7330.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   199807
ED   Entered STN: 19980716
     Last Updated on STN: 19980716
     Entered Medline: 19980702

L4   ANSWER 340 OF 473   MEDLINE on STN
AN   1998276681   MEDLINE
DN   PubMed ID: 9614497
TI   Contribution of reverse-mode sodium-calcium exchange to contractions in
     failing   ***human***   left ventricular myocytes.
AU   Mattiello J A; Margulies K B; Jeevanandam V; Houser S R
CS   Department of Physiology, Temple University School of Medicine,
     Philadelphia, PA 19140, USA.
SO   Cardiovascular research,   ***(1998 Feb)***   37 (2) 424-31.
     Journal code: 0077427. ISSN: 0008-6363.
CY   Netherlands
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   199806
ED   Entered STN: 19980625
     Last Updated on STN: 19980625
     Entered Medline: 19980615

L4   ANSWER 341 OF 473   MEDLINE on STN
AN   1998263786   MEDLINE
DN   PubMed ID: 9601480
TI   Changes in intracellular Ca^{2+} mobilization and Ca^{2+} sensitization as
     mechanisms of action of physiological interventions and inotropic agents
     in intact myocardial cells.

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L4    ANSWER 345 OF 473      MEDLINE on STN
AN    1998191135      MEDLINE
DN    PubMed ID: 9530104
TI    ATP stimulation of Na+/Ca2+ exchange in cardiac sarcolemmal vesicles.
AU    Berberian G; Hidalgo C; DiPolo R; Beauge L
CS    Instituto de Investigacion Medica Mercedes y Martin Ferreyra, Cordoba,
      Argentina.
SO    American journal of physiology,   ***(1998 Mar)***   274 (3 Pt 1) C724-33.
      Journal code: 0370511. ISSN: 0002-9513.
CY    United States
DT    Journal; Article; (JOURNAL ARTICLE)
LA    English
FS    Priority Journals
EM    199804
ED    Entered STN: 19980507
      Last Updated on STN: 19980507
      Entered Medline: 19980424

L4    ANSWER 346 OF 473      MEDLINE on STN
AN    1998182628      MEDLINE
DN    PubMed ID: 9522160
TI    Review of some actions of taurine on ion channels of cardiac muscle cells
      and others.
AU    Satoh H; Sperelakis N
CS    Department of Pharmacology, Nara Medical University, Japan.
SO    General pharmacology,   ***(1998 Apr)***   30 (4) 451-63.   Ref: 106
      Journal code: 7602417. ISSN: 0306-3623.
CY    ENGLAND: United Kingdom
DT    Journal; Article; (JOURNAL ARTICLE)
      General Review; (REVIEW)
      (REVIEW, TUTORIAL)
LA    English
FS    Priority Journals
EM    199805
ED    Entered STN: 19980520
      Last Updated on STN: 19980520
      Entered Medline: 19980512

L4    ANSWER 347 OF 473      MEDLINE on STN
AN    1998181480      MEDLINE
DN    PubMed ID: 9520863
TI    Calcium-dependent inhibition of the sodium-calcium exchange current by
      KB-R7943.
AU    Watano T; Kimura J
CS    Department of Pharmacology, Fukushima Medical College, Japan.
SO    Canadian journal of cardiology,   ***(1998 Feb)***   14 (2) 259-62.
      Journal code: 8510280. ISSN: 0828-282X.
CY    Canada
DT    Journal; Article; (JOURNAL ARTICLE)
LA    English
FS    Priority Journals
EM    199804
ED    Entered STN: 19980416
      Last Updated on STN: 19980416
      Entered Medline: 19980406

L4    ANSWER 348 OF 473      MEDLINE on STN
AN    1998138491      MEDLINE
DN    PubMed ID: 9478004
TI    cDNA cloning of the   ***human***   retinal rod Na-Ca + K exchanger:
      comparison with a revised bovine sequence.
AU    Tucker J E; Winkfein R J; Cooper C B; Schnetkamp P P
CS    Department of Medical Biochemistry, Faculty of Medicine, University of
      Calgary, Canada.
SO    Investigative ophthalmology & visual science,   ***(1998 Feb)***   39 (2)
      435-40.
      Journal code: 7703701. ISSN: 0146-0404.
CY    United States
DT    Journal; Article; (JOURNAL ARTICLE)
LA    English
FS    Priority Journals
OS    GENBANK-AF025480
EM    199803
ED    Entered STN: 19980312
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L4   ANSWER 349 OF 473   MEDLINE on STN
AN   1998051754   MEDLINE
DN   PubMed ID: 9395572
TI   Cellular calcium and sodium regulation, salt-sensitivity and essential
      hypertension in African Americans.
AU   Aviv A
CS   Hypertension Research Program, University of Medicine and Dentistry of New
      Jersey, New Jersey Medical School, Newark 07103-2714, USA.
NC   HL34807 (NHLBI)
      HL42856 (NHLBI)
SO   Ethnicity & health,   ***(1996 Sep)***   1 (3) 275-81. Ref: 32
      Journal code: 9608374. ISSN: 1355-7858.
CY   ENGLAND: United Kingdom
DT   Journal; Article; (JOURNAL ARTICLE)
      General Review; (REVIEW)
      (REVIEW, TUTORIAL)
LA   English
FS   Priority Journals
EM   199712
ED   Entered STN: 19980122
      Last Updated on STN: 19980122
      Entered Medline: 19971231

L4   ANSWER 350 OF 473   MEDLINE on STN
AN   97476084   MEDLINE
DN   PubMed ID: 9336335
TI   Effect of cyclopiazonic acid on the force-frequency relationship in
      human   nonfailing myocardium.
AU   Schwinger R H; Brixius K; Bavendiek U; Hoischen S; Muller-Ehmsen J; Bolck
      B; Erdmann E
CS   Klinik III fur Innere Medizin der Universitat zu Koln, Germany.
SO   Journal of pharmacology and experimental therapeutics,   ***(1997 Oct)***
      283 (1) 286-92.
      Journal code: 0376362. ISSN: 0022-3565.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   199711
ED   Entered STN: 19971224
      Last Updated on STN: 19971224
      Entered Medline: 19971103

L4   ANSWER 351 OF 473   MEDLINE on STN
AN   97471773   MEDLINE
DN   PubMed ID: 9330714
TI   Ca(2+)-signaling in cardiac myocytes: evidence from evolutionary and
      transgenic models.
AU   Morad M; Suzuki Y J
CS   Department of Pharmacology, Georgetown University Medical Center,
      Washington, DC 20007-2197, USA.
NC   RO1-16152
SO   Advances in experimental medicine and biology,   ***(1997)***   430 3-12.
      Ref: 13
      Journal code: 0121103. ISSN: 0065-2598.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
      General Review; (REVIEW)
      (REVIEW, TUTORIAL)
LA   English
FS   Priority Journals
EM   199711
ED   Entered STN: 19971224
      Last Updated on STN: 19971224
      Entered Medline: 19971119

L4   ANSWER 352 OF 473   MEDLINE on STN
AN   97353731   MEDLINE
DN   PubMed ID: 9209972
TI   Role of intracellular sodium overload in the genesis of cardiac
      arrhythmias.
AU   Levi A J; Dalton G R; Hancox J C; Mitcheson J S; Issberner J; Bates J A;
      Evans S J; Howarth F C; Hobai I A; Jones J V

DT   Journal; Article; (JOURNAL ARTICLE)
     General Review; (REVIEW)
     (REVIEW, ACADEMIC)
LA   English
FS   Priority Journals
EM   199708
ED   Entered STN: 19970902
     Last Updated on STN: 19980206
     Entered Medline: 19970815

L4   ANSWER 353 OF 473   MEDLINE on STN
AN   97346426   MEDLINE
DN   PubMed ID: 9202843
TI   Sodium-calcium exchange: recent advances.
AU   Hryshko L V; Philipson K D
CS   Division of Cardiovascular Sciences, St. Boniface General Hospital,
     Winnipeg, Manitoba, Canada.
SO   Basic research in cardiology,   ***(1997)***   92 Suppl 1 45-51. Ref: 90
     Journal code: 0360342. ISSN: 0300-8428.
CY   GERMANY: Germany, Federal Republic of
DT   Journal; Article; (JOURNAL ARTICLE)
     General Review; (REVIEW)
     (REVIEW, TUTORIAL)
LA   English
FS   Priority Journals
EM   199708
ED   Entered STN: 19970908
     Last Updated on STN: 19980206
     Entered Medline: 19970827

L4   ANSWER 354 OF 473   MEDLINE on STN
AN   97343141   MEDLINE
DN   PubMed ID: 9199770
TI   Electrophysiological characterization of ionic transport by the retinal
     exchanger expressed in   ***human***   embryonic kidney cells.
AU   Navanglone A; Rispoli G; Gabellini N; Carafoli E
CS   Instituto Nazionale per la Fisica della Materia (INFM), Dipartimento di
     Biologia dell'Universita, Ferrara, Italy.
SO   Biophysical journal,   ***(1997 Jul)***   73 (1) 45-51.
     Journal code: 0370626. ISSN: 0006-3495.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   199708
ED   Entered STN: 19970908
     Last Updated on STN: 19970908
     Entered Medline: 19970827

L4   ANSWER 355 OF 473   MEDLINE on STN
AN   97338732   MEDLINE
DN   PubMed ID: 9195292
TI   Na(+)-Ca2+ exchanger: physiology and pharmacology.
AU   Matsuda T; Takuma K; Baba A
CS   Department of Pharmacology, Faculty of Pharmaceutical Sciences, Osaka
     University, Japan.
SO   Japanese journal of pharmacology,   ***(1997 May)***   74 (1) 1-20. Ref:
     277
     Journal code: 2983305R. ISSN: 0021-5198.
CY   Japan
DT   Journal; Article; (JOURNAL ARTICLE)
     General Review; (REVIEW)
     (REVIEW, ACADEMIC)
LA   English
FS   Priority Journals
EM   199708
ED   Entered STN: 19970813
     Last Updated on STN: 19980206
     Entered Medline: 19970805

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AN      97289536      MEDLINE
DN      PubMed ID: 9144441
TI      Mechanism of calcium entry during axon injury and degeneration.
AU      LoPachin R M; Lehning E J
CS      Department of Anesthesiology, Montefiore Medical Center, Albert Einstein
        College of Medicine, Bronx, New York 10467, USA.
SO      Toxicology and applied pharmacology,   ***(1997 Apr)***   143 (2) 233-44.
        Ref: 108
        Journal code: 0416575. ISSN: 0041-008X.
CY      United States
DT      Journal; Article; (JOURNAL ARTICLE)
        General Review; (REVIEW)
        (REVIEW, TUTORIAL)
LA      English
FS      Priority Journals
EM      199706
ED      Entered STN: 19970612
        Last Updated on STN: 19980206
        Entered Medline: 19970602


L4      ANSWER 357 OF 473       MEDLINE on STN
AN      97094294      MEDLINE
DN      PubMed ID: 8940382
TI      Possible role for mitochondrial calcium in angiotensin II- and
        potassium-stimulated steroidogenesis in bovine adrenal glomerulosa cells.
AU      Brandenburger Y; Kennedy E D; Python C P; Rossier M F; Vallotton M B;
        Wollheim C B; Capponi A M
CS      Division of Endocrinology and Diabetology, Faculty of Medicine, Geneva,
        Switzerland.
SO      Endocrinology,   ***(1996 Dec)***   137 (12) 5544-51.
        Journal code: 0375040. ISSN: 0013-7227.
CY      United States
DT      Journal; Article; (JOURNAL ARTICLE)
LA      English
FS      Abridged Index Medicus Journals; Priority Journals
EM      199701
ED      Entered STN: 19970219
        Last Updated on STN: 19980206
        Entered Medline: 19970123


L4      ANSWER 358 OF 473       MEDLINE on STN
AN      97070613      MEDLINE
DN      PubMed ID: 8913539
TI      Distribution and signal transduction of angiotensin II AT1 and AT2
        receptors.
AU      Capponi A M
CS      Division of Endocrinology, University Hospital, Geneva, Switzerland.
SO      Blood pressure. Supplement,   ***(1996)***   2 41-6.   Ref: 55
        Journal code: 9300787. ISSN: 0803-8023.
CY      Norway
DT      Journal; Article; (JOURNAL ARTICLE)
        General Review; (REVIEW)
        (REVIEW, TUTORIAL)
LA      English
FS      Priority Journals
EM      199703
ED      Entered STN: 19970313
        Last Updated on STN: 19970313
        Entered Medline: 19970303


L4      ANSWER 359 OF 473       MEDLINE on STN
AN      97006060      MEDLINE
DN      PubMed ID: 8853354
TI      Contribution of Na+/Ca2+ exchange to action potential of   ***human***
        atrial myocytes.
AU      Benardeau A; Hatem S N; Rucker-Martin C; Le Grand B; Mace L; Dervanian P;
        Mercadier J J; Coraboeuf E
CS      Laboratoire de Cardiologie Moleculaire et Cellulaire, Universite de Paris
        XI-Centre National de la Recherche Scientifique Unite de Recherche
        Associee 1159, Hopital Marie Lannelongue, Le Plessis Robinson, France.
SO      American journal of physiology,   ***(1996 Sep)***   271 (3 Pt 2)
        H1151-61.
        Journal code: 0370511. ISSN: 0002-9513.
CY      United States
DT      Journal; Article; (JOURNAL ARTICLE)
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L4   ANSWER 360 OF 473   MEDLINE on STN
AN   96437036   MEDLINE
DN   PubMed ID: 8839852
TI   Affinity modulation of the platelet integrin alpha IIb beta 3 by
      alpha-chymotrypsin: a possible role for Na+/Ca2+ exchanger.
AU   Shiraga M; Tomiyama Y; Honda S; Kashiwagi H; Kosugi S; Handa M; Ikeda Y;
      Kanakura Y; Kurata Y; Matsuzawa Y
CS   Second Department of Internal Medicine, Osaka University Medical School,
      Japan.
SO   Blood,   ***(1996 Oct 1)***   88 (7) 2594-602.
      Journal code: 7603509. ISSN: 0006-4971.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Abridged Index Medicus Journals; Priority Journals
EM   199611
ED   Entered STN: 19961219
      Last Updated on STN: 19980206
      Entered Medline: 19961107

L4   ANSWER 361 OF 473   MEDLINE on STN
AN   96382173   MEDLINE
DN   PubMed ID: 8790037
TI   Evidence for functional relevance of an enhanced expression of the
      Na(+)-Ca2+ exchanger in failing   ***human***   myocardium.
AU   Flesch M; Schwinger R H; Schiffer F; Frank K; Sudkamp M; Kuhn-Regnier F;
      Arnold G; Bohm M
CS   Klinik III fur Innere Medizin Universitat zu Koln, FRG.
SO   Circulation,   ***(1996 Sep 1)***   94 (5) 992-1002.
      Journal code: 0147763. ISSN: 0009-7322.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Abridged Index Medicus Journals; Priority Journals
EM   199610
ED   Entered STN: 19961025
      Last Updated on STN: 19980206
      Entered Medline: 19961017

L4   ANSWER 362 OF 473   MEDLINE on STN
AN   96372590   MEDLINE
DN   PubMed ID: 8776405
TI   The role of Na-Ca exchange current in the cardiac action potential.
AU   Janvier N C; Boyett M R
CS   Department of Physiology, University of Leeds, UK.
SO   Cardiovascular research,   ***(1996 Jul)***   32 (1) 69-84. Ref: 74
      Journal code: 0077427. ISSN: 0008-6363.
CY   Netherlands
DT   Journal; Article; (JOURNAL ARTICLE)
      General Review; (REVIEW)
      (REVIEW, ACADEMIC)
LA   English
FS   Priority Journals
EM   199610
ED   Entered STN: 19961106
      Last Updated on STN: 19980206
      Entered Medline: 19961024

L4   ANSWER 363 OF 473   MEDLINE on STN
AN   96285996   MEDLINE
DN   PubMed ID: 8659814
TI   3rd International Conference on Sodium-Calcium Exchange. Woods Hole,
      Massachusetts, April 23-26, 1995. Proceedings.
AU   Anonymous
SO   Annals of the New York Academy of Sciences,   ***(1996 Apr 15)***   779
      1-589.
      Journal code: 7506858. ISSN: 0077-8923.
CY   United States
DT   Conference; Conference Article; (CONGRESSES)

L4   ANSWER 364 OF 473   MEDLINE on STN
AN   96250118   MEDLINE
DN   PubMed ID: 8659869
TI   Demonstration of an inward Na(+)-Ca2+ exchange current in adult
       human   atrial myocytes.
AU   Li G R; Nattel S
CS   Research Center, Montreal Heart Institute, Quebec, Canada.
SO   Annals of the New York Academy of Sciences,   ***(1996 Apr 15)***   779
       525-8.
       Journal code: 7506858. ISSN: 0077-8923.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   199607
ED   Entered STN: 19960808
       Last Updated on STN: 19980206
       Entered Medline: 19960726

L4   ANSWER 365 OF 473   MEDLINE on STN
AN   96250107   MEDLINE
DN   PubMed ID: 8659857
TI   Calcium in the cardiac diadic cleft. Implications for sodium-calcium
       exchange.
AU   Langer G A; Peskoff A
CS   Department of Medicine, University of California, Los Angeles School of
       Medicine 90095, USA.
SO   Annals of the New York Academy of Sciences,   ***(1996 Apr 15)***   779
       408-16. Ref: 24
       Journal code: 7506858. ISSN: 0077-8923.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
       General Review; (REVIEW)
       (REVIEW, TUTORIAL)
LA   English
FS   Priority Journals
EM   199607
ED   Entered STN: 19960808
       Last Updated on STN: 19980206
       Entered Medline: 19960726

L4   ANSWER 366 OF 473   MEDLINE on STN
AN   96250066   MEDLINE
DN   PubMed ID: 8659816
TI   Expression of Na(+)-Ca2+ exchanger with modified C-terminal hydrophobic
       domains and enhanced activity.
AU   Gabellini N; Iwata T; Carafoli E
CS   Department of Biological Chemistry University of Padova, Italy.
SO   Annals of the New York Academy of Sciences,   ***(1996 Apr 15)***   779
       110-4. Ref: 9
       Journal code: 7506858. ISSN: 0077-8923.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
       General Review; (REVIEW)
       (REVIEW, TUTORIAL)
LA   English
FS   Priority Journals
OS   GENBANK-Z49266
EM   199607
ED   Entered STN: 19960808
       Last Updated on STN: 19980206
       Entered Medline: 19960726

L4   ANSWER 367 OF 473   MEDLINE on STN
AN   96250060   MEDLINE
DN   PubMed ID: 8659862
TI   Alternative splicing of the Na(+)-Ca2+ exchanger gene, NCX1.
AU   Schulze D H; Kofuji P; Valdivia C; He S; Luo S; Ruknudin A; Wisel S; Kirby

AN   96250058   MEDLINE
DN   PubMed ID: 8659840
TI   The structural basis of Na(+)-Ca2+ exchange activity.
AU   Rahamimoff H; Low W; Cook O; Furman I; Kasir J; Vatashski R
CS   Department of Biochemistry Hebrew University-Hadassah Medical School
      Jerusalem, Israel.
SO   Annals of the New York Academy of Sciences,   ***(1996 Apr 15)***   779
      29-36. Ref: 16
      Journal code: 7506858. ISSN: 0077-8923.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
      General Review; (REVIEW)
      (REVIEW, TUTORIAL)
LA   English
FS   Priority Journals
EM   199607
ED   Entered STN: 19960808
      Last Updated on STN: 19980206
      Entered Medline: 19960726

AN   96250056   MEDLINE
DN   PubMed ID: 8659882
TI   The molecular biology of the Na(+)-Ca2+ exchanger and its functional roles
      in heart, smooth muscle cells, neurons, glia, lymphocytes, and
      nonexcitable cells.
AU   Lederer W J; He s; Luo S; duBell W; Kofuji P; Kieval R; Neubauer C F;
      Ruknudin A; Cheng H; Cannell M B; Rogers T B; Schulze D H
CS   Department of Physiology, University of Maryland School of Medicine,
      Baltimore, Maryland 21201, USA.
SO   Annals of the New York Academy of Sciences,   ***(1996 Apr 15)***   779
      7-17. Ref: 60
      Journal code: 7506858. ISSN: 0077-8923.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
      General Review; (REVIEW)
      (REVIEW, TUTORIAL)
LA   English
FS   Priority Journals
EM   199607
ED   Entered STN: 19960808
      Last Updated on STN: 19980206
      Entered Medline: 19960726

AN   96162572   MEDLINE
DN   PubMed ID: 8576853
TI   Species differences in the activity of the Na(+)-Ca2+ exchanger in
      mammalian cardiac myocytes.
AU   Sham J S; Hatem S N; Morad M
CS   Department of Pharmacology, Georgetown University Medical Center,
      Washington, DC 20007, USA.
NC   R01-HL16152 (NHLBI)
SO   Journal of physiology,   ***(1995 Nov 1)***   488 (Pt 3) 623-31.
      Journal code: 0266262. ISSN: 0022-3751.
CY   ENGLAND: United Kingdom
DT   Journal; Article; (JOURNAL ARTICLE)

L4   ANSWER 371 OF 473   MEDLINE on STN
AN   95306881   MEDLINE
DN   PubMed ID: 7787264
TI   Recent insights into the regulation of cardiac Ca2+ flux during perinatal
      development and in cardiac failure.
AU   Fisher D J
CS   Texas Children's Hospital, Houston, USA.
SO   Current opinion in cardiology,   ***(1995 Jan)***   10 (1) 44-51.   Ref: 75
      Journal code: 8608087. ISSN: 0268-4705.
CY   ENGLAND: United Kingdom
DT   Journal; Article; (JOURNAL ARTICLE)
      General Review; (REVIEW)
      (REVIEW, TUTORIAL)
LA   English
FS   Priority Journals
EM   199507
ED   Entered STN: 19950807
      Last Updated on STN: 19980206
      Entered Medline: 19950727

L4   ANSWER 372 OF 473   MEDLINE on STN
AN   95306268   MEDLINE
DN   PubMed ID: 7786694
TI   New concepts in the cardioprotective action of magnesium and taurine
      during the calcium paradox and ischaemia of the heart.
AU   Suleiman M S
CS   Department of Physiology, University of Bristol, UK.
SO   Magnesium research : official organ of the International Society for the
      Development of Research on Magnesium,   ***(1994 Dec)***   7 (3-4)
      295-312. Ref: 138
      Journal code: 8900948. ISSN: 0953-1424.
CY   ENGLAND: United Kingdom
DT   Journal; Article; (JOURNAL ARTICLE)
      General Review; (REVIEW)
      (REVIEW, ACADEMIC)
LA   English
FS   Priority Journals
EM   199507
ED   Entered STN: 19950807
      Last Updated on STN: 19980206
      Entered Medline: 19950724

L4   ANSWER 373 OF 473   MEDLINE on STN
AN   95269801   MEDLINE
DN   PubMed ID: 7750570
TI   Specific inhibition of Na-Ca exchange function by antisense
      oligodeoxynucleotides.
CM   Erratum in: FEBS Lett 1995 Aug 21;370(3):280
AU   Lipp P; Schwaller B; Niggli E
CS   Department of Physiology, University of Bern, Switzerland.
SO   FEBS letters,   ***(1995 May 8)***   364 (2) 198-202.
      Journal code: 0155157. ISSN: 0014-5793.
CY   Netherlands
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   199506
ED·   Entered STN: 19950629
      Last Updated on STN: 19980206
      Entered Medline: 19950622

L4   ANSWER 374 OF 473   MEDLINE on STN
AN   95202443   MEDLINE
DN   PubMed ID: 7895054
TI   Studies of the mechanism underlying increased Na+/Ca2+ exchange activity
      in Alzheimer's disease brain.
AU   Colvin R A; Davis N; Wu A; Murphy C A; Levengood J
CS   Department of Biological Sciences, Ohio University College of Osteopathic
      Medicine, Athens 45701.

L4   ANSWER 375 OF 473   MEDLINE on STN
AN   95168956   MEDLINE
DN   PubMed ID: 7864717
TI   Heart failure: an update on pathophysiology.
AU   Drexler H
CS   Medizinische Klinik III, University of Freiburg, Germany.
SO   Archives des maladies du coeur et des vaisseaux,   ***(1994 Jun)***   87
      Spec No 2 13-6.
      Journal code: 0406011. ISSN: 0003-9683.
CY   France
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   199503
ED   Entered STN: 19950404
      Last Updated on STN: 20000303
      Entered Medline: 19950323

L4   ANSWER 376 OF 473   MEDLINE on STN
AN   95150354   MEDLINE
DN   PubMed ID: 7847687
TI   Ion transport systems and Ca2+ regulation in aging neurons.
AU   Michaelis M L
CS   Department of Pharmacology, University of Kansas, Lawrence 66045.
SO   Annals of the New York Academy of Sciences,   ***(1994 Dec 15)***   747
      407-18. Ref: 52
      Journal code: 7506858. ISSN: 0077-8923.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
      General Review; (REVIEW)
      (REVIEW, TUTORIAL)
LA   English
FS   Priority Journals
EM   199503
ED   Entered STN: 19950316
      Last Updated on STN: 19980206
      Entered Medline: 19950308

L4   ANSWER 377 OF 473   MEDLINE on STN
AN   95150189   MEDLINE
DN   PubMed ID: 7847532
TI   Role of the sodium-calcium exchange mechanism and the effect of magnesium
      on sodium-free and high-potassium contractures in pregnant   ***human***
      myometrium.
AU   Morishita F; Kawarabayashi T; Sakamoto Y; Shirakawa K
CS   Department of Obstetrics and Gynecology, School of Medicine, Fukuoka
      University, Japan.
SO   American journal of obstetrics and gynecology,   ***(1995 Jan)***   172 (1
      Pt 1) 186-95.
      Journal code: 0370476. ISSN: 0002-9378.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Abridged Index Medicus Journals; Priority Journals
EM   199503
ED   Entered STN: 19950316
      Last Updated on STN: 19980206
      Entered Medline: 19950309

L4   ANSWER 378 OF 473   MEDLINE on STN
AN   95123339   MEDLINE
DN   PubMed ID: 7823035
TI   Na+/Ca2+ antiport in the mammalian heart.
AU   Reeves J P; Condrescu M; Chernaya G; Gardner J P

Medical School, Newark 07103.
SO   Journal of experimental biology,   ***(1994 Nov)***   196 375-88.   Ref: 40
      Journal code: 0243705. ISSN: 0022-0949.
CY   ENGLAND: United Kingdom
DT   Journal; Article; (JOURNAL ARTICLE)
      General Review; (REVIEW)
      (REVIEW, TUTORIAL)
LA   English
FS   Priority Journals
EM   199502
ED   Entered STN: 19950223
      Last Updated on STN: 19980206
      Entered Medline: 19950216

L4   ANSWER 379 OF 473   MEDLINE on STN
AN   95123334   MEDLINE
DN   PubMed ID: 7823030
TI   Cation antiports of animal plasma membranes.
AU   Grinstein S; Wieczorek H
CS   Division of Cell Biology, Hospital for Sick Children, Toronto, Canada.
SO   Journal of experimental biology,   ***(1994 Nov)***   196 307-18.   Ref: 41
      Journal code: 0243705. ISSN: 0022-0949.
CY   ENGLAND: United Kingdom
DT   Journal; Article; (JOURNAL ARTICLE)
      General Review; (REVIEW)
      (REVIEW, TUTORIAL)
LA   English
FS   Priority Journals
EM   199502
ED   Entered STN: 19950223
      Last Updated on STN: 19980206
      Entered Medline: 19950216

L4   ANSWER 380 OF 473   MEDLINE on STN
AN   95116246   MEDLINE
DN   PubMed ID: 7816552
TI   A novel two-compartment culture dish allows microscopic evaluation of two
      different treatments in one cell culture simultaneously. Influence of
      external pH on Na+/Ca2+ exchanger activity in cultured rat cardiomyocytes.
AU   Atsma D E; Bastiaanse E M; Ince C; van der Laarse A
CS   Department of Cardiology, University Hospital, Leiden, The Netherlands.
SO   Pflugers Archiv : European journal of physiology,   ***(1994 Oct)***   428
      (3-4) 296-9.
      Journal code: 0154720. ISSN: 0031-6768.
CY   GERMANY: Germany, Federal Republic of
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   199502
ED   Entered STN: 19950217
      Last Updated on STN: 19980206
      Entered Medline: 19950208

L4   ANSWER 381 OF 473   MEDLINE on STN
AN   95103184   MEDLINE
DN   PubMed ID: 7804751
TI   Crosstalk and epithelial ion transport.
AU   Harvey B J
CS   Department of Physiology, University College Cork, Ireland.
SO   Current opinion in nephrology and hypertension,   ***(1994 Sep)***   3 (5)
      523-8.
      Journal code: 9303753. ISSN: 1062-4821.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   199502
ED   Entered STN: 19950215
      Last Updated on STN: 19980206
      Entered Medline: 19950202

L4   ANSWER 382 OF 473   MEDLINE on STN
AN   95097406   MEDLINE
DN   PubMed ID: 7799453
TI   Comparison of the action potential prolonging and positive inotropic

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        myocardium.
AU      Hoey A; Amos G J; Ravens U
CS      Department of Pharmacology, University of Essen, Germany.
SO      Journal of molecular and cellular cardiology,   ***(1994 Aug)***    26 (8)
        985-94.
        Journal code: 0262322. ISSN: 0022-2828.
CY      ENGLAND: United Kingdom
DT      Journal; Article; (JOURNAL ARTICLE)
LA      English
FS      Priority Journals
EM      199501
ED      Entered STN: 19950215
        Last Updated on STN: 19980206
        Entered Medline: 19950125


L4      ANSWER 383 OF 473       MEDLINE on STN
AN      95081902     MEDLINE
DN      PubMed ID: 7527459
TI      Inhibition of Ca2+ entry by Ca2+ overloading of intracellular Ca2+ stores
        in   ***human***   platelets.
AU      Kimura M; Cho J H; Reeves J P; Aviv A
CS      Hypertension Research Center, University of Medicine and Dentistry of New
        Jersey, New Jersey Medical School, Newark 07103-2714.
NC      HL34807 (NHLBI)
        HL42856 (NHLBI)
        HL49932 (NHLBI)
SO      Journal of physiology,   ***(1994 Aug 15)***    479 ( Pt 1) 1-10.
        Journal code: 0266262. ISSN: 0022-3751.
CY      ENGLAND: United Kingdom
DT      Journal; Article; (JOURNAL ARTICLE)
LA      English
FS      Priority Journals
EM      199501
ED      Entered STN: 19950124
        Last Updated on STN: 19980206
        Entered Medline: 19950111


L4      ANSWER 384 OF 473       MEDLINE on STN
AN      95077943     MEDLINE
DN      PubMed ID: 7986536
TI      Mammalian exchangers and co-transporters.
AU      Reithmeier R A
CS      Department of Medicine, University of Toronto, Canada.
SO      Current opinion in cell biology,   ***(1994 Aug)***    6 (4) 583-94.   Ref:
        106
        Journal code: 8913428. ISSN: 0955-0674.
CY      United States
DT      Journal; Article; (JOURNAL ARTICLE)
        General Review; (REVIEW)
        (REVIEW, ACADEMIC)
LA      English
FS      Priority Journals
EM      199501
ED      Entered STN: 19950124
        Last Updated on STN: 19980206
        Entered Medline: 19950111


L4      ANSWER 385 OF 473       MEDLINE on STN
AN      95054028     MEDLINE
DN      PubMed ID: 7964733
TI      Characterization of exchange inhibitory peptide effects on Na+/Ca2+
        exchange in rat and   ***human***   brain plasma membrane vesicles.
AU      Wu A; Colvin R A
CS      Department of Biological Sciences, Ohio University College of Osteopathic
        Medicine, Athens 45701.
NC      NS30384 (NINDS)
SO      Journal of neurochemistry,   ***(1994 Dec)***    63 (6) 2136-43.
        Journal code: 2985190R. ISSN: 0022-3042.
CY      United States
DT      Journal; Article; (JOURNAL ARTICLE)
LA      English
FS      Priority Journals
EM      199412
ED      Entered STN: 19950110
        Last Updated on STN: 19980206
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L4      ANSWER 386 OF 473      MEDLINE on STN
AN      95051546      MEDLINE
DN      PubMed ID: 7962546
TI      Na+/Ca2+ exchange-mediated calcium entry in   ***human***   lymphocytes.
AU      Balasubramanyam M; Rohowsky-Kochan C; Reeves J P; Gardner J P
CS      Hypertension Research Center, University of Medicine and Dentistry-New
        Jersey Medical School, Newark 07103.
NC      HL44196 (NHLBI)
        HL49932 (NHLBI)
SO      Journal of clinical investigation,   ***(1994 Nov)***   94 (5) 2002-8.
        Journal code: 7802877. ISSN: 0021-9738.
CY      United States
DT      Journal; Article; (JOURNAL ARTICLE)
LA      English
FS      Abridged Index Medicus Journals; Priority Journals
EM      199412
ED      Entered STN: 19950110
        Last Updated on STN: 19980206
        Entered Medline: 19941202


L4      ANSWER 387 OF 473      MEDLINE on STN
AN      94367220      MEDLINE
DN      PubMed ID: 8085015
TI      The cellular actions of digitalis glycosides on the heart.
AU      Levi A J; Boyett M R; Lee C O
CS      Department of Physiology, School of Medical Sciences, University of
        Bristol, University Walk, U.K.
SO      Progress in biophysics and molecular biology,   ***(1994)***   62 (1)
        1-54.  Ref: 228
        Journal code: 0401233. ISSN: 0079-6107.
CY      ENGLAND: United Kingdom
DT      Journal; Article; (JOURNAL ARTICLE)
        General Review; (REVIEW)
        (REVIEW, ACADEMIC)
LA      English
FS      Priority Journals
EM      199410
ED      Entered STN: 19941021
        Last Updated on STN: 19980206
        Entered Medline: 19941010


L4      ANSWER 388 OF 473      MEDLINE on STN
AN      94363504      MEDLINE
DN      PubMed ID: 7521769
TI      Cyclic nucleotides inhibit Na+/Ca2+ exchange in cultured   ***human***
        mesangial cells.
AU      Mene P; Pugliese F; Cinotti G A
CS      Chair of Nephrology, University of Rome La Sapienza, Italy.
SO      Experimental nephrology,   ***(1993 Jul-Aug)***   1 (4) 245-52.
        Journal code: 9302239. ISSN: 1018-7782.
CY      Switzerland
DT      Journal; Article; (JOURNAL ARTICLE)
LA      English
FS      Priority Journals
EM      199410
ED      Entered STN: 19941021
        Last Updated on STN: 19980206
        Entered Medline: 19941013


L4      ANSWER 389 OF 473      MEDLINE on STN
AN      94346468      MEDLINE
DN      PubMed ID: 8067429
TI      Furazolidone increases thapsigargin-sensitive Ca(2+)-ATPase in chick
        cardiac myocytes.
AU      Lax D; Martinez-Zaguilan R; Gillies R J
CS      Department of Pediatrics, Steele Memorial Children's Research Center,
        Tucson, Arizona.
SO      American journal of physiology,   ***(1994 Aug)***   267 (2 Pt 2) H734-41.
        Journal code: 0370511. ISSN: 0002-9513.
CY      United States
DT      Journal; Article; (JOURNAL ARTICLE)
LA      English
FS      Priority Journals
EM      199409
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Last Updated on STN: 19980206
Entered Medline: 19940921

L4   ANSWER 390 OF 473   MEDLINE on STN
AN   94340771   MEDLINE
DN   PubMed ID: 8062418
TI   Gene expression of the cardiac Na(+)-Ca2+ exchanger in end-stage
        human   heart failure.
AU   Studer R; Reinecke H; Bilger J; Eschenhagen T; Bohm M; Hasenfuss G; Just
        H; Holtz J; Drexler H
CS   Arbeitsgruppe Molekulare Kardiologie, Universitat Freiburg, Germany.
SO   Circulation research,   ***(1994 Sep)***   75 (3) 443-53.
        Journal code: 0047103. ISSN: 0009-7330.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   199409
ED   Entered STN: 19941005
        Last Updated on STN: 19980206
        Entered Medline: 19940920

L4   ANSWER 391 OF 473   MEDLINE on STN
AN   94292759   MEDLINE
DN   PubMed ID: 8021471
TI   Differences in platelet calcium regulation between African Americans and
        Caucasians: implications for the predisposition of African Americans to
        essential hypertension.
AU   Kimura M; Cho J H; Lasker N; Aviv A
CS   Hypertension Research Center, University of Medicine and Dentistry of New
        Jersey, New Jersey Medical School, Newark 07103-2714.
NC   HL34807 (NHLBI)
        HL42856 (NHLBI)
SO   Journal of hypertension,   ***(1994 Feb)***   12 (2) 199-207.
        Journal code: 8306882. ISSN: 0263-6352.
CY   ENGLAND: United Kingdom
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   199407
ED   Entered STN: 19940815
        Last Updated on STN: 19980206
        Entered Medline: 19940729

L4   ANSWER 392 OF 473   MEDLINE on STN
AN   94260944   MEDLINE
DN   PubMed ID: 8201934
TI   [Energetics of ionic behavior in heart muscle contraction. Physiologic and
        physiopathologic aspects].
        Energetica del comportamiento ionico en la contraccion muscular cardiaca.
        Aspectos fisiologicos y fisiopatologicos.
AU   Ponce-Hornos J E; Bonazzola P; Taquini A C
CS   Instituto de Investigaciones Cardiologicas, Facultad de Medicina,
        Universidad de Buenos Aires.
SO   Medicina,   ***(1993)***   53 (5) 445-58.   Ref: 52
        Journal code: 0204271. ISSN: 0025-7680.
CY   Argentina
DT   Journal; Article; (JOURNAL ARTICLE)
        General Review; (REVIEW)
        (REVIEW, TUTORIAL)
LA   Spanish
FS   Priority Journals
EM   199407
ED   Entered STN: 19940714
        Last Updated on STN: 19940714
        Entered Medline: 19940705

L4   ANSWER 393 OF 473   MEDLINE on STN
AN   94232511   MEDLINE
DN   PubMed ID: 8177473
TI   Increased cytosolic free sodium in platelets from patients with
        early-stage chronic renal failure.
AU   Tepel M; Bauer S; Kegel M; Raffelsiefer A; Wischniowski H; Zidek W
CS   Medizinische Universitats-Poliklinik, University of Munster, Germany.
SO   Nephrology, dialysis, transplantation : official publication of the

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L4     ANSWER 394 OF 473        MEDLINE on STN
AN     94133698      MEDLINE
DN     PubMed ID: 7508043
TI     Na+, K(+)-ATPase and Na+/Ca2+ exchange isoforms: physiological and
       physiopathological relevance.
AU     Decollogne S; Bertrand I B; Ascensio M; Drubaix I; Lelievre L G
CS     Laboratoire de Pharmacologie des Transports Ioniques Membranaires,
       Universite Paris 7, France.
SO     Journal of cardiovascular pharmacology,    ***(1993)***    22 Suppl 2 S96-8.
       Ref: 29
       Journal code: 7902492. ISSN: 0160-2446.
CY     United States
DT     Journal; Article; (JOURNAL ARTICLE)
       General Review; (REVIEW)
       (REVIEW, TUTORIAL)
LA     English
FS     Priority Journals
EM     199403
ED     Entered STN: 19940318
       Last Updated on STN: 20000303
       Entered Medline: 19940310
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L4     ANSWER 395 OF 473        MEDLINE on STN
AN     94126946      MEDLINE
DN     PubMed ID: 8296399
TI     Modulation of intramitochondrial free Ca2+ concentration by antagonists of
       Na(+)-Ca2+ exchange.
AU     Cox D A; Matlib M A
CS     Lilly Research Laboratories, Indianapolis, IN 46285.
NC     T32-HL07382 (NHLBI)
SO     Trends in pharmacological sciences,    ***(1993 Nov)***    14 (11) 408-13.
       Ref: 39
       Journal code: 7906158. ISSN: 0165-6147.
CY     ENGLAND: United Kingdom
DT     Journal; Article; (JOURNAL ARTICLE)
       General Review; (REVIEW)
       (REVIEW, TUTORIAL)
LA     English
FS     Priority Journals
EM     199403
ED     Entered STN: 19940314
       Last Updated on STN: 19980206
       Entered Medline: 19940303
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L4     ANSWER 396 OF 473        MEDLINE on STN
AN     94101659      MEDLINE
DN     PubMed ID: 8275516
TI     Reconstructing the heart: a challenge for integrative physiology.
AU     Noble D; Bett G
CS     University Laboratory of Physiology, Oxford, United Kingdom.
SO     Cardiovascular research,    ***(1993 Oct)***    27 (10) 1701-12.
       Journal code: 0077427. ISSN: 0008-6363.
CY     ENGLAND: United Kingdom
DT     Journal; Article; (JOURNAL ARTICLE)
LA     English
FS     Priority Journals
EM     199402
ED     Entered STN: 19940218
       Last Updated on STN: 19980206
       Entered Medline: 19940204
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L4     ANSWER 397 OF 473        MEDLINE on STN
AN     94091534      MEDLINE
DN     PubMed ID: 8267157
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       main pulmonary artery.
AU     Abdalla S S; Laravuso R B; Will J A
CS     Department of Animal Health, University of Wisconsin, Madison 53706.
SO     Anesthesia and analgesia,   ***(1994 Jan)***   78 (1) 17-22.
       Journal code: 1310650. ISSN: 0003-2999.
CY     United States
DT     Journal; Article; (JOURNAL ARTICLE)
LA     English
FS     Abridged Index Medicus Journals; Priority Journals
EM     199401
ED     Entered STN: 19940209
       Last Updated on STN: 19980206
       Entered Medline: 19940125


L4     ANSWER 398 OF 473      MEDLINE on STN
AN     94081304     MEDLINE
DN     PubMed ID: 8258673
TI     Na(+)-Ca2+ exchange modulates Ca2+ handling of   ***human***   platelets
       by altering intracellular Ca2+ store size.
AU     Ishida T; Matsuura H; Ishida-Kainouchi M; Ozono R; Watanabe M; Kajiyama G;
       Oshima T
CS     First Department of Internal Medicine, Hiroshima University School of
       Medicine, Japan.
SO     Journal of hypertension,   ***(1993 Oct)***   11 (10) 1089-95.
       Journal code: 8306882. ISSN: 0263-6352.
CY     ENGLAND: United Kingdom
DT     Journal; Article; (JOURNAL ARTICLE)
LA     English
FS     Priority Journals
EM     199401
ED     Entered STN: 19940203
       Last Updated on STN: 19980206
       Entered Medline: 19940119


L4     ANSWER 399 OF 473      MEDLINE on STN
AN     94016601     MEDLINE
DN     PubMed ID: 8411189
TI     Is "fuzzy space" necessary for Ca2+ extrusion on the Na(+)-Ca+ exchanger
       in cardiac myocytes?.
CM     Comment on: J Mol Cell Cardiol. 1993 Jun;25(6):637-9. PubMed ID: 8411188
AU     Barry W H
NC     HL30478 (NHLBI)
       HL42535 (NHLBI)
SO     Journal of molecular and cellular cardiology,   ***(1993 Jun)***   25 (6)
       641-3; discussion 645-6.
       Journal code: 0262322. ISSN: 0022-2828.
CY     ENGLAND: United Kingdom
DT     Commentary
       Editorial
LA     English
FS     Priority Journals
EM     199311
ED     Entered STN: 19940117
       Last Updated on STN: 20030114
       Entered Medline: 19931104


L4     ANSWER 400 OF 473      MEDLINE on STN
AN     94016600     MEDLINE
DN     PubMed ID: 8411188
TI     How does the Na(+)-Ca2+ exchanger work in the intact cardiac cell?.
CM     Comment in: J Mol Cell Cardiol. 1993 Jun;25(6):641-3; discussion 645-6.
       PubMed ID: 8411189
AU     Langer G A; Peskoff A; Post J A
NC     HL 28539-10 (NHLBI)
SO     Journal of molecular and cellular cardiology,   ***(1993 Jun)***   25 (6)
       637-9.
       Journal code: 0262322. ISSN: 0022-2828.
CY     ENGLAND: United Kingdom
DT     Editorial
LA     English
FS     Priority Journals
EM     199311
ED     Entered STN: 19940117
       Last Updated on STN: 20030114
       Entered Medline: 19931104
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AN   94016522   MEDLINE
DN   PubMed ID: 8411123
TI   Platelet activating factor-induced increase in cytosolic calcium and
      transmembrane current in   ***human***   macrophages.
AU   Katnik C; Nelson D J
CS   University of Chicago, Dept. of Neurology, Illinois 60637.
SO   Journal of membrane biology,   ***(1993 Jun)***   134 (3) 213-24.
      Journal code: 0211301. ISSN: 0022-2631.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   199310
ED   Entered STN: 19940117
      Last Updated on STN: 19980206
      Entered Medline: 19931022

AN   93278803   MEDLINE
DN   PubMed ID: 8389258
TI   Intracellular calcium homeostasis in cardiac myocytes.
AU   Barry W H; Bridge J H
CS   Division of Cardiology, University of Utah School of Medicine, Salt Lake
      City.
SO   Circulation,   ***(1993 Jun)***   87 (6) 1806-15. Ref: 87
      Journal code: 0147763. ISSN: 0009-7322.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
      General Review; (REVIEW)
      (REVIEW, TUTORIAL)
LA   English
FS   Abridged Index Medicus Journals; Priority Journals
EM   199307
ED   Entered STN: 19930716
      Last Updated on STN: 19980206
      Entered Medline: 19930702

AN   93226470   MEDLINE
DN   PubMed ID: 8385772
TI   Regulation of the cytosolic pH set point for activation of the Na+/H+
      antiport in   ***human***   platelets: the roles of the Na+/Ca2+ exchange,
      the Na(+)-K(+)-2Cl- cotransport and cellular volume.
AU   Kimura M; Aviv A
CS   Hypertension Research Center, University of Medicine and Dentistry of
      NJ-NJ Medical School, Newark 07103-2714.
NC   HL34807 (NHLBI)
      HL42856 (NHLBI)
SO   Pflugers Archiv : European journal of physiology,   ***(1993 Mar)***   422
      (6) 585-90.
      Journal code: 0154720. ISSN: 0031-6768.
CY   GERMANY: Germany, Federal Republic of
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   199305
ED   Entered STN: 19930521
      Last Updated on STN: 19980206
      Entered Medline: 19930507

AN   93167758   MEDLINE
DN   PubMed ID: 7679565
TI   Molecular dissection of the myelinated axon.
AU   Waxman S G; Ritchie J M
CS   Department of Neurology, Yale University School of Medicine, New Haven,
      CT.
SO   Annals of neurology,   ***(1993 Feb)***   33 (2) 121-36. Ref: 172
      Journal code: 7707449. ISSN: 0364-5134.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
      General Review; (REVIEW)
      (REVIEW, TUTORIAL)
LA   English

EM   199303
ED   Entered STN: 19930402
       Last Updated on STN: 19980206
       Entered Medline: 19930316

L4   ANSWER 405 OF 473   MEDLINE on STN
AN   93110167   MEDLINE
DN   PubMed ID: 8417464
TI   Anoxic injury of central myelinated axons: ionic mechanisms and
       pharmacology.
AU   Ransom B R; Waxman S G; Stys P K
CS   Department of Neurology, Yale University School of Medicine, New Haven,
       Connecticut 06510.
SO   Research publications - Association for Research in Nervous and Mental
       Disease,   ***(1993)***   71 121-51.   Ref: 91
       Journal code: 7505942. ISSN: 0091-7443.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
       General Review; (REVIEW)
       (REVIEW, TUTORIAL)
LA   English
FS   Priority Journals
EM   199301
ED   Entered STN: 19930212
       Last Updated on STN: 19980206
       Entered Medline: 19930126

L4   ANSWER 406 OF 473   MEDLINE on STN
AN   93042766   MEDLINE
DN   PubMed ID: 1384746
TI   The impact of single cell voltage clamp on the understanding of the
       cardiac ventricular action potential.
AU   Varro A; Papp J G
CS   Department of Pharmacology, Albert Szent-Gyorgyi Medical University,
       Szeged, Hungary.
SO   Cardioscience,   ***(1992 Sep)***   3 (3) 131-44.   Ref: 139
       Journal code: 9014943. ISSN: 1015-5007.
CY   Italy
DT   Journal; Article; (JOURNAL ARTICLE)
       General Review; (REVIEW)
       (REVIEW, TUTORIAL)
LA   English
FS   Priority Journals
EM   199212
ED   Entered STN: 19930122
       Last Updated on STN: 19980206
       Entered Medline: 19921222

L4   ANSWER 407 OF 473   MEDLINE on STN
AN   93040297   MEDLINE
DN   PubMed ID: 1419049
TI   Sodium-calcium exchange.
AU   Philipson K D; Nicoll D A
CS   University of California, Los Angeles.
SO   Current opinion in cell biology,   ***(1992 Aug)***   4 (4) 678-83.   Ref:
       45
       Journal code: 8913428. ISSN: 0955-0674.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
       General Review; (REVIEW)
       (REVIEW, TUTORIAL)
LA   English
FS   Priority Journals
EM   199212
ED   Entered STN: 19930122
       Last Updated on STN: 19980206
       Entered Medline: 19921204

L4   ANSWER 408 OF 473   MEDLINE on STN
AN   92374100   MEDLINE
DN   PubMed ID: 1507528
TI   Regulation of vascular smooth muscle contractility: roles of the
       sarcoplasmic reticulum (SR) and the   ***sodium***   /   ***calcium***
       exchanger .
AU   Blaustein M P; Ambesi A; Bloch R J; Goldman W F; Juhaszova M; Lindenmayer

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DT    Journal; Article; (JOURNAL ARTICLE)
LA    English
FS    Priority Journals
EM    199203
ED    Entered STN: 19920405
      Last Updated on STN: 19980206
      Entered Medline: 19920317


L4    ANSWER 412 OF 473        MEDLINE on STN
AN    92152800     MEDLINE
DN    PubMed ID: 1785897
TI    Mechanism of partial reactions in the cardiac Na(+)-Ca2+ exchange system.
AU    Khananshvili D
CS    Department of Biochemistry, Weizmann Institute of Science, Rehovot,
      Israel.
SO    Annals of the New York Academy of Sciences,    ***(1991)***    639 85-95.
      Ref: 26
      Journal code: 7506858. ISSN: 0077-8923.
CY    United States
DT    Journal; Article; (JOURNAL ARTICLE)
      General Review; (REVIEW)
      (REVIEW, TUTORIAL)
LA    English
FS    Priority Journals
EM    199203
ED    Entered STN: 19920405
      Last Updated on STN: 19980206
      Entered Medline: 19920317


L4    ANSWER 413 OF 473        MEDLINE on STN
AN    92152795     MEDLINE
DN    PubMed ID: 1785893
TI    Characterization of Na(+)-Ca2+ exchange in the beta cell.
AU    Hoenig M; Culberson L H; Wheeler C A; Ferguson D C
CS    Department of Physiology and Pharmacology, College of Veterinary Medicine,
      University of Georgia, Athens 30602.
SO    Annals of the New York Academy of Sciences,    ***(1991)***    639 657-9.
      Ref: 11
      Journal code: 7506858. ISSN: 0077-8923.
CY    United States
DT    Journal; Article; (JOURNAL ARTICLE)
      General Review; (REVIEW)
      (REVIEW, TUTORIAL)
LA    English
FS    Priority Journals
EM    199203
ED    Entered STN: 19920405
      Last Updated on STN: 19980206
      Entered Medline: 19920317


L4    ANSWER 414 OF 473        MEDLINE on STN
AN    92152794     MEDLINE
DN    PubMed ID: 1785892
TI    Sodium-calcium exchange in the pancreatic B cell.
AU    Herchuelz A; Plasman P O
CS    Laboratoire de Pharmacodynamie et de Therapeutique, Universite Libre de
      Bruxelles, Faculte de Medecine, Belgium.
SO    Annals of the New York Academy of Sciences,    ***(1991)***    639 642-56.
      Ref: 77
      Journal code: 7506858. ISSN: 0077-8923.
CY    United States
DT    Journal; Article; (JOURNAL ARTICLE)
      General Review; (REVIEW)
      (REVIEW, TUTORIAL)
LA    English
FS    Priority Journals
EM    199203
ED    Entered STN: 19920405
      Last Updated on STN: 19980206
      Entered Medline: 19920317


L4    ANSWER 415 OF 473        MEDLINE on STN
AN    92152792     MEDLINE
DN    PubMed ID: 1664709
TI    The role of Na(+)-Ca2+ exchange in    ***human***    neutrophil function.
```

CS Department of Medicine, Veterans Administration Medical Center, St. Louis,
    Missouri 63106.
NC GM-38094 (NIGMS)
SO Annals of the New York Academy of Sciences,   ***(1991)***   639 616-30.
    Ref: 40
    Journal code: 7506858. ISSN: 0077-8923.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
    General Review; (REVIEW)
    (REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 199203
ED Entered STN: 19920405
    Last Updated on STN: 19980206
    Entered Medline: 19920317

L4 ANSWER 416 OF 473   MEDLINE on STN
AN 92152788   MEDLINE
DN PubMed ID: 1785887
TI The role of Na-Ca exchange in renal epithelia. An overview.
AU Windhager E E; Frindt G; Milovanovic S
CS Department of Physiology and Biophysics, Cornell University Medical
    College, New York, New York 10021.
SO Annals of the New York Academy of Sciences,   ***(1991)***   639 577-91.
    Ref: 49
    Journal code: 7506858. ISSN: 0077-8923.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
    General Review; (REVIEW)
    (REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 199203
ED Entered STN: 19920405
    Last Updated on STN: 19980206
    Entered Medline: 19920317

L4 ANSWER 417 OF 473   MEDLINE on STN
AN 92152779   MEDLINE
DN PubMed ID: 1785880
TI Role of sarcolemmal membrane sodium-calcium exchange in vascular smooth
    muscle tension.
AU Matlib M A
CS Department of Pharmacology and Cell Biophysics, University of Cincinnati
    College of Medicine, Ohio 45267-0575.
NC RO1-HL34664 (NHLBI)
SO Annals of the New York Academy of Sciences,   ***(1991)***   639 531-42.
    Ref: 80
    Journal code: 7506858. ISSN: 0077-8923.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
    General Review; (REVIEW)
    (REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 199203
ED Entered STN: 19920405
    Last Updated on STN: 19980206
    Entered Medline: 19920317

L4 ANSWER 418 OF 473   MEDLINE on STN
AN 92152778   MEDLINE
DN PubMed ID: 1785879
TI Evidence for Na-Ca exchange in   ***human***   resistance arteries.
AU Aaronson P I; Poston L; Woolfson R G; Smirnov S V
CS United Medical School, St. Thomas' Hospital, London, United Kingdom.
SO Annals of the New York Academy of Sciences,   ***(1991)***   639 521-30.
    Journal code: 7506858. ISSN: 0077-8923.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199203
ED Entered STN: 19920405

Entered Medline: 19920317

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L4     ANSWER 419 OF 473      MEDLINE on STN
AN     92152777     MEDLINE
DN     PubMed ID: 1785878
TI     Sodium-calcium exchange in aortic myocytes and renal epithelial cells.
       Dependence on metabolic energy and intracellular sodium.
AU     Smith J B; Lyu R M; Smith L
CS     Department of Pharmacology, School of Medicine, University of Alabama,
       Birmingham 35294.
NC     DK39258 (NIDDK)
       HL44408 (NHLBI)
SO     Annals of the New York Academy of Sciences,    ***(1991)***   639 505-20.
       Ref: 42
       Journal code: 7506858. ISSN: 0077-8923.
CY     United States
DT     Journal; Article; (JOURNAL ARTICLE)
       General Review; (REVIEW)
       (REVIEW, TUTORIAL)
LA     English
FS     Priority Journals
EM     199203
ED     Entered STN: 19920405
       Last Updated on STN: 19980206
       Entered Medline: 19920317


L4     ANSWER 420 OF 473      MEDLINE on STN
AN     92152753     MEDLINE
DN     PubMed ID: 1785858
TI     Na(+)-Ca2+ exchange activity is increased in Alzheimer's disease brain
       tissues.
AU     Colvin R A; Bennett J W; Colvin S L
CS     Department of Zoological and Biomedical Sciences, Ohio University College
       of Osteopathic Medicine, Athens 45701.
SO     Annals of the New York Academy of Sciences,    ***(1991)***   639 325-7.
       Journal code: 7506858. ISSN: 0077-8923.
CY     United States
DT     Journal; Article; (JOURNAL ARTICLE)
LA     English
FS     Priority Journals
EM     199203
ED     Entered STN: 19920405
       Last Updated on STN: 19980206
       Entered Medline: 19920317


L4     ANSWER 421 OF 473      MEDLINE on STN
AN     92152752     MEDLINE
DN     PubMed ID: 1785857
TI     Neuron-specific and state-specific differences in calcium regulation.
       Their role in the development of neuronal architecture.
AU     Mills L R
CS     Playfair Neuroscience Unit, University of Toronto, Ontario, Canada.
NC     NS15350 (NINDS)
       NS24683 (NINDS)
SO     Annals of the New York Academy of Sciences,    ***(1991)***   639 312-24.
       Ref: 48
       Journal code: 7506858. ISSN: 0077-8923.
CY     United States
DT     Journal; Article; (JOURNAL ARTICLE)
       General Review; (REVIEW)
       (REVIEW, TUTORIAL)
LA     English
FS     Priority Journals
EM     199203
ED     Entered STN: 19920405
       Last Updated on STN: 19980206
       Entered Medline: 19920317


L4     ANSWER 422 OF 473      MEDLINE on STN
AN     92152749     MEDLINE
DN     PubMed ID: 1785854
TI     Sodium-calcium exchange and phototransduction in retinal photoreceptors.
AU     Yau K W; Nakatani K; Tamura T
CS     Howard Hughes Medical Institute, Baltimore, Maryland.
NC     EY 06837 (NEI)
```

CY United States
DT Journal; Article; (JOURNAL ARTICLE)
    General Review; (REVIEW)
    (REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 199203
ED Entered STN: 19920405
    Last Updated on STN: 19980206
    Entered Medline: 19920317

L4 ANSWER 423 OF 473   MEDLINE on STN
AN 92152727   MEDLINE
DN PubMed ID: 1785834
TI Regulation of Na-Ca exchange. An overview.
AU DiPolo R; Beauge L
CS Centro de Biofiisica y Bioquimica, IVIC, Caracas, Venezuela.
NC R01 HL-39243-03 (NHLBI)
SO Annals of the New York Academy of Sciences,   ***(1991)***   639 100-11.
    Ref: 26
    Journal code: 7506858. ISSN: 0077-8923.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
    General Review; (REVIEW)
    (REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 199203
ED Entered STN: 19920405
    Last Updated on STN: 19980206
    Entered Medline: 19920317

L4 ANSWER 424 OF 473   MEDLINE on STN
AN 91355993   MEDLINE
DN PubMed ID: 2151738
TI Plasma membrane Ca^{2+} pumps and Na^+/Ca^{2+} exchangers.
AU Strehler E E
CS Laboratory for Biochemistry, Swiss Federal Institute of Technology,
    Zurich.
SO Seminars in cell biology,   ***(1990 Aug)***   1 (4) 283-95. Ref: 104
    Journal code: 9007587. ISSN: 1043-4682.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
    General Review; (REVIEW)
    (REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 199110
ED Entered STN: 19911027
    Last Updated on STN: 19980206
    Entered Medline: 19911008

L4 ANSWER 425 OF 473   MEDLINE on STN
AN 91317885   MEDLINE
DN PubMed ID: 1650372
TI Characterization of calcium transport by basal plasma membranes from
    human   placental syncytiotrophoblast.
AU Lafond J; Leclerc M; Brunette M G
CS Maisonneuve-Rosemont Hospital, Montreal, Quebec, Canada.
SO Journal of cellular physiology,   ***(1991 Jul)***   148 (1) 17-23.
    Journal code: 0050222. ISSN: 0021-9541.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199109
ED Entered STN: 19910922
    Last Updated on STN: 19980206
    Entered Medline: 19910905

L4 ANSWER 426 OF 473   MEDLINE on STN
AN 91274932   MEDLINE
DN PubMed ID: 1647256

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         tissues.
AU       Colvin R A; Bennett J W; Colvin S L; Allen R A; Martinez J; Miner G D
CS       Department of Zoological and Biomedical Sciences, Ohio University College
         of Osteopathic Medicine, Athens 45701.
SO       Brain research,   ***(1991 Mar 8)***   543 (1) 139-47.
         Journal code: 0045503. ISSN: 0006-8993.
CY       Netherlands
DT       Journal; Article; (JOURNAL ARTICLE)
LA       English
FS       Priority Journals
EM       199108
ED       Entered STN: 19910818
         Last Updated on STN: 19980206
         Entered Medline: 19910801


L4       ANSWER 427 OF 473      MEDLINE on STN
AN       91176440     MEDLINE
DN       PubMed ID: 1826093
TI       Inhibitor action on placental calcium transport.
AU       Williams J M; Abramovich D R; Dacke C G; Mayhew T M; Page K R
CS       Department of Anatomy, University of Aberdeen, Marischal College, United
         Kingdom.
SO       Calcified tissue international,   ***(1991 Jan)***   48 (1) 7-12.
         Journal code: 7905481. ISSN: 0171-967X.
CY       United States
DT       Journal; Article; (JOURNAL ARTICLE)
LA       English
FS       Priority Journals
EM       199104
ED       Entered STN: 19910519
         Last Updated on STN: 19980206
         Entered Medline: 19910426


L4       ANSWER 428 OF 473      MEDLINE on STN
AN       91162935     MEDLINE
DN       PubMed ID: 2074662
TI       Identification and characteristics of a Na+/Ca2+ exchanger in cultured
           ***human***   mesangial cells.
AU       Mene P; Pugliese F; Faraggiana T; Cinotti G A
CS       Cattedra di Nefrologia Medica, University of Rome La Sapienza, Italy.
SO       Kidney international,   ***(1990 Dec)***   38 (6) 1199-205.
         Journal code: 0323470. ISSN: 0085-2538.
CY       United States
DT       Journal; Article; (JOURNAL ARTICLE)
LA       English
FS       Priority Journals
EM       199104
ED       Entered STN: 19910505
         Last Updated on STN: 19980206
         Entered Medline: 19910418


L4       ANSWER 429 OF 473      MEDLINE on STN
AN       91109877     MEDLINE
DN       PubMed ID: 1703282
TI       Characterization of Na(+)-Ca2+ exchange activity in plasma membrane
         vesicles from postmortem   ***human***   brain.
AU       Hoel G; Michaelis M L; Freed W J; Kleinman J E
CS       Department of Pharmacology and Toxicology, University of Kansas, Lawrence
         66047.
NC       AA 04732 (NIAAA)
         AG04762 (NIA)
SO       Neurochemical research,   ***(1990 Sep)***   15 (9) 881-7.
         Journal code: 7613461. ISSN: 0364-3190.
CY       United States
DT       Journal; Article; (JOURNAL ARTICLE)
LA       English
FS       Priority Journals
EM       199102
ED       Entered STN: 19910329
         Last Updated on STN: 19980206
         Entered Medline: 19910228


L4       ANSWER 430 OF 473      MEDLINE on STN
AN       90355219     MEDLINE
DN       PubMed ID: 2167385
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          calcium paradox.
CM        Comment on: J Mol Cell Cardiol. 1990 May;22(5):499-501. PubMed ID: 2167384
AU        Chapman R a
CS        British Heart Foundation Research Group in Cellular Cardiology, Department
          of Physiology, School of Veterinary Science, Bristol, England.
SO        Journal of molecular and cellular cardiology,   ***(1990 May)***   22 (5)
          503-5.
          Journal code: 0262322. ISSN: 0022-2828.
CY        ENGLAND: United Kingdom
DT        Commentary
          Journal; Article; (JOURNAL ARTICLE)
LA        English
FS        Priority Journals
EM        199009
ED        Entered STN: 19901026
          Last Updated on STN: 19980206
          Entered Medline: 19900927


L4        ANSWER 431 OF 473      MEDLINE on STN
AN        90355218      MEDLINE
DN        PubMed ID: 2167384
TI        Is an increase of intracellular Na+ during Ca2+ depletion essential for
          the occurrence of the calcium paradox?.
CM        Comment in: J Mol Cell Cardiol. 1990 May;22(5):503-5. PubMed ID: 2167385
AU        Ruigrok T J
CS        Department of Cardiology, University Hospital, Utrecht, The Netherlands.
SO        Journal of molecular and cellular cardiology,   ***(1990 May)***   22 (5)
          499-501.
          Journal code: 0262322. ISSN: 0022-2828.
CY        ENGLAND: United Kingdom
DT        Journal; Article; (JOURNAL ARTICLE)
LA        English
FS        Priority Journals
EM        199009
ED        Entered STN: 19901026
          Last Updated on STN: 19980206
          Entered Medline: 19900927


L4        ANSWER 432 OF 473      MEDLINE on STN
AN        90325890      MEDLINE
DN        PubMed ID: 1973777
TI        Na(+)-Ca2+ exchanger and cardiac contraction.
AU        Anonymous
SO        Lancet,   ***(1990 Jul 28)***   336 (8709) 219-20.
          Journal code: 2985213R. ISSN: 0140-6736.
CY        ENGLAND: United Kingdom
DT        Editorial
LA        English
FS        Abridged Index Medicus Journals; Priority Journals
EM        199008
ED        Entered STN: 19901012
          Last Updated on STN: 19980206
          Entered Medline: 19900827


L4        ANSWER 433 OF 473      MEDLINE on STN
AN        90284028      MEDLINE
DN        PubMed ID: 2191788
TI        The cardiac Na(+)-Ca2+ exchanger: dependence on membrane environment.
AU        Philipson K D
CS        Department of Medicine, UCLA School of Medicine 90024-1760.
SO        Cell biology international reports,   ***(1990 Apr)***   14 (4) 305-9.
          Ref: 20
          Journal code: 7708050. ISSN: 0309-1651.
CY        ENGLAND: United Kingdom
DT        Journal; Article; (JOURNAL ARTICLE)
          General Review; (REVIEW)
          (REVIEW, TUTORIAL)
LA        English
FS        Priority Journals
EM        199007
ED        Entered STN: 19900824
          Last Updated on STN: 19980206
          Entered Medline: 19900726


L4        ANSWER 434 OF 473      MEDLINE on STN
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DN   PubMed ID: 2335019
TI   Canine cardiac sarcolemmal vesicles demonstrate rapid initial Na(+)-Ca2+
      exchange activity.
AU   Gruver C L; Katz A M; Messineo F C
CS   Department of Medicine, University of Connecticut Health Center,
      Farmington 06032.
NC   HL-07420 (NHLBI)
      HL-33026 (NHLBI)
SO   Circulation research,   ***(1990 May)***   66 (5) 1171-7.
      Journal code: 0047103. ISSN: 0009-7330.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   199006
ED   Entered STN: 19900706
      Last Updated on STN: 19980206
      Entered Medline: 19900611

L4   ANSWER 435 OF 473   MEDLINE on STN
AN   90193175   MEDLINE
DN   PubMed ID: 2156295
TI   Aspects of hepatic calcium metabolism.
AU   Heilmann C; Spamer C; Gerok W
SO   Progress in liver diseases,   ***(1990)***   9 261-79.   Ref: 159
      Journal code: 0376447. ISSN: 1060-913X.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
      General Review; (REVIEW)
      (REVIEW, ACADEMIC)
LA   English
FS   Priority Journals
EM   199004
ED   Entered STN: 19900601
      Last Updated on STN: 19980206
      Entered Medline: 19900419

L4   ANSWER 436 OF 473   MEDLINE on STN
AN   89384166   MEDLINE
DN   PubMed ID: 2550727
TI   Sodium-calcium and sodium-proton exchangers in red blood cells.
AU   Parker J C
NC   AM 11357 (NIADDK)
SO   Methods in enzymology,   ***(1989)***   173 292-300.
      Journal code: 0212271. ISSN: 0076-6879.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   198910
ED   Entered STN: 19900309
      Last Updated on STN: 19980206
      Entered Medline: 19891026

L4   ANSWER 437 OF 473   MEDLINE on STN
AN   89103446   MEDLINE
DN   PubMed ID: 2912132
TI   Relationship between cytosolic free Ca2+ and Na+-Ca2+ exchange in aortic
      muscle cells.
AU   Smith J B; Zheng T; Smith L
CS   Department of Pharmacology, University of Alabama, Birmingham 35294.
NC   DK-39258 (NIDDK)
      HL-01671 (NHLBI)
SO   American journal of physiology,   ***(1989 Jan)***   256 (1 Pt 1) C147-54.
      Journal code: 0370511. ISSN: 0002-9513.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   198902
ED   Entered STN: 19900308
      Last Updated on STN: 19980206
      Entered Medline: 19890221

L4   ANSWER 438 OF 473   MEDLINE on STN

DN   PubMed ID: 3213678
TI   Sodium-calcium exchange in platelet plasma membrane vesicles.
AU   Rengasamy A; Feinberg H
CS   Department of Pharmacology, University of Illinois College of Medicine,
     Chicago.
SO   Advances in experimental medicine and biology,   ***(1988)***   232 105-8.
     Journal code: 0121103. ISSN: 0065-2598.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   198902
ED   Entered STN: 19900308
     Last Updated on STN: 19980206
     Entered Medline: 19890216

L4   ANSWER 439 OF 473   MEDLINE on STN
AN   88057421   MEDLINE
DN   PubMed ID: 2445679
TI   Vascular muscle membrane cation mechanisms and total peripheral
     resistance.
AU   Hermsmeyer R K
CS   Department of Pharmacology, University of Iowa, Iowa City.
NC   HL 14388 (NHLBI)
     HL 16328 (NHLBI)
SO   Hypertension,   ***(1987 Nov)***   10 (5 Pt 2) I20-2. Ref: 28
     Journal code: 7906255. ISSN: 0194-911X.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
     General Review; (REVIEW)
     (REVIEW, TUTORIAL)
LA   English
FS   Priority Journals
EM   198801
ED   Entered STN: 19900305
     Last Updated on STN: 19980206
     Entered Medline: 19880104

L4   ANSWER 440 OF 473   MEDLINE on STN
AN   86308026   MEDLINE
DN   PubMed ID: 2943901
TI   The homeostasis of calcium in heart cells.
AU   Carafoli E
SO   Journal of molecular and cellular cardiology,   ***(1985 Mar)***   17 (3)
     203-12.
     Journal code: 0262322. ISSN: 0022-2828.
CY   ENGLAND: United Kingdom
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   198610
ED   Entered STN: 19900321
     Last Updated on STN: 19980206
     Entered Medline: 19861023

L4   ANSWER 441 OF 473   MEDLINE on STN
AN   85197812   MEDLINE
DN   PubMed ID: 3888080
TI   Sodium-calcium exchange in plasma membrane vesicles.
AU   Philipson K D
SO   Annual review of physiology,   ***(1985)***   47 561-71. Ref: 56
     Journal code: 0370600. ISSN: 0066-4278.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
     General Review; (REVIEW)
LA   English
FS   Priority Journals
EM   198505
ED   Entered STN: 19900320
     Last Updated on STN: 19980206
     Entered Medline: 19850528

L4   ANSWER 442 OF 473 PASCAL   COPYRIGHT 2004 INIST-CNRS. ALL RIGHTS
     RESERVED. on STN
AN   1999-0448929   PASCAL

TIEN   Sodium/calcium exchange contributes to contraction and relaxation in
        failed   ***human***   ventricular myocytes
AU   GAUGHAN J. P.; FURUKAWA S.; JEEVANANDAM V.; HEFNER C. A.; KUBO H.;
        MARGULIES K. B.; MCGOWAN B. S.; MATTIELLO J. A.; DIPLA K.; PIACENTINO V.
        III; SIYUN LI; HOUSER S. R.
CS   Departments of Physiology and Cardio-Thoracic Surgery, Temple University
        School of Medicine, Philadelphia, Pennsylvania 19140, United States
SO   American journal of physiology. Heart and circulatory physiology,
        (1999)   , 46(2), H714-H724, 30 refs.
        ISSN: 0363-6135   CODEN: AJPPDI
DT   Journal
BL   Analytic
CY   United States
LA   English
AV   INIST-670D, 354000089395720340

L4   ANSWER 443 OF 473   PASCAL   COPYRIGHT 2004 INIST-CNRS. ALL RIGHTS
        RESERVED. on STN
AN   1998-0057087   PASCAL
CP   Copyright .COPYRGT. 1998 INIST-CNRS. All rights reserved.
TIEN   Molecular biology of calcium channels in the cardiovascular system
AU   KATZ A. M.
        DZAU Victor J. (ed.)
CS   Cardiology Division, University of Connecticut Health Center, Farmington,
        Connecticut, United States
        Department of Medicine, Brigham and Women's Hospital, Boston,
        Massachusetts, United States; Harvard Medical School, Boston,
        Massachusetts, United States
SO   The American journal of cardiology,   ***(1997)***   , 80(9A), 17I-22I, 25
        refs.
        Conference: New Approaches to Cardiovascular Therapy. Symposium, Anaheim,
        California (United States), 15 Mar 1997
        ISSN: 0002-9149   CODEN: AJCDAG
DT   Journal; Conference
BL   Analytic
CY   United States
LA   English
AV   INIST-8674, 354000079384920030

L4   ANSWER 444 OF 473   PASCAL   COPYRIGHT 2004 INIST-CNRS. ALL RIGHTS
        RESERVED. on STN
AN   1996-0272799   PASCAL
CP   Copyright .COPYRGT. 1996 INIST-CNRS. All rights reserved.
TIEN   Pathophysiological targets for beta-blocker therapy in congestive heart
        failure
AU   JUST H.
        TAYLOR S. H. (ed.)
CS   Medizinische Universitaetsklinik Freiburg im Breisgau Abteilung Innere
        Medizin III/Kardiologie, Angiologie, Germany, Federal Republic of
        University Department of Cardiovascular Studies, Department of Medical
        Cardiology, The General Infirmary, Leeds, United Kingdom
        European Society of Cardiology. Drug Therapy Working Group, EUR (patr.)
SO   European heart journal,   ***(1996)***   , 17(APR, SUPB), 1-7 [6 p.], 5
        refs.
        Conference: Beta-blockers in heart failure -- myths and realities.
        Satellite symposium, Berlin (Germany, Federal Republic of), 13 Sep 1994
        ISSN: 0195-668X
DT   Journal; Conference
BL   Analytic
CY   United Kingdom
LA   English
AV   INIST-18785, 354000043212540010

L4   ANSWER 445 OF 473   PHIN COPYRIGHT 2004 PJB on STN

AN   1998:4227   PHIN
DN   B00570226
DED   1 Feb 1998
TI   Physiome Sciences Inc.: Matters of the Heart
SO   Bioventure-View (***1998***) No. 1302 p14
DT   Newsletter
FS   FULL

L4   ANSWER 446 OF 473   SCISEARCH   COPYRIGHT 2004 THOMSON ISI on STN
AN   2001:704332   SCISEARCH

AN   1999:621920   SCISEARCH
GA   The Genuine Article (R) Number: 223XA
TI   Sodium/calcium exchange contributes to contraction and relaxation in
      failed   ***human***   ventricular myocytes
AU   Gaughan J P (Reprint); Furukawa S; Jeevanandam V; Hefner C A; Kubo H;
      Margulies K B; McGowan B S; Mattiello J A; Dipla K; Piacentino V; Li S Y;
      Houser S R
CS   TEMPLE UNIV, SCH MED, DEPT PHYSIOL, 3420 N BROAD ST, PHILADELPHIA, PA
      19140 (Reprint); TEMPLE UNIV, SCH MED, DEPT CARDIOTHORAC SURG,
      PHILADELPHIA, PA 19140
CYA   USA

AN   1999:337223   SCISEARCH
GA   The Genuine Article (R) Number: 189VE
TI   Transmembrane regulation of intracellular calcium by a plasma membrane
      sodium / ***calcium***   ***exchanger***   in mouse ova
AU   Pepperell J R (Reprint); Kommineni K; Buradagunta S; Smith P J S; Keefe D
      L
CS   BROWN UNIV, WOMEN & INFANTS HOSP, DEPT OBSTET & GYNECOL, 101 DUDLEY ST,
      PROVIDENCE, RI 02905 (Reprint); WOODS HOLE OCEANOG INST, BIOL MARINE LAB,
      WOODS HOLE, MA 02543
CYA   USA

AN   1998:516471   SCISEARCH
GA   The Genuine Article (R) Number: ZX213
TI   Ionic mechanisms underlying   ***human***   atrial action potential
      properties: insights from a mathematical model
AU   Courtemanche M (Reprint); Ramirez R J; Nattel S
CS   MONTREAL HEART INST, RES CTR, 5000 E BELANGER ST, MONTREAL, PQ H1T 1C8,
      CANADA (Reprint); UNIV MONTREAL, DEPT PHYSIOL, MONTREAL, PQ H3C 3J7,
      CANADA; UNIV MONTREAL, DEPT MED, MONTREAL, PQ H3C 3J7, CANADA; MCGILL
      UNIV, DEPT PHARMACOL, MONTREAL, PQ H3G 1Y6, CANADA
CYA   CANADA

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L4      ANSWER 453 OF 473  SCISEARCH  COPYRIGHT 2004 THOMSON ISI on STN
AN      97:543597  SCISEARCH
GA      The Genuine Article (R) Number: XK487
TI      Na+/Ca2+ exchanger in Drosophila: Cloning, expression, and transport
        differences
AU      Ruknudin A; Valdivia C; Kofuji P; Lederer W J; Schulze D H (Reprint)
CS      UNIV MARYLAND, SCH MED, DEPT MICROBIOL & IMMUNOL, 655 W BALTIMORE ST,
        BALTIMORE, MD 21201 (Reprint); UNIV MARYLAND, SCH MED, DEPT MICROBIOL &
        IMMUNOL, BALTIMORE, MD 21201; UNIV MARYLAND, SCH MED, DEPT PHYSIOL,
        BALTIMORE, MD 21201; UNIV MARYLAND, SCH MED, DEPT PHARMACOL & EXPT
        THERAPEUT, BALTIMORE, MD 21201; CTR MED BIOTECHNOL, BALTIMORE, MD 21201
CYA     USA
SO      AMERICAN JOURNAL OF PHYSIOLOGY-CELL PHYSIOLOGY, (  ***JUL 1997***  ) Vol.
        42, No. 1, pp. C257-C265.
        Publisher: AMER PHYSIOLOGICAL SOC, 9650 ROCKVILLE PIKE, BETHESDA, MD
        20814.
        ISSN: 0363-6143.
DT      Article; Journal
FS      LIFE
LA      English
REC     Reference Count: 34
        *ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS*


L4      ANSWER 454 OF 473  SCISEARCH  COPYRIGHT 2004 THOMSON ISI on STN
AN      96:798258  SCISEARCH
GA      The Genuine Article (R) Number: VN119
TI      RELATIONSHIP BETWEEN DIASTOLIC FUNCTION AND PROTEIN-LEVELS OF
        ***SODIUM***  -  ***CALCIUM***  -  ***EXCHANGER***   IN END-STAGE FAILIN(
        ***HUMAN***   HEARTS
AU      HASENFUSS G (Reprint); PREUSS M; LEHNART S; PRESTLE J; MEYER M; JUST H
CS      UNIV FREIBURG, D-7800 FREIBURG, GERMANY
CYA     GERMANY
SO      CIRCULATION, (  ***15 OCT 1996***  ) Vol. 94, No. 8, Supp. S, pp. 2527.
        ISSN: 0009-7322.
DT      Conference; Journal
FS      LIFE; CLIN
LA      ENGLISH
REC     No References


L4      ANSWER 455 OF 473  SCISEARCH  COPYRIGHT 2004 THOMSON ISI on STN
AN      94:471364  SCISEARCH
GA      The Genuine Article (R) Number: NX999
TI      THE   ***HUMAN***   CARDIAC   ***SODIUM***  -  ***CALCIUM***
        ***EXCHANGER***   EXPRESSED IN SF9 CELLS
AU      NIGGLI E (Reprint); LIPP P; KOFUJI P; SCHULZE D H; LEDERER W J
CS      UNIV BERN, DEPT PHYSIOL, CH-3012 BERN, SWITZERLAND; UNIV MARYLAND, DEPT
        PHYSIOL, BALTIMORE, MD, 21201; UNIV MARYLAND, DEPT MICROBIOL, BALTIMORE,
        MD, 21201
CYA     SWITZERLAND; USA
SO      JOURNAL OF PHYSIOLOGY-LONDON, (  ***JUN 1994***  ) Vol. 477P, pp. P17.
        ISSN: 0022-3751.
DT      Conference; Journal
FS      LIFE
LA      ENGLISH
REC     Reference Count: 4


L4      ANSWER 456 OF 473  SCISEARCH  COPYRIGHT 2004 THOMSON ISI on STN
AN      93:558095  SCISEARCH
GA      The Genuine Article (R) Number: LW031
TI      KINETICS OF CALCIUM-TRANSPORT ACROSS THE LYMPHOCYTE PLASMA-MEMBRANE
AU      BALASUBRAMANYAM M; KIMURA M; AVIV A; GARDNER J P (Reprint)
CS      UNIV MED & DENT NEW JERSEY, NEW JERSEY MED SCH, HYPERTENS RES CTR, 185 S
        ORANGE AVE, NEWARK, NJ, 07103; UNIV MED & DENT NEW JERSEY, NEW JERSEY MED
        SCH, DEPT PHYSIOL, NEWARK, NJ, 07103; UNIV MED & DENT NEW JERSEY, NEW
        JERSEY MED SCH, DEPT PEDIAT, NEWARK, NJ, 07103
CYA     USA
SO      AMERICAN JOURNAL OF PHYSIOLOGY, (  ***AUG 1993***  ) Vol. 265, No. 2, Part
        1, pp. C321-C327.
        ISSN: 0002-9513.
DT      Article; Journal
FS      LIFE
LA      ENGLISH
REC     Reference Count: 32
        *ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS*
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DT        Utility
FS        Granted
LN.CNT    1169
INCL      INCLM: 514/355.000
          INCLS: 514/906.000
NCL       NCLM:  514/355.000
          NCLS:  514/906.000
IC        [7]
          ICM: A61P015-10
          ICS: A61K031-4406
EXF       514/355; 514/906; 514/356
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4     ANSWER 461 OF 473   USPATFULL on STN
AN        2000:28005   USPATFULL
TI        Method for protection of heart by limiting metabolic and ionic
          abnormalities developed during ischemia following ischemia or resulting
          from ischemia
IN        Ramasamy, Ravichandran, Davis, CA, United States
          Schaefer, Saul, Davis, CA, United States
PA        The Regents of the University of California, Oakland, CA, United States
          (U.S. corporation)
PI        US 6034109          20000307                              <--
AI        US 1998-118521      19980717 (9)
RLI       Division of Ser. No. US 1995-574899, filed on 19 Dec 1995, now patented,
          Pat. No. US 5834466 which is a continuation-in-part of Ser. No. US
          1994-362400, filed on 22 Dec 1994, now abandoned
DT        Utility
FS        Granted
LN.CNT    1591
INCL      INCLM: 514/345.000
          INCLS: 514/429.000; 514/471.000; 514/646.000
NCL       NCLM:  514/345.000
          NCLS:  514/429.000; 514/471.000; 514/646.000
IC        [7]
          ICM: A61K031-44
          ICS: A61K031-40; A61K031-34; A61K031-135
EXF       514/471; 514/429; 514/646; 514/345
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4     ANSWER 462 OF 473   USPATFULL on STN
AN        1999:155719   USPATFULL
TI        Method of inhibiting proliferation of cells by administering an
          aminosterol compound
IN        Zasloff, Michael, Merion Station, PA, United States
          Shinnar, Ann, Teaneck, NJ, United States
          Kinney, William, Churchville, PA, United States
          Rao, Meena, Horsham, PA, United States
PA        Magainin Pharmaceuticals Inc., Plymouth Meeting, PA, United States (U.S.
          corporation)
PI        US 5994336          19991130                              <--
AI        US 1995-479455      19950607 (8)
DT        Utility
FS        Granted
LN.CNT 3505
INCL      INCLM: 514/182.000
NCL       NCLM:  514/182.000
IC        [6]
          ICM: A61K031-575
EXF       514/182
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4     ANSWER 463 OF 473   USPATFULL on STN
AN        1999:78751   USPATFULL
TI        Inhibition of noninactivating Na channels of mammalian optic nerve as a
          means of preventing optic nerve degeneration associated with glaucoma
IN        Adorante, Joseph S., Irvine, CA, United States
PA        Allergan, Waco, TX, United States (U.S. corporation)
PI        US 5922746          19990713                              <--
AI        US 1997-827194      19970327 (8)
DT        Utility
FS        Granted
LN.CNT    424
INCL      INCLM: 514/373.000
          INCLS: 514/912.000
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       NCLS:   514/912.000
IC        [6]
          ICM: A61K031-425
EXF    514/373; 514/912
CAS INDEXING IS AVAILABLE FOR THIS PATENT.


L4     ANSWER 464 OF 473   USPATFULL on STN
AN        1999:24813   USPATFULL
TI        Certain aminosterol compounds and pharmaceutical compositions including
          these compounds
IN        Jones, Steven, West Chester, PA, United States
PA        Magainin Pharmaceuticals, Inc., Plymouth Meeting, PA, United States
          (U.S. corporation)
PI        US 5874597                   19990223                              <--
AI        US 1995-476855               19950607 (8)
DT        Utility
FS        Granted
LN.CNT 3435
INCL   INCLM: 552/521.000
NCL    NCLM:  552/521.000
IC        [6]
          ICM: C07J041-00
EXF    552/521; 514/182
CAS INDEXING IS AVAILABLE FOR THIS PATENT.


L4     ANSWER 465 OF 473   USPATFULL on STN
AN        1998:154470   USPATFULL
TI        Certain aminosterol compounds and pharmaceutical compositions including
          these compounds
IN        Zasloff, Michael, Merion Station, PA, United States
          Shinnar, Ann, Teaneck, NJ, United States
          Kinney, William, Churchville, PA, United States
          Jones, Steven, West Chester, PA, United States
PA        Magainin Pharmaceuticals Inc., Plymouth Meeting, PA, United States (U.S.
          corporation)
PI        US 5847172                   19981208                              <--
AI        US 1995-487443               19950607 (8)
DT        Utility
FS        Granted
LN.CNT 3533
INCL   INCLM: 552/521.000
NCL    NCLM:  552/521.000
IC        [6]
          ICM: C07J041-00
EXF    552/521
CAS INDEXING IS AVAILABLE FOR THIS PATENT.


L4     ANSWER 466 OF 473   USPATFULL on STN
AN        1998:147645   USPATFULL
TI        Aminosterol compounds useful as inhibitors of the sodium/proton
          exchanger (NHE)
IN        Zasloff, Michael, Merion Station, PA, United States
          Shinnar, Ann, Teaneck, NJ, United States
          Rao, Meena, Horsham, PA, United States
          Kinney, William, Churchville, PA, United States
PA        Magainin Pharmaceuticals Inc., Plymouth Meeting, PA, United States (U.S.
          corporation)
PI        US 5840936                   19981124                              <--
AI        US 1995-475572               19950607 (8)
DT        Utility
FS        Granted
LN.CNT 3497
INCL   INCLM: 552/521.000
       INCLS: 558/029.000
NCL    NCLM:  552/521.000
       NCLS:  558/029.000
IC        [6]
          ICM: C07C305-12
          ICS: C07J041-00
EXF    552/521; 558/29
CAS INDEXING IS AVAILABLE FOR THIS PATENT.


L4     ANSWER 467 OF 473   USPATFULL on STN
AN        1998:147455   USPATFULL
TI        Aminosterol compounds and a method of treating infection using the
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IN       Zasloff, Michael, Merion Station, PA, United States
         Shinnar, Ann, Teaneck, NJ, United States
         Kinney, William, Churchville, PA, United States
         Rao, Meena, Horsham, PA, United States
PA       Magainin Pharmaceuticals Inc., Plymouth Meeting, PA, United States (U.S.
         corporation)
PI       US 5840740               19981124                              <--
AI       US 1995-483059           19950607 (8)
DT       Utility
FS       Granted
LN.CNT   3513
INCL     INCLM:  514/182.000
         INCLS:  552/521.000
NCL      NCLM:   514/182.000
         NCLS:   552/521.000
IC       [6]
         ICM: A01K031-575
         ICS: A07J041-00
EXF      552/521; 514/182
CAS INDEXING IS AVAILABLE FOR THIS PATENT.


L4       ANSWER 468 OF 473   USPATFULL on STN
AN       1998:138899   USPATFULL
TI       Method for protecting of heart by limiting metabolic and ionic
         abnormalities developed during ischemia, following ischemia or resulting
         from ischemia
IN       Ramasamy, Ravichandran, Davis, CA, United States
         Schaefer, Saul, Davis, CA, United States
PA       The Regents of the University of California, Oakland, CA, United States
         (U.S. corporation)
PI       US 5834466               19981110                              <--
AI       US 1995-574899           19951219 (8)
RLI      Continuation-in-part of Ser. No. US 1994-362400, filed on 22 Dec 1994,
         now abandoned
DT       Utility
FS       Granted
LN.CNT   1609
INCL     INCLM:  514/227.500
         INCLS:  514/248.000;  514/356.000
NCL      NCLM:   514/227.500
         NCLS:   514/248.000;  514/356.000
IC       [6]
         ICM: A61K031-54
         ICS: A61K031-495;  A61K031-44
EXF      514/356;  514/227.5;  514/248
CAS INDEXING IS AVAILABLE FOR THIS PATENT.


L4       ANSWER 469 OF 473   USPATFULL on STN
AN       1998:98909   USPATFULL
TI       Method of inhibiting profileration of cells by administering an
         aminosterol compound
IN       Zasloff, Michael, Merion Station, PA, United States
         Shinnar, Ann, Teaneck, NJ, United States
         Kinney, William, Churchville, PA, United States
         Anderson, Mark, Norristown, PA, United States
         Williams, Jon, Robbinsville, NJ, United States
         McLane, Michael, Lansdale, PA, United States
PA       Magainin Pharmaceuticals Inc., Plymouth Meeting, PA, United States (U.S.
         corporation)
PI       US 5795885               19980818                              <--
AI       US 1995-483057           19950607 (8)
DT       Utility
FS       Granted
LN.CNT   3513
INCL     INCLM:  514/182.000
NCL      NCLM:   514/182.000
IC       [6]
         ICM: A61K031-56
EXF      514/182
CAS INDEXING IS AVAILABLE FOR THIS PATENT.


L4       ANSWER 470 OF 473   USPATFULL on STN
AN       1998:95412   USPATFULL
TI       Method of inhibiting the sodium/proton exchanger NHE3 and method of
         inhibiting growth by administering squalamine
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PA      Magainin Pharmaceuticals, Inc., Plymouth Meeting, PA, United States
        (U.S. corporation)
PI      US 5792635              19980811                            <--
AI      US 1995-474799          19950607 (8)
DT      Utility
FS      Granted
LN.CNT  3485
INCL    INCLM:  435/184.000
        INCLS:  514/182.000;  552/521.000
NCL     NCLM:   435/184.000
        NCLS:   514/182.000;  552/521.000
IC      [6]
        ICM:  C12N009-99
        ICS:  A61K031-56
EXF     435/184;  514/182;  552/521
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4      ANSWER 471 OF 473   USPATFULL on STN
AN      1998:65213   USPATFULL
TI      Method of treating a viral infection by administering a steroid compound
IN      Zasloff, Michael, Merion Station, PA, United States
PA      Magainin Pharmaceuticals Inc., Plymouth Meeting, PA, United States (U.S.
        corporation)
PI      US 5763430              19980609                            <--
AI      US 1995-479457          19950607 (8)
DT      Utility
FS      Granted
LN.CNT  3495
INCL    INCLM:  514/169.000
        INCLS:  514/170.000;  514/171.000;  514/172.000;  514/173.000;  514/174.000;
                514/175.000;  514/176.000;  514/177.000;  514/178.000;  514/179.000;
                514/180.000;  514/181.000;  514/182.000
NCL     NCLM:   514/169.000
        NCLS:   514/170.000;  514/171.000;  514/172.000;  514/173.000;  514/174.000;
                514/175.000;  514/176.000;  514/177.000;  514/178.000;  514/179.000;
                514/180.000;  514/181.000;  514/182.000
IC      [6]
        ICM:  A61K031-56
        ICS:  A61K031-565;  A61K031-57;  A61K031-58
EXF     514/169;  514/170;  514/171;  514/172;  514/173;  514/174;  514/175;  514/176;
        514/177;  514/178;  514/179;  514/180;  514/181;  514/182
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4      ANSWER 472 OF 473   USPATFULL on STN
AN      97:109916   USPATFULL
TI      Compounds having both potent calcium antagonist and antioxidant activity
        and use thereof as cytoprotective agents
IN      Hellberg, Mark R., Arlington, TX, United States
        Barnes, George, Arlington, TX, United States
        Collier, Jr., Robert J., Arlington, TX, United States
PA      Alcon Laboratories, Inc., Fort Worth, TX, United States (U.S.
        corporation)
PI      US 5691360              19971125                            <--
AI      US 1995-471550          19950606 (8)
RLI     Division of Ser. No. US 1993-164267, filed on 8 Dec 1993, now patented,
        Pat. No. US 5424321
DT      Utility
FS      Granted
LN.CNT  765
INCL    INCLM:  514/337.000
        INCLS:  514/338.000
NCL     NCLM:   514/337.000
        NCLS:   514/338.000
IC      [6]
        ICM:  A61K031-44
EXF     514/337;  514/338
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4      ANSWER 473 OF 473   USPATFULL on STN
AN      97:59207   USPATFULL
TI      Compounds having both potent calcium antagonist and antioxidant activity
        and use thereof as cytoprotective agents
IN      Hellberg, Mark R., Arlington, TX, United States
        Barnes, George, Arlington, TX, United States
        Collier, Jr., Robert J., Arlington, TX, United States
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               corporation)
PI        US 5646149              19970708                              <--
AI        US 1995-472685          19950607 (8)
RLI       Continuation of Ser. No. US 1993-163980, filed on 8 Dec 1993, now
          abandoned
DT        Utility
FS        Granted
LN.CNT 1610
INCL      INCLM: 514/253.000
          INCLS: 514/255.000; 514/292.000; 514/317.000; 514/320.000; 514/323.000;
                 514/324.000; 514/331.000; 544/361.000; 544/372.000; 544/376.000;
                 544/377.000; 544/396.000; 546/086.000; 546/192.000; 546/197.000;
                 546/200.000; 546/202.000; 546/230.000; 546/240.000
NCL       NCLM: 514/254.110
          NCLS: 514/292.000; 514/317.000; 514/320.000; 514/323.000; 514/324.000;
                514/331.000; 544/361.000; 544/372.000; 544/376.000; 544/377.000;
                544/396.000; 546/086.000; 546/192.000; 546/197.000; 546/200.000;
                546/202.000; 546/230.000; 546/240.000
IC        [6]
          ICM: A61K031-495
          ICS: A61K031-445; C07D405-06; C07D411-06
EXF       544/376; 544/377; 514/253
CAS INDEXING IS AVAILABLE FOR THIS PATENT.


=> S SLC8A
   53 FILES SEARCHED...
L5               1 SLC8A

=> D L5

L5     ANSWER 1 OF 1   USPATFULL on STN
AN         2003:206874   USPATFULL
TI         Methods and compositions for the treatment and diagnosis of pain
           disorders using 57749
IN         Silos-Santiago, Inmaculada, Jamaica Plain, MA, UNITED STATES
PA         Millennium Pharmaceuticals, Inc. (U.S. corporation)
PI         US 2003143231       A1    20030731
AI         US 2002-281868      A1    20021028 (10)
PRAI       US 2001-335046P        20011031 (60)
DT         Utility
FS         APPLICATION
LN.CNT 2876
INCL       INCLM: 424/146.100
           INCLS: 514/001.000; 514/044.000; 435/006.000; 435/007.200
NCL        NCLM: 424/146.100
           NCLS:  514/001.000; 514/044.000; 435/006.000; 435/007.200
IC         [7]
           ICM: A61K039-395
           ICS: A61K031-00; C12Q001-68; G01N033-53; G01N033-567; A61K048-00
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
STN INTERNATIONAL LOGOFF AT 15:23:05 ON 13 JUL 2004
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